

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

Title: US-09-713-136-1
Perfect score: 22
Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A-COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B-COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A-COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS-COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	92.7	22	4 US-09-092-314-2	Sequence 2, Appli
2	18.8	85.5	22	4 US-09-092-314-1	Sequence 1, Appli
3	18.8	85.5	22	4 US-09-092-314-3	Sequence 3, Appli
4	18.8	85.5	22	4 US-09-092-314-10	Sequence 10, Appli
5	17.2	78.2	22	4 US-09-092-314-4	Sequence 4, Appli
6	15.6	70.9	22	4 US-09-092-314-5	Sequence 5, Appli
7	15.6	70.9	22	4 US-09-092-314-7	Sequence 7, Appli
8	15.6	70.9	22	4 US-09-092-314-8	Sequence 8, Appli
9	15.6	70.9	1418	1 US-08-391-615-7	Sequence 7, Appli
10	15.6	70.9	1830	4 US-09-019-931-2	Sequence 2, Appli
11	15.6	70.9	2505	1 US-08-391-615-1	Sequence 1, Appli
12	15.6	70.9	6909	2 US-08-804-196-1	Sequence 1, Appli
13	15.6	70.9	6909	3 US-08-658-340-1	Sequence 1, Appli
14	15.6	70.9	6909	2 US-08-746-111-26	Sequence 26, Appli
15	15.2	69.1	1892	2 US-08-933-750C-66	Sequence 66, Appli
16	15.2	69.1	1892	3 US-09-234-613-66	Sequence 66, Appli
17	15.2	69.1	6638	2 US-08-070-301-2	Sequence 2, Appli
18	14.8	67.3	882	1 US-08-622-354-4	Sequence 4, Appli
19	14.6	66.4	404	4 US-09-060-756-303	Sequence 303, App
20	14.6	66.4	913	2 US-08-975-316-61	Sequence 61, Appli
21	14.6	66.4	1532	3 US-09-118-324-1	Sequence 1, Appli
22	14.6	66.4	1614	4 US-09-046-894-29	Sequence 29, Appli
23	14.6	66.4	2694	3 US-08-975-703-5	Sequence 5, Appli
24	14.6	66.4	2694	4 US-09-515-884-5	Sequence 5, Appli
25	14.6	66.4	5408	1 US-08-471-058-20	Sequence 20, Appli
26	14.6	66.4	5408	1 US-08-471-057-20	Sequence 20, Appli
27	14.2	64.5	864	4 US-08-998-416-297	Sequence 297, App

28	14.2	64.5	1166	1 US-08-121-063-7	Sequence 7, Appli
29	14.2	64.5	176373	3 US-09-128-153-17	Sequence 17, Appli
30	14	63.6	77	1 US-08-399-412A-58	Sequence 58, Appli
31	14	63.6	95	5 PCT-US96-09455A-258	Sequence 258, App
32	14	63.6	657	2 US-08-479-733A-22	Sequence 22, Appli
33	14	63.6	657	3 US-08-487-427-22	Sequence 22, Appli
34	14	63.6	657	3 US-08-479-727A-22	Sequence 22, Appli
35	14	63.6	657	3 US-08-482-369A-22	Sequence 22, Appli
36	14	63.6	657	3 US-09-009-217-10	Sequence 10, Appli
37	14	63.6	657	3 US-09-009-656-10	Sequence 10, Appli
38	14	63.6	657	5 PCT-US95-07439-22	Sequence 22, Appli
39	14	63.6	672	1 US-07-816-679A-2	Sequence 2, Appli
40	14	63.6	672	5 PCT-US92-11270-2	Sequence 2, Appli
41	14	63.6	795	1 US-07-882-202A-1	Sequence 1, Appli
42	14	63.6	795	1 US-07-683-682B-3	Sequence 3, Appli
43	14	63.6	795	1 US-08-021-615A-1	Sequence 1, Appli
44	14	63.6	795	1 US-08-321-777-1	Sequence 1, Appli
45	14	63.6	795	1 US-08-463-931-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match 92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.044; 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22
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RESULT 2
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
||||| ||| |||||
Db 1 tgactgtgaagcttagatga 22

RESULT 3
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
||||| ||| |||||
Db 1 tgactgtgaaccttagatga 22

RESULT 4
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10

; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
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Db 1 tgactgtgaatgttagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match 78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.9;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
||||| ||| |||||
Db 1 tgactgtgaagcttagatga 22

RESULT 6
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-09-092-314-5

;
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-5

Query Match 70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
||||||| | |||||
DB 1 tgactgtgttccttagagatga 22
||||||| | |||||

RESULT 7

US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-7

Query Match 70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
||||||| | |||||
DB 1 tgactgtgagggtcagagatga 22
||||||| | |||||

RESULT 8

US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-8

Query Match 70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
||||||| | |||||
DB 1 tgactgtgagggtcagagatga 22
||||||| | |||||

RESULT 9

US-08-391-615-7
; Sequence 7, Application US/08391615
; Patent No. 5550054
; GENERAL INFORMATION:
; APPLICANT: Witte, Owen
; APPLICANT: Tsukada, Satoshi
; APPLICANT: Saffran, David
; APPLICANT: Rawlings, David
; TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,615
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,449
; FILING DATE: 21-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-391-615-7

Query Match 70.9%; Score 15.6; DB 1; Length 1418;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
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DB 218 TGACTTTGACGTCGGAGAGA 239
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RESULT 10

US-09-019-931-2
; Sequence 2, Application US/09019931
; Patent No. 6194148

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; GENERAL INFORMATION:
; APPLICANT: Hori, Kunio, Takahashi, Takeo, Okada, Takao
; TITLE OF INVENTION: A Method For Detecting A Hybridized
; TITLE OF INVENTION: Nucleic Acid Molecule
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frischauf, Holtz, Goodman, Langer & Chick
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3+ Inch, 1.44 mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,931
; FILING DATE: 06-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-025291
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Barth, Richard
; REGISTRATION NUMBER: 28,180
; REFERENCE/DOCKET NUMBER: 980048/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 319-4900
; TELEFAX: (212) 319-5101
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; IMMEDIATE SOURCE:
; LIBRARY: pGEX-PH
;
US-09-019-931-2

Query Match 70.9%; Score 15.6; DB 4; Length 1830;
Best Local Similarity 81.8%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
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Db 881 TGACTTTGAACGTGGGAGA 902

RESULT 11
US-08-391-615-1
; Sequence 1, Application US/08391615
; Patent No. 5550054
; GENERAL INFORMATION:
; APPLICANT: Witte, Owen
; APPLICANT: Tsukada, Satoshi
; APPLICANT: Saffran, Douglas
; APPLICANT: Rawlings, David
; TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,615
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/006,449
; FILING DATE: 21-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Berttram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 137..2116
;
US-08-391-615-1

Query Match 70.9%; Score 15.6; DB 1; Length 2505;
Best Local Similarity 81.8%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
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Db 262 TGACTTTGAACGTGGGAGA 283

RESULT 12
US-08-804-196-1/c
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:

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Qy 1 tgactgtgaacgttcgcgatga 22
||||| | | | |

RESULT 15
US-08-933-750C-66/c
; Sequence 66, Application US/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

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; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933.750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-08-933-750C-66

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Query Match          69.1%; Score 15.2; DB 2; Length 1892;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 tgactgtgaacgttcgagat 20
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Db 1278 TGAATGTGAAGGTTCCGAGCT 1259

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Search completed: October 9, 2001, 15:41:58
Job time: 288 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-1
Perfect score: 22
Sequence: 1 tgactgtgaagttcagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDSB/gcgdata/geneseq/geneseq/NA1980.DAT.*
- 2: /SIDSB/gcgdata/geneseq/geneseq/NA1981.DAT.*
- 3: /SIDSB/gcgdata/geneseq/geneseq/NA1982.DAT.*
- 4: /SIDSB/gcgdata/geneseq/geneseq/NA1983.DAT.*
- 5: /SIDSB/gcgdata/geneseq/geneseq/NA1984.DAT.*
- 6: /SIDSB/gcgdata/geneseq/geneseq/NA1985.DAT.*
- 7: /SIDSB/gcgdata/geneseq/geneseq/NA1986.DAT.*
- 8: /SIDSB/gcgdata/geneseq/geneseq/NA1987.DAT.*
- 9: /SIDSB/gcgdata/geneseq/geneseq/NA1988.DAT.*
- 10: /SIDSB/gcgdata/geneseq/geneseq/NA1989.DAT.*
- 11: /SIDSB/gcgdata/geneseq/geneseq/NA1990.DAT.*
- 12: /SIDSB/gcgdata/geneseq/geneseq/NA1991.DAT.*
- 13: /SIDSB/gcgdata/geneseq/geneseq/NA1992.DAT.*
- 14: /SIDSB/gcgdata/geneseq/geneseq/NA1993.DAT.*
- 15: /SIDSB/gcgdata/geneseq/geneseq/NA1994.DAT.*
- 16: /SIDSB/gcgdata/geneseq/geneseq/NA1995.DAT.*
- 17: /SIDSB/gcgdata/geneseq/geneseq/NA1996.DAT.*
- 18: /SIDSB/gcgdata/geneseq/geneseq/NA1997.DAT.*
- 19: /SIDSB/gcgdata/geneseq/geneseq/NA1998.DAT.*
- 20: /SIDSB/gcgdata/geneseq/geneseq/NA1999.DAT.*
- 21: /SIDSB/gcgdata/geneseq/geneseq/NA2000.DAT.*
- 22: /SIDSB/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	19	AAV32079
2	22	100.0	22	20	AAV36624
3	22	100.0	22	20	AAV80097
4	22	100.0	22	20	AAV80102
5	22	100.0	22	20	AAV80103
6	22	100.0	22	21	AAV80101
7	22	100.0	22	21	AAV80104
8	22	100.0	22	21	AAV80106
9	22	100.0	22	21	AAV80105
10	22	100.0	22	21	AAV80107
11	22	100.0	22	21	AAV80108

12	22	100.0	22	21	AAV38072	Immunostimulatory
13	22	100.0	22	21	AAV55876	Immunomodulatory o
14	22	100.0	22	22	AAV77040	Cholera toxin immu
15	22	100.0	22	22	AAV29800	Oligonucleotide OD
16	22	100.0	22	22	AAV82107	CG motif and CFA c
17	22	100.0	22	22	AAV92377	Immunostimulatory
18	21.2	96.4	22	22	AAV77046	Immunomodulatory o
19	21	95.5	22	21	AAV55880	Oligo used in expe
20	20.4	92.7	22	20	AAV80105	Immunomodulatory o
21	20.4	92.7	22	20	AAV80096	Immunomodulatory o
22	20.4	92.7	22	20	AAV80099	Immunomodulatory o
23	20.4	92.7	22	20	AAV80101	Immunomodulatory o
24	20.4	92.7	22	21	AAV86254	Sequence of a stab
25	20.4	92.7	22	21	AAV38066	Immunostimulatory
26	20.4	92.7	22	21	AAV38068	Immunostimulatory
27	20.4	92.7	22	21	AAV38070	Immunostimulatory
28	20.4	92.7	22	22	AAV77041	Immunostimulatory
29	20.4	92.7	22	22	AAV77043	Immunostimulatory
30	20.4	92.7	22	22	AAV77047	Immunostimulatory
31	20	90.9	22	21	AAV55881	Immunomodulatory o
32	19.6	89.1	22	22	AAV77045	Immunostimulatory
33	19.4	88.2	22	21	AAV55877	Immunomodulatory o
34	18.8	85.5	22	19	AAV32080	Nucleotide sequenc
35	18.8	85.5	22	20	AAV36625	ISS-ODN mutant Dv1
36	18.8	85.5	22	20	AAV55790	Immunostimulatory
37	18.8	85.5	22	20	AAV55797	Immunostimulatory
38	18.8	85.5	22	20	AAV55788	Immunostimulatory
39	18.8	85.5	22	20	AAV80106	Oligo used in expe
40	18.8	85.5	22	20	AAV80104	Oligo used in expe
41	18.8	85.5	22	21	AAV64052	Non-CpG control ph
42	18.8	85.5	22	21	AAV86252	Sequence of a stab
43	18.8	85.5	22	21	AAV96260	Sequence of a stab
44	18.8	85.5	22	21	AAV90459	CpG adjuvant oligo
45	18.8	85.5	22	22	AAV92378	CG motif and CFA c

ALIGNMENTS

RESULT 1

AAV32079

ID AAV32079 standard; DNA; 22 BP.

AC AAV32079;

DT 09-SEP-1998 (first entry)

DE Nucleotide sequence of DY1018.

KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;

KW Immunisation; anaphylaxis; IgE; retinopathies; ss.

OS synthetic.

FT Key Location/Qualifiers

FT modified_base 1..22

FT /*tag= a

FT /note= "phosphothioate backbone"

PN WO9816247-A1.

PD 23-APR-1998.

PF 09-OCT-1997; 97WO-US19004.

PR 11-OCT-1996; 96US-0028118.

PA (REGC) UNIV CALIFORNIA.

PI Carson DA, Raz E, Roman M;

DR WPI; 1998-261028/23.

XX

PT New immunomodulatory compositions - comprising an antigen conjugated
 PT to a polynucleotide that contains an immunostimulatory sequence
 XX
 PS Example 1; Page 36; 69pp; English.
 XX
 CC This is the nucleotide sequence of DY1018, which is conjugated to
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
 CC (IMM), which comprises an antigen conjugated to a polynucleotide
 CC (PN), that contains at least one immunostimulatory nucleotide
 CC (ISS). The conjugate synergistically boost the magnitude of the host
 CC immune response against an antigen to a level greater than the host
 CC immune response to either the IMM, antigen or ISS-PN alone. These
 CC responses to ISS-PN/IMM conjugates are particularly acute during
 CC the important early phase of the host immune response to an antigen.
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular
 CC (Th1 type) immune responses of the host. Thus, use of the method to
 CC boost the immune responsiveness of a host to subsequent challenge by a
 CC sensitising antigen without immunisation avoids the risk of
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IGE
 CC production in response to the antigen challenge. The conjugates can
 CC also be used to combat pathogenic infection and to stimulate
 CC therapeutic angiogenesis to treat conditions in which localised blood
 CC flow plays a significant etiological role, e.g. retinopathies.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 2
 AAX36624
 ID AAX36624 standard; DNA; 22 BP.
 AC AAX36624;
 XX
 DT 09-JUL-1999 (first entry)
 DE ISS-ODN DY1018 nucleotide sequence.
 XX
 KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.
 XX
 OS Synthetic.
 XX
 XX WO9911275-A2.
 XX
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18382.
 XX
 PR 05-SEP-1997; 97US-0927120.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Ray E;
 XX
 XX WPI; 1999-312404/26.
 DR
 XX Reducing antigen-stimulated granulocyte-mediated inflammation
 XX
 PS Example 2; Page 30; 69pp; English.
 XX

CC This is the ISS-ODN DY1018 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen.
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
 AAV80097
 ID AAV80097 standard; DNA; 22 BP.
 XX
 AC AAV80097;
 XX
 DT 12-MAR-1999 (first entry)
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX
 OS Synthetic.
 XX
 XX WO9855495-A2.
 PN
 XX 10-DEC-1998.
 PD
 XX 05-JUN-1998; 98WO-US11578.
 PF
 XX 06-JUN-1997; 97US-0048793.
 PR
 XX (DYNA-) DYNAX TECHNOLOGIES CORP.
 PA
 XX Dina D, Roman M, Schwartz D;
 PI
 XX WPI; 1999-059898/05.
 DR
 XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 5; Page 29; 63pp; English.
 XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC CACGTTCC, and CACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 CC
 CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
 AAV80102
 ID AAV80102 standard; DNA; 22 BP.
 AC AAV80102;
 XX
 XX 12-MAR-1999 (first entry)
 DT
 DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX Synthetic.

XX Key Location/Qualifiers
 FH modified_base 11
 FT /*tag= a
 FT /note= "5-bromocytosine"

XX WO9855495-A2.
 XX 10-DEC-1998.
 XX 05-JUN-1998; 98WO-US11578.
 XX 06-JUN-1997; 97US-0048793.
 XX (DYNA-) DYNVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 PI WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 CC
 CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
 AAV80103
 ID AAV80103 standard; DNA; 22 BP.
 XX
 XX AAV80103;
 XX
 XX 12-MAR-1999 (first entry)
 DT
 DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX Synthetic.

XX Key Location/Qualifiers
 FH modified_base 11
 FT /*tag= a
 FT /note= "5-bromocytosine"

XX WO9855495-A2.
 XX 10-DEC-1998.
 XX 05-JUN-1998; 98WO-US11578.
 XX 06-JUN-1997; 97US-0048793.
 XX (DYNA-) DYNVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 PI WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6

AAC64051

ID AAC64051 standard; DNA; 22 BP.

AC

XX AAC64051;

DT

XX 15-FEB-2001 (first entry)

XX

DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX

KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;

KW enhanced antigen presentation; antigen-presenting cell; APC;

KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;

KW vaccine; ss.

XX

OS Synthetic.

XX

PN WO200062787-A1.

XX

XX 26-OCT-2000.

PD

XX 11-APR-2000; 2000WO-US09664.

PF

XX 15-APR-1999; 99US-0292278.

PR

XX (REGC) UNIV CALIFORNIA.

XX

PI Raz E, Martin-Orozco E;

XX

DR WPI; 2000-679548/66.

XX

PT Enhancing antigen-presentation capabilities of T-cells for cancer

PT immunotherapy, by contacting cells with an immunostimulatory

PT oligonucleotide

XX

PS Example 1; Page 18; 42pp; English.

XX

CC The invention relates to a method of inducing activation of T-cells
CC to respond to an antigen, comprising contacting antigen-presenting cells
CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC thus treated have enhanced antigen presenting capabilities compared to
CC antigen-activated APCs. APCs with enhanced antigen-presentation
CC capabilities then present the antigen to T-cells. The method is useful
CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC antigen presenting capacity of tumour cells, thereby inducing T-cell
CC activation, and is therefore useful for treating tumours. Additionally,
CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
CC ISS-ODN treated APCs are induced to take up antigen through upregulation
CC of Fe-receptor expression, to present antigen through upregulation of
CC major histocompatibility complex (MHC) Class I and II expression and
CC CD8 expression, to produce co-stimulatory factors (B7 and CD40), to
CC provide cell-to-cell adhesion through upregulation of intercellular
CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
CC cytokine production, all at levels greater than that achieved through
CC contact of APC with antigen alone. The present sequence represents
CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC invention.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7

AAA96253

ID AAA96253 standard; DNA; 22 BP.

XX

AC AAA96253;

XX

DT 08-FEB-2001 (first entry)

XX

DE Sequence of a stabilised oligonucleotide with antitumour activity.

XX

KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;

KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.

XX

OS Synthetic.

XX

PN WO200056342-A2.

XX

PD 28-SEP-2000.

XX

PF 17-MAR-2000; 2000WO-FR00676.

XX

PR 19-MAR-1999; 99FR-0003433.

XX

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

XX

PI (INRM) INST NAT SANTE & RECH MEDICALE.

XX

PI Carpentier A;

XX

DR WPI; 2000-602192/57.

XX

PT Use of stabilized oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic

XX

PS Example 2; Page 16; 57pp; French.

XX

CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

RESULT 8

AAA90458

ID AAA90458 standard; DNA; 22 BP.

XX

AC AAA90458;

Query Match 100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

XX 10-JAN-2001 (first entry)
 XX CpG adjuvant oligonucleotide, SEQ ID NO:19.
 XX
 XX CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;
 KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.
 XX
 XX Synthetic.
 OS
 XX WO200050006-A2.
 PN
 XX 31-AUG-2000.
 XX
 XX 09-FEB-2000; 2000WO-US03331.
 PF
 XX 26-FEB-1999; 99US-0121858.
 PR
 XX 29-JUL-1999; 99US-0146391.
 PR
 XX 28-OCT-1999; 99US-0161997.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Ugozzoli M, Singh M;
 PI Barackman J;
 PI WPI; 2000-587123/55.
 DR
 XX Microemulsion having an adsorbent surface comprising a microdroplet
 PT emulsion consisting of a metabolizable oil and an emulsifying agent
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,
 PT and parasitic infection
 XX
 XX Claim 17; Page 40; 95pp; English.
 XX
 XX The invention relates to a microdroplet emulsion (microemulsion) with an
 CC adsorbent surface, and which comprises a metabolizable oil and an
 CC emulsifying agent (a detergent). It also relates to a composition
 CC comprising the microemulsion and a microparticle with an adsorbent
 CC surface, where the microparticle comprises a polymer selected from a
 CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a
 CC polycaprolactone, a polyorthoester, a polyvanhydride, and a
 CC polycyanoacrylate, and a second detergent. The surface of the
 CC microparticles efficiently adsorb biologically active macromolecules such
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,
 CC mediators of transcription or translation, metabolic intermediates and
 CC adjuvants. Additionally, a second biologically active molecule may be
 CC encapsulated within the microparticle. The microemulsion can be used in
 CC methods of immunising a host animal, particularly a human, against a
 CC viral, bacterial or parasitic infection, and in methods of increasing a
 CC Th1 immune response. The microemulsions (having the appropriate antigens
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif
 CC which are claimed for use as adjuvants in the compositions of the
 CC invention.
 XX
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22
 RESULT 9
 AAA14467
 ID AAA14467 standard; DNA; 22 BP.
 XX
 XX AAA14467;
 AC
 XX 21-AUG-2000 (first entry)
 DT
 XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.
 DE
 XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
 KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.
 KW
 XX Synthetic.
 OS
 XX WO200020039-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 15-SEP-1999; 99WO-US21203.
 PF
 XX 05-OCT-1998; 98US-0167039.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Raz E, Horner AA, Carson DA;
 PI
 XX WPI; 2000-303647/26.
 DR
 XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
 PT an antigen in a mammalian host through production of secretory
 PT immunoglobulin A
 PT
 XX Claim 8; Page 21; 64pp; English.
 XX
 XX The invention relates to a method of inducing mucosal immunity to an
 CC antigen in a mammalian host, including the production of secretory
 CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal
 CC site of entry of most foreign antigens) is mediated by mucosa-associated
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
 CC cell sub-populations. The primary immune response which characterises
 CC the induction of mucosal immunity to an antigen is sIgA production by
 CC activated B-cells. The method comprises introducing an immunostimulatory
 CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
 CC ISS-ODN includes a core nucleotide sequence. The core nucleotide
 CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A
 CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The
 CC level of sIgA production induced in the host is at least 3 times the
 CC magnitude of sIgA production achievable in response to introduction of
 CC antigen alone into the mucosal tissue and is equivalent or greater than
 CC the magnitude of sIgA production achievable in response to introduction
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The
 CC host immune response is stimulated to antigen specific IgA production,
 CC biased towards the Th1 phenotype while antigen-induced IgE production is
 CC avoided. The adjuvant has little or no known toxicity in mammals and its
 CC efficacy is comparable to that of cholera toxin which is used as a
 CC mucosal adjuvant. The present sequence represents the immunostimulatory
 CC oligonucleotide DY1018.
 XX
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22

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Db      1 tgactgtgaacgttcgagatga 22
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RESULT 10
AAA38065
ID      AAA38065 standard; DNA; 22 BP.
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XX      AAA38065;
XX
XX      24-AUG-2000 (first entry)
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XX      Immunostimulatory sequence (ISS) #1.
XX
XX      Immunostimulatory sequence; ISS: immunomodulator; glycoprotein 120;
KW      gp120; human immunodeficiency virus; HIV; immune response; infection;
KW      development; ss.
XX
XX      Synthetic.
XX
XX      WO200021556-A1.
XX
XX      20-APR-2000.
XX
XX      08-OCT-1999; 99WO-US23677.
XX
XX      09-OCT-1998; 98US-0103733.
XX      07-OCT-1999; 99US-0415186.
XX
XX      (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX      Tighe H, Raz E, Schwartz D, Takabayashi K;
XX      WPI: 2000-317846/27.
XX
XX      Anti-HIV composition comprises immunostimulatory polynucleotides and
PT      HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT      response against HIV in an HIV infected individual.
XX
XX      Claim 3; Page 16; 65pp; English.
XX
XX      The present invention relates to an immunostimulatory composition
CC      comprising a human immunodeficiency virus (HIV) antigen, and an
CC      immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC      (ISS). This sequence represents an ISS that can be used in the
CC      composition. An immunostimulatory composition which comprises a gp120
CC      conjugated to an immunomodulatory polynucleotide, or is proximately
CC      associated to it and not conjugated, is used for modulating or
CC      stimulating a specific immune response against gp120 in an individual by
CC      producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC      is also used for suppressing or delaying development of HIV infection in
CC      an individual infected with HIV or an individual at risk of infection
CC      with HIV, respectively. It is also used for treating an individual
CC      infected with HIV in need of immune modulation.
XX
XX      Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ
Query Match      100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db      1 tgactgtgaacgttcgagatga 22
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RESULT 11
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ID      AAA38071 standard; DNA; 22 BP.
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XX      AAA38071;
XX
XX

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DT      24-AUG-2000 (first entry)
XX
XX      Immunostimulatory sequence (ISS) #7.
XX
XX      Immunostimulatory sequence; ISS: immunomodulator; glycoprotein 120;
KW      gp120; human immunodeficiency virus; HIV; immune response; infection;
KW      development; ss.
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XX      Synthetic.
XX
XX      Key      Location/Qualifiers
FT      modified_base 11
FT      FT      /*tag= a
FT      FT      /mod_base= OTHER
XX      FT      /note= "5-Bromocytosine"
XX
XX      WO200021556-A1.
XX
XX      20-APR-2000.
XX
XX      08-OCT-1999; 99WO-US23677.
XX
XX      09-OCT-1998; 98US-0103733.
XX      07-OCT-1999; 99US-0415186.
XX
XX      (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX      Tighe H, Raz E, Schwartz D, Takabayashi K;
XX      WPI: 2000-317846/27.
XX
XX      Anti-HIV composition comprises immunostimulatory polynucleotides and
PT      HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT      response against HIV in an HIV infected individual.
XX
XX      Disclosure; Page 17; 65pp; English.
XX
XX      The present invention relates to an immunostimulatory composition
CC      comprising a human immunodeficiency virus (HIV) antigen, and an
CC      immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC      (ISS). This sequence represents an ISS that can be used in the
CC      composition. An immunostimulatory composition which comprises a gp120
CC      conjugated to an immunomodulatory polynucleotide, or is proximately
CC      associated to it and not conjugated, is used for modulating or
CC      stimulating a specific immune response against gp120 in an individual by
CC      producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC      is also used for suppressing or delaying development of HIV infection in
CC      an individual infected with HIV or an individual at risk of infection
CC      with HIV, respectively. It is also used for treating an individual
CC      infected with HIV in need of immune modulation.
XX
XX      Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ
Query Match      100.0%; Score 22; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 tgactgtgaacgttcgagatga 22
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Db      1 tgactgtgaacgttcgagatga 22
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RESULT 12
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ID      AAA38072 standard; DNA; 22 BP.
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XX      AAA38072;
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XX      24-AUG-2000 (first entry)
XX
XX      Immunostimulatory sequence (ISS) #7.
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Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120; gp120; human immunodeficiency virus; HIV; immune response; infection; development; ss.

Synthetic.

Key modified_base 11 Location/Qualifiers
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 /note= "5-Bromocytosine"

modified_base 15
 /tag= b
 /mod_base= OTHER
 /note= "5-Bromocytosine"

WO200021556-A1.

20-APR-2000.

08-OCT-1999; 99WO-US23677.

09-OCT-1998; 98US-0103733.

07-OCT-1999; 99US-0415186.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Tighe H, Raz E, Schwartz D, Takabayashi K;
 WPI; 2000-317846/27.

Anti-HIV composition comprises immunostimulatory polynucleotides and HIV glycoprotein gp120 useful for modulating, stimulating an immune response against HIV in an HIV infected individual.

Disclosure; Page 17; 65pp; English.

The present invention relates to an immunostimulatory composition comprising a human immunodeficiency virus (HIV) antigen, and an immunostimulatory polynucleotide comprising an immunostimulatory sequence (ISS). This sequence represents an ISS that can be used in the composition. An immunostimulatory composition which comprises a gp120 conjugated to an immunostimulatory polynucleotide, or is proximately associated to it and not conjugated, is used for modulating or stimulating a specific immune response against gp120 in an individual by producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It is also used for suppressing or delaying development of HIV infection in an individual infected with HIV or an individual at risk of infection with HIV, respectively. It is also used for treating an individual infected with HIV in need of immune modulation.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
 |||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
 AAZ55876
 ID AAZ55876 standard; DNA; 22 BP.
 XX AAZ55876;
 AC
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Immunomodulatory oligonucleotide SEQ ID NO: 1.
 XX

Immunomodulation; immunostimulatory sequence; adjuvant; Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy; asthma; immunosuppression; ss.

Mus musculus.
 Synthetic.

Key modified_base 11 Location/Qualifiers
 /tag= a
 /note= "Phosphorothioate linkages"

misc_feature 9..16
 /tag= b
 /note= "Immunostimulatory sequence (ISS)"

WO9962923-A2.

09-DEC-1999.

04-JUN-1999; 99WO-US12538.

05-JUN-1998; 98US-0088310.

01-JUN-1999; 99US-0324191.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Schwartz D;
 WPI; 2000-105687/09.

Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens.

Example 1; Page 35; 54pp; English.

Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory oligonucleotides comprising an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTC, AGCGTC, AGCGTC, AGCGTC, GACGTC, GACGTC, GCGGTT, AACGTC and GACGTC). The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886 contain ISSs comprising at least one bromocytosine, whereas sequence AAZ55876 contains an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect; when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells), while simultaneously downregulating the Th2-type response. The Th1 response is particularly effective for control of viruses and intracellular parasites. The immunomodulatory oligonucleotides are used, particularly when formulated with an antigen or a facilitator, for modulating immune responses. Such compositions may be used in tumour therapy, in treatment of allergy (including asthma), for inducing a vigorous cellular response (against a virus, bacterium, fungus or protozoan), and also in contraceptive vaccines based on sperm antigens.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
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Db 1 tgactgtgaacgttcgagatga 22

RESULT 14
 AAF77040
 ID AAF77040 standard; DNA; 22 BP.
 XX
 AC AAF77040;

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XX 15-MAY-2001 (first entry)
DT Immunomodulatory DNA.
DE Modulate; immune; antigen; immunostimulatory; ds.
KW Synthetic.
XX WO200112223-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000WO-US22835.
XX 19-AUG-1999; 99US-0149768.
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX Van Nest G;
XX WPI; 2001-211136/21.
XX Modulating immune response to a second antigen in humans involves
PT administering an immunostimulatory polynucleotide comprising an
PT immunostimulatory sequence and a first antigen.
XX Claim 31; Page 15; 63pp; English.
XX The present invention relates to modulating an immune response to
CC a second antigen in an individual, involving
CC administering to the individual an immunomodulatory polynucleotide
CC comprising an immunostimulatory sequence (ISS) and a first antigen.
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
AAF29800
ID AAF29800 standard; DNA; 22 BP.
XX
AC AAF29800;
XX
DT 12-APR-2001 (first entry)
XX
DE Cholera toxin immunostimulatory nucleotide sequence.
XX
KW Immunostimulatory nucleotide sequence; immune response; cancer;
KW antibody production; IFNgamma release; CTL activity; Th1 response;
KW infection; allergy; ds.
XX
OS Unidentified.
XX
PN WO200102007-A1.
XX
XX 11-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18229.
XX
XX 02-JUL-1999; 99US-0347343.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Raz E, Kobayashi H;

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XX WPI; 2001-138066/14.
XX Enhancing immune response against pathogen or antigen associated with
PT infectious diseases, an allergen or cancer, involves administering
PT immunostimulatory nucleotide sequence prior to antigen exposure -
XX
XX Example 1; Page 14; 47pp; English.
XX The present invention describes a method for enhancing an immune response
CC to a substance, comprising administering an immunostimulatory nucleotide
CC sequence to a subject prior to exposure to the substance. This can be
CC used to enhance antibody production, IFNgamma release, CTL activity and
CC Th1 related effects. The method can be used in the prevention and
CC treatment of allergies, cancer and infections.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

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Job time: 2977 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 2150.93 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	9 AX036945	AX036945 Sequence
2	22	100.0	22	9 AX046993	AX046993 Sequence
3	22	100.0	22	10 AX083675	AX083675 Sequence
4	21	95.5	22	10 AX083681	AX083681 Sequence
5	20.4	92.7	22	9 AX036946	AX036946 Sequence
6	20.4	92.7	22	10 AX083676	AX083676 Sequence
7	20.4	92.7	22	10 AX083678	AX083678 Sequence
8	20	90.9	22	10 AX083682	AX083682 Sequence

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9 19.4 88.2 22 10 AX083680 Sequence
10 18.8 85.5 22 9 AX036944 Sequence
11 18.8 85.5 22 9 AX036952 Sequence
12 17.8 80.9 145939 79 AL158143 Homo sapi
13 17.8 80.9 165337 70 AC027442 Homo sapi
14 17.8 80.9 167237 86 AC007938 Homo sapi
15 17.8 80.9 201214 75 AC074012 Homo sapi
16 17.8 80.9 209777 69 AC024934 Homo sapi
17 17.2 78.2 127 5 AGXH8
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19 17.2 78.2 12545 6 CEP42G10
20 17.2 78.2 85219 88 AC073520 Homo sapi
21 17.2 78.2 128216 93 HSDJ319M7
22 17.2 78.2 149912 76 AC079336 Homo sapi
23 17.2 78.2 169277 75 AC078940 Homo sapi
24 17.2 78.2 171777 81 AL451162 Homo sapi
25 17.2 78.2 183827 86 AC005899 Homo sapi
26 17.2 78.2 185784 61 AC009719 Homo sapi
27 16.8 76.4 72383 71 AC027746 Homo sapi
28 16.8 76.4 102798 78 AL138730 Homo sapi
29 16.8 76.4 135714 90 AL160037 Human DNA
30 16.8 76.4 136410 67 AC023308 Homo sapi
31 16.8 76.4 139399 13 AP002865 Oryza sat
32 16.8 76.4 150379 13 AP003074 Oryza sat
33 16.8 76.4 151992 61 AC009939 Homo sapi
34 16.8 76.4 157180 14 NCBI18D24
35 16.8 76.4 172091 60 AC007962 Homo sapi
36 16.8 76.4 178255 87 AC019197 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE synthetic construct.
ORGANISM Carpentier,A.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)
PATENT: FR 2790955-A 2 22-SEP-2000;
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Db 1 TGACTGTGAACGTTCCGAGATGA 22

RESULT 4
AX083681
LOCUS AX083681 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 7 from Patent WO0112223.

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RESULT 2
AX046993
LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss,R.B.
JOURNAL Hiv immunogenic compositions and methods
TITLE Patent: WO 0067787-A 2 16-NOV-2000;
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Db 1 TGACTGTGAACGTTCCGAGATGA 22

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LOCUS AX083675 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
TITLE equences and compositions for use therein
PATENT: WO 0112223-A 1 22-FEB-2001;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGACTGTGAACGTTCCGAGATGA 22

RESULT 4
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DEFINITION Sequence 7 from Patent WO0112223.

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ACCESSION AX083681 GI:13185413
VERSION AX083681.1
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;
Dynamax Technologies Corporation (US)
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QY 1 tgactgtgaacgttcgagatga 22
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Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 5
AX036946 LOCUS 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036946
VERSION AX036946.1 GI:11226374
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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QY 1 tgactgtgaacgttcgagatga 22
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Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 6
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DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
Dynamax Technologies Corporation (US)
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            /db_xref="taxon:32630"
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            /mod_base=OTHER
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BASE COUNT 6 a 7 g 6 t 1 others
ORIGIN

    Query Match 92.7%; Score 20.4; DB 10; Length 22;
    Best Local Similarity 95.5%; Pred. No. 1.5;
    Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 7
AX083678 LOCUS 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083678
VERSION AX083678.1 GI:13185410
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
    source
        1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic construct"
            /mod_base=OTHER
        6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN

    Query Match 92.7%; Score 20.4; DB 10; Length 22;
    Best Local Similarity 95.5%; Pred. No. 1.5;
    Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 8
AX083682 LOCUS 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 8 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
    source
        1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic construct"
            /mod_base=OTHER
        6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN
```



```

Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj107418
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
Dye-terminator Big Dye; 9% of reads
Consensus quality: 137464 bases at least Q40
Consensus quality: 141229 bases at least Q30
Consensus quality: 143037 bases at least Q20
Insert size: 144339; sum-of-contigs
Quality size: 111741; 30.4% error; agarose-fp
Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.27x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 3024: contig of 3024 bp in length
* 3025 3124: gap of 100 bp
* 3125 10834: contig of 7710 bp in length
* 10835 10934: gap of 100 bp
* 10935 13593: contig of 2661 bp in length
* 13596 13693: gap of 100 bp
* 13696 16092: contig of 2397 bp in length
* 16093 16192: gap of 100 bp
* 16193 22530: contig of 6338 bp in length
* 22531 22630: gap of 100 bp
* 22631 27253: contig of 4623 bp in length
* 27254 27353: gap of 100 bp
* 27354 30261: contig of 2908 bp in length
* 30262 30361: gap of 100 bp
* 30362 33611: contig of 3250 bp in length
* 33612 33711: gap of 100 bp
* 33712 38262: contig of 4551 bp in length
* 38263 38362: gap of 100 bp
* 38363 40615: contig of 2253 bp in length
* 40616 40715: gap of 100 bp
* 40716 44299: contig of 3584 bp in length
* 44300 44399: gap of 100 bp
* 44400 47229: contig of 2830 bp in length
* 47230 47329: gap of 100 bp
* 47330 52776: contig of 5447 bp in length
* 52777 52876: gap of 100 bp
* 52877 60226: contig of 7350 bp in length
* 60227 60326: gap of 100 bp
* 60327 62930: contig of 2604 bp in length
* 62931 63030: gap of 100 bp
* 63031 67419: contig of 4389 bp in length
* 67420 67519: gap of 100 bp
* 67520 145939: contig of 78420 bp in length.
*
* Location/Qualifiers
* 1..145939
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="X"
* /clone="RP5-107418"
* /clone_lib="RC1-5"
* /clone="1"
* 1..3024
* /note="assembly_fragment:00567"
* vector_side:left
* clone_end:SP6
* 3125..10834
* /note="assembly_fragment:00921"
* fragment_chain:1

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misc_feature 10935..13595
              /note="assembly_fragment:01789"
              fragment_chain:1
misc_feature 13696..16092
              /note="assembly_fragment:01424"
              fragment_chain:2
misc_feature 16193..22530
              /note="assembly_fragment:01022"
              fragment_chain:2
misc_feature 22631..27253
              /note="assembly_fragment:00011"
              fragment_chain:1
misc_feature 27354..30261
              /note="assembly_fragment:00127"
              fragment_chain:1
misc_feature 30362..33611
              /note="assembly_fragment:00247"
              fragment_chain:1
misc_feature 33712..38262
              /note="assembly_fragment:00335"
              fragment_chain:1
misc_feature 38363..40615
              /note="assembly_fragment:00495"
              fragment_chain:1
misc_feature 40716..44299
              /note="assembly_fragment:00561"
              fragment_chain:1
misc_feature 44400..47229
              /note="assembly_fragment:00700"
              fragment_chain:1
misc_feature 47330..52776
              /note="assembly_fragment:00832"
              fragment_chain:1
misc_feature 52877..60226
              /note="assembly_fragment:00912"
              fragment_chain:1
misc_feature 60327..62930
              /note="assembly_fragment:01119"
              fragment_chain:1
misc_feature 63031..67419
              /note="assembly_fragment:01935"
              fragment_chain:1
misc_feature 67520..145939
              /note="assembly_fragment:02239"
              fragment_chain:1
BASE COUNT 45121 a 27951 c 28095 g 43161 t 1611 others
ORIGIN
Query Match      80.9%; Score 17.8; DB 79; Length,145939;
Best Local Similarity 90.5%; Pred. No.73;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 gactgtgaacttcgagatga 22
   ||||| ||||| ||||| |||||
Db 37628 GACTGTGAATGTTCCAGATGA 37648

RESULT 13
AC027442 165337 bp DNA HTG 27-APR-2000
LOCUS Homo sapiens clone RP11-439K16, WORKING DRAFT SEQUENCE, 31
DEFINITION Homo sapiens clone RP11-439K16, WORKING DRAFT SEQUENCE, 31
ACCESSION AC027442
VERSION AC027442.2 GI:7651981
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165337)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens, clone RP11-439K16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165337)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Collins, S.,
Dodge, S., Domino, M., Doyle, M., Ferrel, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczek, J.,

```

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Melgrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollivier, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 27, 2000 this sequence version replaced gi:7342171.

COMMENT
All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8145

Center clone name: 439_K_16

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 149010 bases at least Q40

Consensus quality: 157303 bases at least Q30

Consensus quality: 160628 bases at least Q20

Insert size: 170000; agarose-fp

Insert size: 162337; sum-of-ctngs

Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.8 in Q20 bases; sum-of-ctngs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1105: contig of 1105 bp in length
* 1106 1205: gap of 100 bp
* 1206 2479: contig of 1274 bp in length
* 2480 2579: gap of 100 bp
* 2580 4211: contig of 1632 bp in length
* 4212 4311: gap of 100 bp
* 4312 5781: contig of 1470 bp in length
* 5782 5881: gap of 100 bp
* 5882 7830: contig of 1949 bp in length
* 7831 7930: gap of 100 bp
* 7931 9913: contig of 1983 bp in length
* 9914 10013: gap of 100 bp
* 10014 12486: contig of 2473 bp in length
* 12487 12586: gap of 100 bp
* 12587 15592: contig of 3006 bp in length
* 15593 15692: gap of 100 bp
* 15693 19721: contig of 4029 bp in length
* 19722 19821: gap of 100 bp
* 19822 23269: contig of 3448 bp in length
* 23270 23369: gap of 100 bp
* 23370 26785: contig of 3416 bp in length
* 26786 26885: gap of 100 bp
* 26886 30363: contig of 3478 bp in length
* 30364 30463: gap of 100 bp
* 30464 33964: contig of 3501 bp in length
* 33965 34064: gap of 100 bp
* 34065 37794: contig of 3730 bp in length

* 37795 37894: gap of 100 bp
* 37895 43354: contig of 5460 bp in length
* 43355 43454: gap of 100 bp
* 43455 47839: contig of 4385 bp in length
* 47840 47939: gap of 100 bp
* 47940 53326: contig of 5387 bp in length
* 53327 53426: gap of 100 bp
* 53427 58576: contig of 5150 bp in length
* 58577 58676: gap of 100 bp
* 58677 64554: contig of 5878 bp in length
* 64555 64654: gap of 100 bp
* 64655 68538: contig of 3884 bp in length
* 68539 68638: gap of 100 bp
* 68639 74650: contig of 6012 bp in length
* 74651 74750: gap of 100 bp
* 74751 80037: contig of 5287 bp in length
* 80038 80137: gap of 100 bp
* 80138 85646: contig of 5509 bp in length
* 85647 85746: gap of 100 bp
* 85747 92718: contig of 6972 bp in length
* 92719 92818: gap of 100 bp
* 92819 101098: contig of 8280 bp in length
* 101099 101198: gap of 100 bp
* 101199 108560: contig of 7362 bp in length
* 108561 108660: gap of 100 bp
* 108661 118118: contig of 9458 bp in length
* 118119 118218: gap of 100 bp
* 118219 128612: contig of 10394 bp in length
* 128613 128712: gap of 100 bp
* 128713 139860: contig of 11148 bp in length
* 139861 139960: gap of 100 bp
* 139961 151029: contig of 11069 bp in length
* 151030 151129: gap of 100 bp
* 151130 165337: contig of 14208 bp in length.

FEATURES Location/Qualifiers

source
1. 165337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPC1-11 Human Male BAC"
misc_feature
1. 1105
/note="assembly_fragment"
misc_feature
1206. 2479
/note="assembly_fragment"
misc_feature
2580. 4211
/note="assembly_fragment"
misc_feature
4312. 5781
/note="assembly_fragment"
misc_feature
5882. 7830
/note="assembly_fragment"
misc_feature
7931. 9913
/note="assembly_fragment"
misc_feature
10014. 12486
/note="assembly_fragment"
misc_feature
12587. 15592
/note="assembly_fragment"
misc_feature
15693. 19721
/note="assembly_fragment"
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19822. 23269
/note="assembly_fragment"
misc_feature
23370. 26785
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26886. 30363
/note="assembly_fragment"
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30464. 33964
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34065. 37794
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37895. 43354
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43455. 47839
/note="assembly_fragment"
misc_feature
47940. 53326

misc_feature	/note="assembly_fragment" 53427. .58576
misc_feature	/note="assembly_fragment" 59677. .64554
misc_feature	/note="assembly_fragment" 64655. .68538
	/note="assembly_fragment" clone_end:T7 vector_side:right"
misc_feature	68639. .74650
misc_feature	/note="assembly_fragment" 74751. .80037
misc_feature	/note="assembly_fragment" 80138. .85646
misc_feature	/note="assembly_fragment" 85747. .92718
misc_feature	/note="assembly_fragment" 92819. .101098
misc_feature	/note="assembly_fragment" 101199. .108360
	/note="assembly_fragment" clone_end:SP6 vector_side:right"
misc_feature	108661. .118118
misc_feature	/note="assembly_fragment" 118219. .128612
misc_feature	/note="assembly_fragment" 128713. .139860
	/note="assembly_fragment"

```
Query Match      80.9%; Score 17.8; DB 70; Length 165337;
Best Local Similarity 90.5%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 gactgtgaacgttcgagatga 22
 ||||| ||| |||||
 Db 34792 GACTGTGAAAGTTTGAGATGA 34812

RESULT 14

AC007938 167237 bp DNA 01-JUL-1999
LOCUS Homo sapiens clone RP11-2E11 from 7q31, complete sequence. PRI
DEFINITION AC007938
ACCESSION AC007938
VERSION AC007938.1 GI:5306288
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167237)
AUTHORS Iadonato,S.P., Yu,J., Wong,G.K.-S., Magness,C.L., Green,E.D.,
Green,P. and Olson,M.V.
TITLE Large-scale MCD Mapping and Sequencing of Human Chromosome 7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 167237)
AUTHORS Bubb,K.L., Desmarais,C.L. and Ramsey,S.A.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1999) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
COMMENT Overlapping Sequences:
5': UWGC:mapping in progress
3': UWGC:mapping in progress

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

```
-----
2391.00 2382.00 1357.00 1347.00
-----
652.00 656.00 14474.00 14507.00
-----
7746.00 7822.00 1021.00 986.00
-----
824.00 820.00 1357.00 1338.00
-----
919.00 898.00 3235.00 3209.00
-----
2000.00 2020.00 4073.00 3995.00
-----
2742.00 2779.00 4844.00 4741.00
-----
1137.00 1127.00 667.00 637.00
-----
7746.00 7672.00 9942.00 9815.00
-----
4401.00 4351.00 9942.00 9798.00
-----
1497.00 1483.00 1122.00 1094.00
-----
1137.00 1141.00 583.00 559.00
-----
3240.00 3204.00 4293.00 4217.00
-----
10233.00 10265.00 1883.00 1853.00
-----
2082.00 2106.00 3007.00 2890.00
-----
5366.00 5430.00 1642.00 1630.00
-----
3156.00 3149.00 -----
3403.00 -----
2082.00 -----
10785.00 -----
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FEATURES
source
  1. 167237
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="7"
  /map="7q31"
  /clone="RP11-2E11"
  /cell_line="Male Blood"
  /clone_lib="RPC1-11 Human Male BAC library"
  19. 57
  /rpt_family="MER33"
  complement(19..202)
  /rpt_family="MER3"
  complement(4274..4485)
  /rpt_family="MER44C"
  4579..4853
  /rpt_family="Alu"
  complement(5201..5265)
  /rpt_family="MER44C"
  complement(9355..9635)
  /rpt_family="Alu"
  complement(9820..10295)
  /rpt_family="Alu"
  complement(10848..11105)
  /rpt_family="Alu"
  12817..13056
  /rpt_family="Alu"
  complement(13484..13707)
  /rpt_family="Alu"
  complement(14659..14767)
  /rpt_family="MIR"
  -----
```

Unmatched fragments are due to vector-containing sequences. We expect 3, 1 and 1-2 such fragments in the BgIII, EcoRI, and NsiI enzyme domains, respectively. The sum of these fragments can be calculated from the sequence of the BAC clone and, in this clone, should be 15 909, 8 992, and 17 890 for the three enzyme domains.

```
repeat_region 17458..17523
/rpt_family="MER5"
repeat_region complement(19439..20044)
/rpt_family="Alu"
repeat_region complement(26649..26806)
/rpt_family="MIR"
repeat_region complement(26993..27274)
/rpt_family="Alu"
repeat_region 30702..31044
/rpt_family="Alu"
repeat_region complement(31117..31171)
/rpt_family="MIR"
STS 31696..31875
/standard_name="SWSS3351"
/standard_name="Genbank Accession: G13133"
repeat_region 31900..32236
/rpt_family="THE1"
repeat_region complement(33690..33730)
/rpt_family="Alu"
repeat_region 33899..34177
/rpt_family="Alu"
repeat_region complement(37893..38494)
```

Query Match 80.9%; Score 17.8; DB 86; Length 167237;
Best Local Similarity 90.5%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatg 21
|||||

Db 21036 TGACTGTGAACGTTCAGAGATG 21056

RESULT 15

AC074012/c

LOCUS

DEFINITION

AC074012

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC074012 201214 bp DNA HTG 16-JUL-2000
Homo sapiens chromosome 7 clone RP11-781M21, WORKING DRAFT
SEQUENCE, 29 unordered pieces.

AC074012.2 GI:9230873

HTG; HTGS_PHASE1; HTGS_DRAFT.

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201214)

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 201214)

Waterston,R.H.

Direct Submission

Submitted (09-JUL-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Jul 16, 2000 this sequence version replaced gi:8980982.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H_NH0781M21

----- Summary Statistics -----

Sequencing vector: M13; 100%

Chemistry: Dye-primer ET; 100% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 185830 bases at least Q40

Consensus quality: 191039 bases at least Q30

Consensus quality: 193172 bases at least Q20

Insert size: 230000; agarose-gel

Insert size: 198414; sum-of-contigs

Search completed: October 9, 2001, 16:18:18
Job time: 2468 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:37:10 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-1
Perfect score: 22
Sequence: 1 tgaactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	gb_est1:
2:	gb_est2:
3:	gb_est3:
4:	gb_est4:
5:	gb_est5:
6:	gb_est6:
7:	gb_est7:
8:	gb_est8:
9:	gb_est9:
10:	gb_est10:
11:	gb_est11:
12:	gb_est12:
13:	gb_est13:
14:	gb_est14:
15:	gb_est15:
16:	gb_est16:
17:	gb_est17:
18:	gb_est18:
19:	gb_est19:
20:	gb_est20:
21:	gb_est21:
22:	gb_est22:
23:	gb_est23:
24:	gb_est24:
25:	gb_est33:
26:	gb_est34:
27:	gb_est35:
28:	gb_est36:
29:	gb_est37:
30:	gb_est38:
31:	gb_est39:
32:	gb_est40:
33:	em_estba:
34:	em_estfun:
35:	em_esthum1:
36:	em_esthum2:
37:	em_esthum3:
38:	em_esthum4:
39:	em_esthum5:
40:	em_esthum6:
41:	em_esthum7:
42:	em_esthum8:
43:	em_esthum9:

44:	em_esthum10:
45:	em_esthum11:
46:	em_esthum12:
47:	em_esthum13:
48:	em_esthum14:
49:	em_esthum15:
50:	em_esthum16:
51:	em_esthum17:
52:	em_esthum18:
53:	em_esthum19:
54:	em_esthum20:
55:	em_esthum21:
56:	em_esthum22:
57:	em_esthum23:
58:	em_esthum24:
59:	em_esthum25:
60:	em_esthum26:
61:	em_esthum27:
62:	em_esthum28:
63:	em_estin1:
64:	em_estin2:
65:	em_estin3:
66:	em_estin4:
67:	em_estin5:
68:	em_estom1:
69:	em_estom2:
70:	em_estov1:
71:	em_estov2:
72:	em_estpl1:
73:	em_estpl2:
74:	em_estpl3:
75:	em_estpl4:
76:	em_estpl5:
77:	em_estpl6:
78:	em_estpl7:
79:	em_estpl8:
80:	em_estpl9:
81:	em_estpl10:
82:	em_estro1:
83:	em_estro2:
84:	em_estro3:
85:	em_estro4:
86:	em_estro5:
87:	em_estro6:
88:	em_estro7:
89:	em_estro8:
90:	em_estro9:
91:	em_estro10:
92:	em_estro11:
93:	em_estro12:
94:	em_estro13:
95:	em_estro14:
96:	em_estro15:
97:	em_estro16:
98:	em_estro17:
99:	em_estro18:
100:	em_estro19:
101:	em_estro20:
102:	gb_est25:
103:	gb_est26:
104:	gb_est27:
105:	gb_est28:
106:	gb_est29:
107:	gb_est30:
108:	gb_est31:
109:	gb_est32:
110:	gb_est41:
111:	gb_est42:
112:	gb_est43:
113:	gb_est44:
114:	gb_est45:
115:	gb_est46:
116:	gb_est47:

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
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222: gb_est153:*
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251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL
COMMENT

Unpublished (2000)
Contact: Friedman TB
Laboratory of Molecular Genetics
National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Court, Room 2A-15, Rockville, MD 20850, USA
Tel: 301 402 7580
Fax: 301 496 7882
Email: friedman@nidcd.nih.gov
Plate: 02 row: g column: 09
Seq primer: -21M13 forward primer (ABI)
Class: random plasmid subclone.
Location/Qualifiers
1..561

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ev02g09"
/clone_lib="PAX3 CASTing Library 'ev'"
/sex="Male"
/lab_host="DH108"
/note="vector: pGEM-T Easy; Human genomic DNA was
partially digested with Sau3AI, ligated to ds linkers,
and enriched for binding to human PAX3D0+ protein using a
Whole Genome PCR-based strategy. DNA fragments containing
putative PAX3D0+ binding sites were amplified by PCR and
cloned into pGEM-T Easy (Promega). The ligation products
were transformed into DH10B electrocompetent cells (Life
Technologies)."

BASE COUNT 126 a 149 c 152 g 134 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 249; Length 561;
Best Local Similarity 90.5%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatg 21
|||||
Db 461 TGACTGTGACGTCAGAGATG 441

RESULT 2

BF971856 961 bp mRNA EST 22-JAN-2001
LOCUS 60224044F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328890 5',
mRNA sequence.
ACCESSION BF971856
VERSION BF971856.1 GI:12339071
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 961)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM1189 row: h column: 11
High quality sequence stop: 555.

FEATURES
source

1..961
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4328890"

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	17.8	80.9	561	249	A2755668	ev02g09.x
C 2	17.8	80.9	961	172	BF971856	60224044
C 3	17.4	79.1	489	231	A2060178	RPCI-23-4
C 4	17.4	79.1	530	251	A2886419	RPCI-23-1
C 5	17.2	78.2	374	226	AQ245026	HS_2056.B
C 6	17.2	78.2	408	245	A2536502	110300.96
C 7	17.2	78.2	424	139	BE723539	193384.MA
C 8	17.2	78.2	463	107	AU083559	AU083559
C 9	17.2	78.2	479	107	AU089685	AU089685
C 10	17.2	78.2	972	222	CNS05PD9	AL347814 Tetraodon
C 11	16.8	76.4	105	2	AA094019	cl1619.se
C 12	16.8	76.4	523	244	A2483488	LM0309M12
C 13	16.8	76.4	526	245	A2501799	LM0340J17
C 14	16.8	76.4	681	32	AV732648	AV732648
C 15	16.8	76.4	705	122	AW916461	EST347765
C 16	16.4	74.5	400	115	AW398307	EST298154
C 17	16.4	74.5	496	110	AW034934	EST279163
C 18	16.4	74.5	546	237	AZ058706	RPCI-23-4
C 19	16.4	74.5	554	241	A2280611	RPCI-23-1
C 20	16.4	74.5	599	237	AZ068022	RPCI-23-4
C 21	16.4	74.5	633	155	BG570577	BG570577
C 22	16.4	74.5	747	174	BG127461	EST473107
C 23	16.4	74.5	934	220	CNS027SC	AL185061 Tetraodon
C 24	16.2	73.6	202	4	AA236074	zs05a04.r
C 25	16.2	73.6	236	127	BB183285	BB183285
C 26	16.2	73.6	236	171	BF932252	IL2-NT019
C 27	16.2	73.6	251	161	BB565758	BB565758
C 28	16.2	73.6	286	16	AI099019	uc02h08.r
C 29	16.2	73.6	297	7	AA445764	vc63b04.s
C 30	16.2	73.6	300	156	C11370	C11370
C 31	16.2	73.6	304	230	AQ581066	RPCI-11-4
C 32	16.2	73.6	317	163	BE119339	UI-R-CAO-
C 33	16.2	73.6	360	26	AV189436	AV189436
C 34	16.2	73.6	398	167	BE428418	MTD006.G1
C 35	16.2	73.6	401	165	BE275964	601120704
C 36	16.2	73.6	416	231	AQ646593	RPCI193-Dp
C 37	16.2	73.6	434	170	BF851024	IL5-EN008
C 38	16.2	73.6	441	22	AI597068	v344e09.x
C 39	16.2	73.6	448	115	AW390277	CM2-ST018
C 40	16.2	73.6	457	166	BE367478	P11.8-F04
C 41	16.2	73.6	472	235	AQ904593	GSSTC0381
C 42	16.2	73.6	473	188	R83554	yq12d03.r1
C 43	16.2	73.6	474	167	BE419241	WNR021.G5
C 44	16.2	73.6	477	149	BF475131	WHE2111.B
C 45	16.2	73.6	479	142	BE946012	UI-M-BH3-

ALIGNMENTS

RESULT 1
A2755668/c 561 bp DNA GSS 01-MAR-2001
LOCUS ev02g09.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone
DEFINITION ev02g09 random, cDNA sequence.
ACCESSION A2755668
VERSION A2755668.1 GI:13175090
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS Barber, T.D., Barber, M.C., Tomescu, O., Barr, F., Ruben, S. and
Friedman, T.B.
TITLE Cyclic amplification and selection of target genes regulated by
pax3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma

/clone_lib="NIH_MGC_46"
 /tissue_type="leiomyosarcoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pOR87; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."
 BASE COUNT 205 a 225 c 240 g 291 t
 ORIGIN

Query Match 80.9%; Score 17.8; DB 172; Length 961;
 Best Local Similarity 90.5%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 gactgtgaacgttcgagatga 22
 ||||| ||||| |||||
 Db 650 GACTGTGACGTTCCGATGA 670

RESULT 3
 AZ060178/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 489)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-405E23.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (inforesgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 405 row: E column: 23
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1. .489
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-405E23"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size

Query Match 80.9%; Score 17.8; DB 172; Length 961;
 Best Local Similarity 90.5%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 gactgtgaacgttcgagatga 22
 ||||| ||||| |||||
 Db 650 GACTGTGACGTTCCGATGA 670

selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 162 a 61 c 67 g 198 t
 ORIGIN

Query Match 79.1%; Score 17.4; DB 237; Length 489;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacgttcgaga 19
 ||||| ||||| |||||
 Db 170 TGACTGTGAACATTCGAGA 152

RESULT 4
 AZ886419/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 530)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-182I6.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 182 row: I column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1. .530
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-182I6"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 174 a 65 c 73 g 218 t
 ORIGIN

Query Match 79.1%; Score 17.4; DB 251; Length 530;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacgttcgaga 19
 ||||| ||||| |||||
 Db 170 TGACTGTGAACATTCGAGA 152

RESULT 4
 AZ886419/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 530)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
 , B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-182I6.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 182 row: I column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1. .530
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-182I6"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 174 a 65 c 73 g 218 t
 ORIGIN

Query Match 79.1%; Score 17.4; DB 251; Length 530;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacgttcgaga 19
 ||||| ||||| |||||
 Db 170 TGACTGTGAACATTCGAGA 152

Qy 1 tgactgtgaacgttcgaga 19
 |||||
 Db 189 TGACTGTGAACATTCGAGA 171

RESULT 5

AQ245026 374 bp DNA GSS 03-OCT-1998
 LOCUS HS_2056_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone plate-2056 Col-5 Row-J, DNA sequence.
 ACCESSION AQ245026
 VERSION AQ245026.1 GI:3691600
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 374)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL PROC. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 2056 row: J column: 5
 Class: BAC ends
 High quality sequence stop: 374.

FEATURES
source

1. 374
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="plate-2056 Col-5 Row-J"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
 E-Coli DH10B."
 BASE COUNT 91 a 73 c 92 g 117 t 1 others
 ORIGIN

Query Match 78.2%; Score 17.2; DB 226; Length 374;
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 207 TGACTGTGAACGATTGAGATCA 228

RESULT 6

AZ536502 408 bp DNA GSS 03-NOV-2000
 LOCUS 110300_96 Planococcus lillacinus DNA Planococcus lillacinus genomic,
 DEFINITION DNA sequence.
 ACCESSION AZ536502
 VERSION AZ536502.1 GI:11093449
 KEYWORDS GSS.
 SOURCE liliac mealybug.
 ORGANISM Planococcus lillacinus
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 Aphidiformes; Coccoidea; Pseudococcidae; Planococcus.
 REFERENCE 1 (bases 1 to 408)

AUTHORS Mohan,K.N. and Chandra,H.S.
 TITLE Mealybug shotgun sequencing
 JOURNAL Unpublished (2000)
 COMMENT Contact: Mohan KN
 Microbiology and Cell Biology
 Indian Institute of Science
 Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India
 Email: mohan@mcbl.iisc.ernet.in

FEATURES
source

1. 408
 Location/Qualifiers
 /organism="Planococcus lillacinus"
 /db_xref="taxon:40930"
 /clone_lib="Planococcus lillacinus DNA"
 BASE COUNT 134 a 83 c 80 g 111 t
 ORIGIN

Query Match 78.2%; Score 17.2; DB 245; Length 408;
 Best Local Similarity 86.4%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
 |||||
 Db 251 TGACTGTGAACGACGATATGA 272

RESULT 7

BE723539 424 bp mRNA EST 14-SEP-2000
 LOCUS 193384 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE723539
 ACCESSION BE723539
 VERSION BE723539.1 GI:10124826
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 424)
 AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
 Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
 W.W. and Keele,J.W.
 TITLE Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCCGATCAGCAGC
 Plate: 92 row: E column: 14
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1. 424
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 4BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
 Library made from pooled tissue from day 20 and day 40
 embryos."
 BASE COUNT 107 a 107 c 87 g 123 t
 ORIGIN

```

Query Match      78.2%  Score 17.2; DB 139; Length 424;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 268 TGACTGTGAACGTTAGAGATGA 289

RESULT 8
LOCUS AU083559 463 bp mRNA EST 21-MAR-2000
DEFINITION AU083559 Rice green shoot Oryza sativa cDNA clone S14862, mRNA
sequence.
ACCESSION AU083559
VERSION AU083559.1 GI:7274015
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 463)
AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from green shoot (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'RGP'
S14862_62.

FEATURES             Location/Qualifiers
     source           1..463
                     /organism="Oryza sativa"
                     /strain="Nipponbare"
                     /db_xref="taxon:4530"
                     /clone="S14862"
                     /clone_lib="Rice green shoot"
                     /note="Green shoot (8 days old)"
BASE COUNT 151 a 74 c 109 g 127 t 2 others
ORIGIN

Query Match      78.2%  Score 17.2; DB 107; Length 463;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 151 TGACTGTGAATGTTAGAGATGA 172

RESULT 9
LOCUS AU089685 479 bp mRNA EST 27-APR-2000
DEFINITION AU089685 Rice callus Oryza sativa subsp. japonica cDNA clone C40060
sequence.
ACCESSION AU089685
VERSION AU089685.1 GI:7652165
KEYWORDS EST.
SOURCE Oryza sativa subsp. japonica.
ORGANISM Oryza sativa subsp. japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 479)

```

```

AUTHORS Sasaki,T. and Yamamoto,K.
TITLE Rice cDNA from callus (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'RGP'
C40060_32.

FEATURES             Location/Qualifiers
     source           1..479
                     /organism="Oryza sativa subsp. japonica"
                     /strain="cultivar Nipponbare, sub_species Japonica"
                     /db_xref="taxon:39947"
                     /clone="C40060"
                     /clone_lib="Rice callus"
                     /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
                     NotI; cDNA prepared from rice callus mRNAs by using
                     oligo(dT) as a primer and ligating to the SalI-NotI site
                     of pBluescript II SK+ phagemid."
BASE COUNT 149 a 96 c 104 g 130 t
ORIGIN

Query Match      78.2%  Score 17.2; DB 107; Length 479;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
    ||| ||||| ||||| |||||
Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 10
LOCUS CNS05PD9/c 972 bp DNA GSS 26-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
005F08 of library A from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL347814
VERSION AL347814.1 GI:8241584
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 972)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 972)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 972)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis

```

genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

FEATURES

source

1. .972

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="005F08"

/clone_lib="A"

/note="Genoscope sequence ID : COAA005DC04C1-end : T7"

BASE COUNT 195 a 268 c 199 g 297 t 13 others

ORIGIN

Query Match 78.2%; Score 17.2; DB 222; Length 972;

Best Local Similarity 86.4%; Pred. No. 1.7e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagatga 22

Db 46 TGGCTGTGAAGGTCGAGATGA 25

RESULT 11

AA094019

LOCUS

DEFINITION

AA094019

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CDNA 5', mRNA sequence.

AA094019.1 GI:1639612

EST

human.

Homosapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Liew.C.C.

CDNAs from fetal heart (1996)

Unpublished (1996)

Contact: Liew CC

Department of Laboratory Medicine and Pathobiology

University of Toronto

Banting Institute, 100 College St., Toronto, Ontario, M5G1L5

Tel: 416/9788758

Fax: 416/9783650

Email: liewcc@utcc.utoronto.ca

PCR Primers

FORWARD: 5' GCCAGCTCGAAATTAACCTCTACTAAAGG 3'

BACKWARD: 5' CCAGTGAATTGTAATACGACTCTACTATAGGCG 3'

Seq primer: 5' GAATTAACCTCTACTAAAGG 3'

Location/Qualifiers

1. .105

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human fetal heart, Lambda ZAP Express"

/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site1: EcoRI; Site2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

BASE COUNT 31 a 21 c 16 g 37 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 2; Length 105;

Best Local Similarity 90.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagat 20

Db 43 TGCATGTGAACCTTCAGAT 62

RESULT 12

AZ483488

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 523)

Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C., Islam.H., Longacre.S., Mahmoud.M., Meenen.E., Pedersen.T., Reilly.M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern.A. and Wright.D., Weiss.R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0309 row: M column: 12

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 523.

Location/Qualifiers

1. .523

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG1M0309M12"

/clone_lib="Mouse 10kb plasmid UUCG1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 162 a 127 c 103 g 131 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 244; Length 523;

Best Local Similarity 90.0%; Pred. No. 2.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 actgtgaacgttcgagatga 22

Db 376 ACTGTGTACTTTCGAGATGA 395

```

RESULT 13
LOCUS AZ501799 526 bp DNA GSS 05-OCT-2000
DEFINITION 1M0340J17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
ACCESSION AZ501799
VERSION AZ501799.1 GI:10683115
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 526)
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0340 row: J column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 526.
FEATURES
Location/Qualifiers
1..526
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0340J17"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1147321141gb1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 121 a 126 c 139 g 140 t
ORIGIN
Query Match 76.4%; Score 16.8; DB 245; Length 526;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tgactgtgaacgttcgagat 20
||||| ||||||| |||||

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Db 60 TGACAGTGAACGTTCTAGAT 79
RESULT 14
LOCUS AV732648/c 681 bp mRNA EST 17-OCT-2000
DEFINITION AV732648 HTF Homo sapiens cDNA clone HTFBLB03 5', mRNA sequence.
ACCESSION AV732648
VERSION AV732648.1 GI:10850193
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA HTF clones
Unpublished (2000)
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
1..681
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTFBLB03"
/clone_lib="HTF"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 202 a 137 c 156 g 184 t 2 others
ORIGIN
Query Match 76.4%; Score 16.8; DB 32; Length 681;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 actgtgaacgttcgagatga 22
||||| ||||| || |||||
Db 382 ACTGTGACATTGTGAGATGA 363

RESULT 15
LOCUS AW916461 705 bp mRNA EST 25-MAY-2000
DEFINITION ES347765 Rat gene index, normalized rat, norvegicus, Bento Soares
Rattus norvegicus cDNA clone RGID049 5' end, mRNA sequence.
ACCESSION AW916461
VERSION AW916461.1 GI:8082187
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 705)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat
Gene Index
Unpublished (1998)
CONTACT: Lee, NH

```

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
Location/Qualifiers
1. .705
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIDQ49"
/clone_lib="Rat gene index, normalized rat, norvegicus,
Bento Soares"
/tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; Estimated insert size approx.1 kb"
BASE COUNT 177 a 201 c 169 g 157 t 1 others
ORIGIN

Query Match 76.4%; Score 16.8; DB 122; Length 705;
Best Local Similarity 90.0%; Pred. NO. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Caps 0;
Qy 3 actgtgaacgttcgagatga 22
||||| |||||
Db 150 ACTGTGACCTTCGAGATGA 169

Search completed: October 9, 2001, 18:20:11
Job time: 9781 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:38:15 ; Search time 10334.3 Seconds
(without alignments)
31.457 Million cell updates/sec

Title: US-09-713-136-1

Perfect score: 22

Sequence: 1 tgactgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
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8: /cgn2_6/ptodata/1/pna/US084_COMB.seq.*
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14: /cgn2_6/ptodata/1/pna/US090_COMB.seq.*
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19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*
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26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*
27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*
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32: /cgn2_6/ptodata/1/pna/US6000_COMB.seq.*
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36: /cgn2_6/ptodata/1/pna/US6004_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US6005_COMB.seq.*
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39: /cgn2_6/ptodata/1/pna/US6007_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US6008_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US6009_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US6010_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US6011_COMB.seq.*

44: /cgn2_6/ptodata/1/pna/US6012_COMB.seq.*
45: /cgn2_6/ptodata/1/pna/US6013_COMB.seq.*
46: /cgn2_6/ptodata/1/pna/US6014_COMB.seq.*
47: /cgn2_6/ptodata/1/pna/US6015_COMB.seq.*
48: /cgn2_6/ptodata/1/pna/US6016_COMB.seq.*
49: /cgn2_6/ptodata/1/pna/US6017_COMB.seq.*
50: /cgn2_6/ptodata/1/pna/US6018_COMB.seq.*
51: /cgn2_6/ptodata/1/pna/US6019_COMB.seq.*
52: /cgn2_6/ptodata/1/pna/US6020_COMB.seq.*
53: /cgn2_6/ptodata/1/pna/US6021_COMB.seq.*
54: /cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
55: /cgn2_6/ptodata/1/pna/US6023_COMB.seq.*
56: /cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
57: /cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
58: /cgn2_6/ptodata/1/pna/US6026_COMB.seq.*
59: /cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
60: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22	100.0	22	1	PCT-US00-18229-32	Sequence 32, Appl
2	22	100.0	22	1	PCT-US00-35064-1	Sequence 1, Appl
3	22	100.0	22	1	PCT-US01-03029-1	Sequence 1, Appl
4	22	100.0	22	1	PCT-US01-06034-1	Sequence 1, Appl
5	22	100.0	22	1	PCT-US01-10118-1	Sequence 1, Appl
6	22	100.0	22	1	PCT-US01-10118-3	Sequence 3, Appl
7	22	100.0	22	1	PCT-US01-11290-1	Sequence 1, Appl
8	22	100.0	22	1	PCT-US01-14508-1	Sequence 1, Appl
9	22	100.0	22	1	PCT-US99-21203-19	Sequence 19, Appl
10	22	100.0	22	13	US-08-927-120-19	Sequence 19, Appl
11	22	100.0	22	15	US-09-167-039-19	Sequence 19, Appl
12	22	100.0	22	16	US-09-235-742-19	Sequence 2, Appl
13	22	100.0	22	16	US-09-296-477-2	Sequence 1, Appl
14	22	100.0	22	17	US-09-308-036A-1	Sequence 1, Appl
15	22	100.0	22	17	US-09-324-191A-1	Sequence 1, Appl
16	22	100.0	22	17	US-09-347-343-32	Sequence 32, Appl
17	22	100.0	22	17	US-09-397-198-1	Sequence 1, Appl
18	22	100.0	22	18	US-09-415-186-1	Sequence 1, Appl
19	22	100.0	22	18	US-09-470-382-69	Sequence 69, Appl
20	22	100.0	22	22	US-09-565-906-2	Sequence 2, Appl
21	22	100.0	22	22	US-09-570-325-19	Sequence 19, Appl
22	22	100.0	22	25	US-09-642-492-1	Sequence 1, Appl
23	22	100.0	22	28	US-09-700-354-1	Sequence 1, Appl
24	22	100.0	22	28	US-09-713-136-1	Sequence 1, Appl
25	22	100.0	22	29	US-09-746-130-1	Sequence 1, Appl
26	22	100.0	22	30	US-09-774-403-1	Sequence 1, Appl
27	22	100.0	22	30	US-09-791-500-1	Sequence 1, Appl
28	22	100.0	22	31	US-09-820-484-1	Sequence 3, Appl
29	22	100.0	22	31	US-09-820-484-3	Sequence 1, Appl
30	22	100.0	22	31	US-09-828-505-1	Sequence 1, Appl
31	21.2	96.4	22	18	US-09-415-186-7	Sequence 7, Appl
32	21	95.5	22	16	US-09-296-477-15	Sequence 15, Appl
33	21	95.5	22	17	US-09-324-191A-5	Sequence 5, Appl
34	21	95.5	22	25	US-09-642-492-7	Sequence 7, Appl
35	21	95.5	22	28	US-09-713-136-7	Sequence 2, Appl
36	20.4	92.7	22	1	PCT-US00-35064-2	Sequence 2, Appl
37	20.4	92.7	22	1	PCT-US01-03029-2	Sequence 4, Appl
38	20.4	92.7	22	1	PCT-US01-06034-4	Sequence 5, Appl
39	20.4	92.7	22	1	PCT-US01-06034-5	Sequence 6, Appl
40	20.4	92.7	22	1	PCT-US01-10118-2	Sequence 2, Appl
41	20.4	92.7	22	1	PCT-US01-10118-6	Sequence 6, Appl
42	20.4	92.7	22	1	PCT-US01-11290-2	Sequence 2, Appl
43	20.4	92.7	22	1	PCT-US01-14508-10	Sequence 10, Appl
44	20.4	92.7	22	31	US-09-828-505-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; FILE REFERENCE: 6510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:

; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.

RESULT 7
PCT-US01-11290-1
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE REFERENCE: 06510-188WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE REFERENCE: 06510-188WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7
PCT-US01-11290-1
; Sequence 1, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 8
PCT-US01-14508-1
; Sequence 1, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE REFERENCE: 06510/168WO1
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-1

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 9
PCT-US99-21203-19
; Sequence 19, Application PC/TUS9921203

GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 865 S. Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/21203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-188
TELEPHONE: 213-892-9200
TELEFAX: 213-680-4518
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
PCT-US99-21203-19

Query Match 100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 10
US-08-927-120-19
Sequence 19, Application US/08927120
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: IMMUNIZATION-FREE METHODS
TITLE OF INVENTION: FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING
TITLE OF INVENTION: INFLAMMATION IN A HOST
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,120

FILING DATE: 22-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/054001
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
US-08-927-120-19

Query Match 100.0%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 11
US-09-167-039-19
Sequence 19, Application US/09167039
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: METHODS AND ADJUVANTS
TITLE OF INVENTION: FOR STIMULATING MUCOSAL IMMUNITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 402 West Broadway, Suite 2300
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,039
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/063001
TELEPHONE: 619-234-6655
TELEFAX: 619-234-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
US-09-167-039-19

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 12
US-09-235-742-19
; Sequence 19, Application US/09235742
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; TITLE OF INVENTION: Phenotype
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

Query Match 100.0%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
US-09-296-477-2
; Sequence 2, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; FILE REFERENCE: 37782000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 22

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-2

Query Match 100.0%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14
US-09-308-036A-1
; Sequence 1, Application US/09308036A
; GENERAL INFORMATION:
; APPLICANT: Carson, Dennis A.
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Immunostimulatory
; TITLE OF INVENTION: Polynucleotide/Immunomodulatory Molecule Conjugates
; FILE REFERENCE: 6510-172CIP
; CURRENT APPLICATION NUMBER: US/09/308,036A
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/US97/19004
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/028,118
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DY1018 polynucleotide
US-09-308-036A-1

Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
US-09-324-191A-1
; Sequence 1, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; TITLE OF INVENTION: MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 37782000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/080,310
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-324-191A-1

Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred No. 0.75;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 tgactgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

Search completed: October 9, 2001, 21:12:35
Job time: 20060 sec


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; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 3778201100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
US-09-802-376-1

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-7

Query Match      95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-376-7

Query Match      95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
    ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-376-7
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Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 7
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match 92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 8
US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22
|||||

RESULT 9
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 10
US-09-802-359-2
; Sequence 2, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-2

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 11
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:


```
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-359-4

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
US-09-802-376-2
; Sequence 2, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-376-2

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; US-09-802-376-4

Query Match          92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
; US-09-802-518-8

Query Match          90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcgagatga 22
   ||||| ||| |||||
Db 1 tgactgtgaangttingagatga 22

Search completed: October 9, 2001, 21:35:59
Job time: 21219 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:18 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-2
Perfect score: 22
Sequence: 1 tgacogtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_ba2:
3: gb_ba3:
4: gb_in1:
5: gb_in2:
6: gb_in3:
7: gb_em:
8: gb_ov:
9: gb_pat1:
10: gb_pat2:
11: gb_ph:
12: gb_pl1:
13: gb_pl2:
14: gb_pl3:
15: gb_pl4:
16: em_ba1:
17: em_ba2:
18: em_fun:
19: em_htgo_hum:
20: em_htgo_inv:
21: em_htgo_rod:
22: em_htg_hum1:
23: em_htg_hum2:
24: em_htg_hum3:
25: em_htg_hum4:
26: em_htg_hum5:
27: em_htg_hum6:
28: em_htg_hum7:
29: em_htg_hum8:
30: em_htg_inv1:
31: em_htg_inv2:
32: em_htg_rod:
33: em_hum1:
34: em_hum2:
35: em_hum3:
36: em_hum4:
37: em_hum5:
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39: em_hum7:
40: em_in:
41: em_in:
42: em_in:
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44: em_ov:
45: em_pat:
46: em_ph:
47: em_pl:
48: em_ro:
49: em_sts:
50: em_sy:
51: em_un:
52: em_v1:
53: gb_sts1:
54: gb_sts2:
55: gb_sts3:
56: gb_sy:
57: gb_un:
58: gb_v1:
59: gb_v12:
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88: gb_pr4:
89: gb_pr5:
90: gb_pr6:
91: gb_pr7:
92: gb_pr8:
93: gb_pr9:
94: gb_rol:
95: gb_rol:
96: gb_in4:
97: gb_pr10:
98: em_ba3:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	10	AX083676 Sequence
2	20.4	92.7	22	9	AX036945 Sequence
3	20.4	92.7	22	9	AX046993 Sequence
4	20.4	92.7	22	10	AX083675 Sequence
5	19.4	88.2	22	10	AX083681 Sequence
6	18.8	85.5	22	9	AX036946 Sequence
7	18.8	85.5	22	10	AX083678 Sequence
8	18.4	83.6	22	10	AX083682 Sequence

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9 17.8 80.9 22 10 AX083680 Sequence
10 17.2 78.2 22 9 AX036944
11 17.2 78.2 22 9 AX036952
12 17.2 78.2 2079 5 AF025951 Dictyoste
13 16.8 76.4 111234 88 AC079157 Homo sapi
14 16.8 76.4 159072 74 AC073123
15 16.8 76.4 159072 74 AC073123
16 16.2 73.6 642 71 AC032512 Giardia i
17 16.2 73.6 781 71 AC035787 Giardia i
18 16.2 73.6 858 72 AC064490 Giardia i
19 16.2 73.6 1014 72 AC048567 Giardia i
20 16.2 73.6 1076 72 AC048568 Giardia i
21 16.2 73.6 1572 15 SCYJL043W
22 16.2 73.6 1736 9 A49990
23 16.2 73.6 3514 2 BPFHABDNA
24 16.2 73.6 3983 7 S57131
25 16.2 73.6 4880 15 SCYJL042W
26 16.2 73.6 6040 2 CTU32622
27 16.2 73.6 7031 94 AF320616
28 16.2 73.6 11830 2 BPFHAB1
29 16.2 73.6 11831 2 BPFHABFH
30 16.2 73.6 11883 10 I06606
31 16.2 73.6 12256 1 AF111796
32 16.2 73.6 93821 66 AC021586
33 16.2 73.6 136282 84 HSDU368B9
34 16.2 73.6 145939 79 AL158143
35 16.2 73.6 149886 94 MMHC438N12
36 16.2 73.6 157647 26 AC069450 Homo sapi
37 16.2 73.6 165337 70 AC027442
38 16.2 73.6 167237 86 AC007938
39 16.2 73.6 169893 66 AC021165
40 16.2 73.6 182271 76 AC080169
41 16.2 73.6 185637 60 AC007979
42 16.2 73.6 189706 75 AC073778
43 16.2 73.6 200905 82 AL590619
44 16.2 73.6 201214 75 AC074012
45 16.2 73.6 209777 69 AC024934

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ALIGNMENTS

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RESULT 1
AX083676
LOCUS AX083676 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM van Nest, G.
REFERENCE 1 (bases 1 to 22)
AUTHORS Methods of modulating an immune response using immunostimulatory s
TITLES sequences and compositions for use therein
JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="synthetic construct"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN
|||||
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||

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Db 1 TGACCGTGAACGTTTCGAGATGA 22
RESULT 2
LOCUS AX036945 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier, A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="oligodeoxynucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
|||||
Query Match 92.7%; Score 20.4; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 TGACCGTGAACGTTTCGAGATGA 22
RESULT 3
AX046993
LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss, R. B.
TITLES Hiv immunogenic compositions and methods
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="phosphorothioate-modified synthetic oligodeoxynucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
|||||
Query Match 92.7%; Score 20.4; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 TGACCGTGAACGTTTCGAGATGA 22
RESULT 4
AX083675
LOCUS AX083675 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 1 from WO0112223.

```

ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest.G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Patent: WO 011223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 3 c 7 g 6 t
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 92.7%; Score 20.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGAAGTGTGAACGTTCCGAGATGA 22
RESULT 5
AX083681
LOCUS AX083681 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 7 from Patent WO0112223.
ACCESSION AX083681
VERSION AX083681.1 GI:13185413
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest.G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Patent: WO 011223-A 7 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5-bromocytosine"
modified_base 11
/mod_base=OTHER
6 a 2 c 7 g 6 t 1 others
BASE COUNT 6 a 2 c 7 g 6 t 1 others
ORIGIN
Query Match 88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGAAGTGTGAACGTTCCGAGATGA 22
RESULT 6
AX083694
LOCUS AX083694 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX083694
VERSION AX083694.1 GI:11226374
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES Location/Qualifiers
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN
Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGAAGTGTGAACGTTCCGAGATGA 22
RESULT 7
AX083678
LOCUS AX083678 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083678
VERSION AX083678.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest.G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Patent: WO 011223-A 4 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN
Query Match 85.5%; Score 18.8; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGAAGTGTGAACGTTCCGAGATGA 22
RESULT 8
AX083682
LOCUS AX083682 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest.G.
TITLE Methods of modulating an immune response using immunostimulatory s
sequences and compositions for use therein

JOURNAL Patent: WO 011223-A 8 22-FEB-2001;
 FEATURES Dynavax Technologies Corporation (US)
 source Location/Qualifiers
 1. 22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 modified_base 11
 /note="5-bromocytosine"
 /mod_base=OTHER
 modified_base 15
 /note="5-bromocytosine"
 /mod_base=OTHER
 BASE COUNT 6 a 1 c 7 g 6 t 2 others
 ORIGIN

Query Match 83.6%; Score 18.4; DB 10; Length 22;
 Best Local Similarity 86.4%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
 |||| |||| |||| |||| ||||
 Db 1 TGACTGTGAANGTTGAGATGA 22

RESULT 9
 AX083680 22 bp DNA PAT 28-FEB-2001
 LOCUS
 DEFINITION Sequence 6 from Patent WO011223.
 ACCESSION AX083680
 VERSION AX083680.1 GI:13185412
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS van Nest,G.
 TITLE Methods of modulating an immune response using immunostimulatory s
 equences and compositions for use therein
 JOURNAL Patent: WO 011223-A 6 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 FEATURES
 source Location/Qualifiers
 1. 22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 modified_base 11
 /note="5-bromocytosine"
 /mod_base=OTHER
 BASE COUNT 6 a 3 c 6 g 6 t 1 others
 ORIGIN

Query Match 80.9%; Score 17.8; DB 10; Length 22;
 Best Local Similarity 86.4%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
 |||| |||| |||| |||| ||||
 Db 1 TGACTGTGAANGTTCCAGATGA 22

RESULT 10
 AX036944 22 bp DNA PAT 16-NOV-2000
 LOCUS
 DEFINITION Sequence 1 from Patent FR2790955.
 ACCESSION AX036944
 VERSION AX036944.1 GI:11226372
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Carpentier,A.

JOURNAL Patent: FR 2790955-A 1 22-SEP-2000;
 FEATURES ASSIST PUBL HOPITAUX DE PARIS (FR)
 source Location/Qualifiers
 1. 22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="oligodesoxynucleotide"
 BASE COUNT 7 a 1 c 8 g 6 t
 ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 22;
 Best Local Similarity 86.4%; Pred. No. 78;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
 |||| |||| |||| |||| ||||
 Db 1 TGACTGTGAAGTTAGATGA 22

RESULT 11
 AX036952 22 bp DNA PAT 16-NOV-2000
 LOCUS
 DEFINITION Sequence 9 from Patent FR2790955.
 ACCESSION AX036952
 VERSION AX036952.1 GI:11226380
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Carpentier,A.
 JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
 ASSIST PUBL HOPITAUX DE PARIS (FR)
 FEATURES
 source Location/Qualifiers
 1. 22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="oligodesoxynucleotide"
 BASE COUNT 7 a 2 c 6 g 7 t
 ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 22;
 Best Local Similarity 86.4%; Pred. No. 78;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
 |||| |||| |||| |||| ||||
 Db 1 TGACTGTGAACGTTATAGATGA 22

RESULT 12
 AF025951/c 2079 bp mRNA INV 26-OCT-1997
 LOCUS Dictyostellium discoideum heat-shock cognate protein 70 (hsc70)
 DEFINITION mRNA, complete cds.
 ACCESSION AF025951
 VERSION AF025951.1 GI:2564919
 KEYWORDS
 SOURCE Dictyostellium discoideum.
 ORGANISM Dictyostellium discoideum
 REFERENCE 1 (bases 1 to 2079)
 AUTHORS Boves,H., Mintert,U., Dittrich,W., Faix,J. and Gerisch,G.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1997) Cellbiology, Max-Planck-Institute of
 Blochemistry, Am Klopferspitz 18a, Martinsried 82152, Germany
 FEATURES
 source Location/Qualifiers
 1. 2079
 /organism="Dictyostellium discoideum"
 /strain="AX3"
 /db_xref="taxon:44689"

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/cell_type="amoeba"
1. .2079
/gene="hsc70"
CDS
123. .2021
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/note="chaperone; localized to filopodias and cortex;
hsc70"
/codon_start=1
/product="heat-shock cognate protein 70"
/protein_id="AA881865.1"
/db_xref="GI:2564920"
/translation="MSSSIGIDLTGTYSCVGMQNDRVEIANDQGNRTTPSYAFNE
TERLIDAAKNQVMTNPITFQAKRLIGRKFSDPVIQSDMKHWPFKVIAKEDGKPHL
OVFEKGEVKTSPFEEVSSVLLKMKETAAYLCKTINNNAVITVPAYENDSOROATKDA
GATAKNVORINEPTAAAIAYGLEKSGOERNILFDLGGTFDVSLLTIETGCVFEV
NATAGTHLGGEDFNRNLVNHVFDEPKRHKHDKLMTNQRHRLRACERAKRTLSS
AQAISIDSLFEGIDFYTSITRAFBEELCADLFRGLDPVKLDSKDKDKKTIHEIV
LVGSTRIPKVOQLQOHFNGELNKSINPDEAVAYGAQAAILNSNEGAKVADILL
LDVAPLSMGLTAGGVTTLIPRNTTIPCKKNOTFTSYSDNQTGVLVQVYVEGERAMTR
DNLLCKFELTNPAPRGVPOIEVTFDIDANGILNVAEDKSTGNKHKITITNDKGR
LTAQTEKMYKDAEMFKAQDEAREVVEKSKNLENYAVTVRSRTKDKKIAAKLSKEDR
KTVEEKSDAEAINLWLANDSATKEEYKAMKDLAVCSPIISKYVGQGGNGENPFGSA
KTTEEDLD"
BASE COUNT      682 a   459 c   372 g   566 t
ORIGIN
Query Match      78.2%; Score 17.2; DB 5; Length 2079;
Best Local Similarity 86.4%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| ||| ||| |||
Db 1957 TGACCGTAAACTTTAGAGATGA 1936

RESULT 13
AC079157 111234 bp DNA PRI 01-NOV-2000
LOCUS
DEFINITION Homo sapiens clone RP11-1285C3, complete sequence.
AC079157
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Waterston, R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 111234)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
REFERENCE
2 (bases 1 to 111234)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
REFERENCE
3 (bases 1 to 111234)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
REFERENCE
3 (bases 1 to 111234)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
Submitted (01-NOV-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Nov 1, 2000 this sequence version replaced gi:9910107.
Center project name: H.NH1285C03.
FEATURES
Location/Qualifiers
1. .111234
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-1285C3"
BASE COUNT      28606 a   22473 c   24546 g   35609 t
ORIGIN
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Query Match      76.4%; Score 16.8; DB 88; Length 111234;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 gaccgtgaacgttcgagatg 21
||||| ||| ||| ||| |||
Db 30683 GACCATGAAGCTGGGAGATG 30702

RESULT 14
AC073123 159072 bp DNA HTG 30-AUG-2000
LOCUS
DEFINITION Homo sapiens chromosome RPCI-11 clone RP11-614N3, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
AC073123
ACCESSION
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Waterston, R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 159072)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
REFERENCE
2 (bases 1 to 159072)
Waterston, R.H.
Direct Submission
TITLE
AUTHORS
JOURNAL
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 30, 2000 this sequence version replaced gi:9690415.
COMMENT
```

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0614N03
----- Summary Statistics -----
Sequencing vector: M13; 66%
Chemistry: Dye-primer ET; 66% of reads
Chemistry: Dye-terminator Big Dye; 34% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154864 bases at least Q40
Consensus quality: 156402 bases at least Q30
Consensus quality: 157217 bases at least Q20
Insert size: 162000; agarose-fp
Quality coverage: 8.21 in Q20 bases; agarose-fp
Quality coverage: 8.38 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1142: contig of 1142 bp in length
* 1143 1242: gap of unknown length
* 1243 3083: contig of 1841 bp in length
* 3084 3183: gap of unknown length
* 3184 6171: contig of 2988 bp in length
* 6172 6271: gap of unknown length
* 6272 14837: contig of 8566 bp in length
* 14838 14937: gap of unknown length
* 14938 22486: contig of 7549 bp in length
* 22487 22586: gap of unknown length
* 22587 38878: contig of 16292 bp in length
```

```

* 38879 38978: gap of unknown length
* 59379 59370: contig of 20392 bp in length
* 59371 59470: gap of unknown length
* 59471 88712: contig of 29242 bp in length
* 88713 88812: gap of unknown length
* 88813 159072: contig of 70260 bp in length.

```

FEATURES

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source
1. .159072
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="RPC1-11"
/clone="RP11-614N3"
1. .1142
/note="assembly_name:Contig11"
misc_feature 1243..3083
/note="assembly_name:Contig12"
misc_feature 3184..6171
/note="assembly_name:Contig13"
misc_feature 6272..14837
/note="assembly_name:Contig14"
misc_feature 14938..22486
/note="assembly_name:Contig15"
misc_feature 22587..38878
/note="assembly_name:Contig16"
misc_feature 38979..59370
/note="assembly_name:Contig17"
misc_feature 59471..88712
/note="assembly_name:Contig18"
misc_feature 88813..159072
/note="assembly_name:Contig19
clone_end:SP6
vector_side:left"

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```

BASE COUNT 48118 a 31947 c 32162 g 46044 t 801 others
ORIGIN

```

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Query Match 76.4%; Score 16.8; DB 74; Length 159072;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 gaccgtgaacgttcgagatg 21
|||||

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Db 82620 GACCATGAACGTGCGAGATG 82639

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RESULT 15

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AC073123/c AC073123 159072 bp DNA HTG 30-AUG-2000
LOCUS Homo sapiens chromosome RPC1-11 clone RP11-614N3, WORKING DRAFT
DEFINITION SQUENCE, 9 unordered pieces.

```

```

ACCESSION AC073123
VERSION AC073123.6 GI:9945292
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.

```

ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159072)

```

AUTHORS

```

TITLE Waterston, R.H.
JOURNAL Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

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COMMENT On Aug 30, 2000 this sequence version replaced gi:9690415.

```

```

----- Genome Center -----

```

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml

```

```

----- Project Information -----
Center project name: H.NH0614N03
----- Summary Statistics -----
Sequencing vector: pBluescript, 34%
Chemistry: Dye-terminator Big Dye; 34% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154864 bases at least Q40
Consensus quality: 156402 bases at least Q30
Consensus quality: 157217 bases at least Q20
Insert size: 162000; agarose-fp
Quality coverage: 8.21 in Q20 bases; agarose-fp
Quality coverage: 8.38 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 1142: contig of 1142 bp in length
* 1143 1242: gap of unknown length
* 1243 3083: contig of 1841 bp in length
* 3084 3183: gap of unknown length
* 3184 6171: contig of 2988 bp in length
* 6172 6271: gap of unknown length
* 6272 14837: contig of 8566 bp in length
* 14838 14937: gap of unknown length
* 14938 22486: contig of 7549 bp in length
* 22487 22586: gap of unknown length
* 22587 38878: contig of 16292 bp in length
* 38879 38978: gap of unknown length
* 38979 59370: contig of 20392 bp in length
* 59371 59470: gap of unknown length
* 59471 88712: contig of 29242 bp in length
* 88713 88812: gap of unknown length
* 88813 159072: contig of 70260 bp in length.

```

FEATURES

source

```

1. .159072
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="RPC1-11"
/clone="RP11-614N3"
1. .1142
/note="assembly_name:Contig11"
misc_feature 1243..3083
/note="assembly_name:Contig12"
misc_feature 3184..6171
/note="assembly_name:Contig13"
misc_feature 6272..14837
/note="assembly_name:Contig14"
misc_feature 14938..22486
/note="assembly_name:Contig15"
misc_feature 22587..38878
/note="assembly_name:Contig16"
misc_feature 38979..59370
/note="assembly_name:Contig17"
misc_feature 59471..88712
/note="assembly_name:Contig18"
misc_feature 88813..159072
/note="assembly_name:Contig19
clone_end:SP6
vector_side:left"

```

```

BASE COUNT 48118 a 31947 c 32162 g 46044 t 801 others
ORIGIN

```

```

Query Match 76.4%; Score 16.8; DB 74; Length 159072;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;

```


Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gaccgtgaacgttcgagatg 21

||||||| ||| |||||

Db 28703 GACCGTGACCTTCCAGATG 28684

Search completed: October 9, 2001, 16:18:29
Job time: 2479 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:11 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: us-09-713-136-2
Perfect score: 22
Sequence: 1 tgaccgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*
- 12: gb_est12.*
- 13: gb_est13.*
- 14: gb_est14.*
- 15: gb_est15.*
- 16: gb_est16.*
- 17: gb_est17.*
- 18: gb_est18.*
- 19: gb_est19.*
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- 21: gb_est21.*
- 22: gb_est22.*
- 23: gb_est23.*
- 24: gb_est24.*
- 25: gb_est25.*
- 26: gb_est26.*
- 27: gb_est27.*
- 28: gb_est28.*
- 29: gb_est29.*
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- 31: gb_est31.*
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- 36: gb_est36.*
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- 45: gb_est45.*
- 46: gb_est46.*
- 47: gb_est47.*

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- 45: em_esthum11.*
- 46: em_esthum12.*
- 47: em_esthum13.*
- 48: em_esthum14.*
- 49: em_esthum15.*
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- 56: em_esthum22.*
- 57: em_esthum23.*
- 58: em_esthum24.*
- 59: em_esthum25.*
- 60: em_esthum26.*
- 61: em_esthum27.*
- 62: em_esthum28.*
- 63: em_estin1.*
- 64: em_estin2.*
- 65: em_estin3.*
- 66: em_estin4.*
- 67: em_estin5.*
- 68: em_estom1.*
- 69: em_estom2.*
- 70: em_estov1.*
- 71: em_estov2.*
- 72: em_estpl1.*
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- 76: em_estpl5.*
- 77: em_estpl6.*
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- 80: em_estpl9.*
- 81: em_estpl10.*
- 82: em_estro1.*
- 83: em_estro2.*
- 84: em_estro3.*
- 85: em_estro4.*
- 86: em_estro5.*
- 87: em_estro6.*
- 88: em_estro7.*
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- 91: em_estro10.*
- 92: em_estro11.*
- 93: em_estro12.*
- 94: em_estro13.*
- 95: em_estro14.*
- 96: em_estro15.*
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- 98: em_estro17.*
- 99: em_estro18.*
- 100: em_estro19.*
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- 102: gb_est25.*
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- 106: gb_est29.*
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- 108: gb_est31.*
- 109: gb_est32.*
- 110: gb_est41.*
- 111: gb_est42.*
- 112: gb_est43.*
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- 114: gb_est45.*
- 115: gb_est46.*
- 116: gb_est47.*

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247: gb_gss30:*
248: gb_gss31:*
249: gb_gss32:*
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251: gb_gss34:*
252: em_gss_inv4:*
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254: em_gss_inv6:*
255: em_gss_inv7:*
256: em_gss_inv8:*
257: gb_gss35:*
258: gb_gss36:*
259: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig, D.O.
Expressed sequences from conidial, mycelial, and sexual stages of *Neurospora crassa*
Fungal Genet. Biol. 21, 348-363 (1997)
97435549
Contact: Natvig, D.O./Nelson, M.A.
Department of Biology
University of New Mexico
Casteretter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu
Deposited in GDB at the National Center for Genome Resources with accession GDB:S1147294
Seq primer: F3.

FEATURES

source

Location/Qualifiers
1..531
/organism="Neurospora crassa"
/strain="74-OR23-IV A (FGSC 2489)"
/db_xref="taxon:5141"
/clone="NM6H2"
/clone_lib="Mycelial"
/sex="Mating type A"
/tissue_type="Mycelium"
/dev_stage="Mycelium"
/lab_host="E. coli"

/note=vector: pBluescript SK (-); Site1: EcoR I; Site2: Xho I; 2% sucrose for 24 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA).
BASE COUNT 105 a 198 c 130 g 98 t
ORIGIN

Query Match 79.1% Score 17.4; DB 13; Length 531;
Best Local Similarity 94.7%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgaga 19
|||||
Db 192 TCACCGTGAACGTCGCGA 210

RESULT

2

AU053757/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1..236
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLJ623"
/clone_lib="Dictyostellium discoideum SL (H. Urushihara)"
/dev_stage="slug"

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17.4	79.1	531	13	AA898422	NC6H2T3
2	17.2	78.2	236	107	AU053757	
3	17.2	78.2	254	107	AU053032	
4	17.2	78.2	265	107	AU054169	
5	17.2	78.2	270	107	AU053754	
6	17.2	78.2	340	107	AU040059	
7	17.2	78.2	371	107	AU039239	
8	17.2	78.2	457	107	AU034234	
9	17.2	78.2	474	107	AU052381	
10	17.2	78.2	509	107	AU039788	
11	17.2	78.2	513	107	AU034515	
12	17.2	78.2	520	107	AU039823	
13	17.2	78.2	669	156	C22959	
14	17.2	78.2	697	174	BG138405	
15	17.2	78.2	699	107	AU034932	
16	17.2	78.2	714	107	AU033417	
17	17.2	78.2	985	139	BE741976	
18	16.8	76.4	526	245	AZ501799	
19	16.4	74.5	360	26	AV192496	
20	16.4	74.5	532	226	AQ270413	
21	16.2	73.6	138	115	AW427585	
22	16.2	73.6	229	107	AU053807	
23	16.2	73.6	310	167	BE406273	
24	16.2	73.6	323	148	BF386464	
25	16.2	73.6	352	137	BE586027	
26	16.2	73.6	398	167	BE428418	
27	16.2	73.6	423	234	AQ815396	
28	16.2	73.6	438	148	BF428883	
29	16.2	73.6	439	229	AQ492115	
30	16.2	73.6	463	13	AA864966	
31	16.2	73.6	474	167	BE419241	
32	16.2	73.6	477	149	BF475131	
33	16.2	73.6	497	229	AQ492226	
34	16.2	73.6	507	229	AQ460797	
35	16.2	73.6	517	235	AQ874041	
36	16.2	73.6	519	229	AQ501248	
37	16.2	73.6	519	235	AQ875722	
38	16.2	73.6	521	229	AQ501128	
39	16.2	73.6	523	229	AQ500252	
40	16.2	73.6	525	235	AQ875251	
41	16.2	73.6	526	249	AZ764668	
42	16.2	73.6	527	167	BE429501	
43	16.2	73.6	538	235	AQ876357	
44	16.2	73.6	542	235	AQ873145	
45	16.2	73.6	542	242	AZ385850	

ALIGNMENTS

RESULT	1
AA898422	
LOCUS	NC6H2T3 Mycelial Neurospora crassa cDNA clone NM6H2 5' end, mRNA
DEFINITION	sequence.
ACCESSION	AA898422
VERSION	AA898422.1 GI:3044855
KEYWORDS	EST.
SOURCE	Neurospora crassa.
ORGANISM	Neurospora crassa
REFERENCE	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
AUTHORS	1 (bases 1 to 531) Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L., Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueves, E., Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S., Trujillo, R.,

BASE COUNT 91 a 42 c 36 g 64 t 3 others
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 236;
Best Local Similarity 86.4%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||| ||||| |||||
Db 104 TGACCGTAACCTTTAGAGATGA 83

RESULT 3
AU053032/c 254 bp mRNA EST 28-APR-1999
LOCUS AU053032 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
DEFINITION AU053032 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLF551, mRNA sequence.
ACCESSION AU053032
VERSION AU053032.1 GI:4701515
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 254)
AUTHORS Yoshino.R., Morio.T. and Tanaka.Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1. .254
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLF551"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 103 a 45 c 40 g 66 t
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 254;
Best Local Similarity 86.4%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||| ||||| |||||
Db 127 TGACCGTAACCTTTAGAGATGA 106

RESULT 4
AU054169/c 265 bp mRNA EST 28-APR-1999
LOCUS AU054169 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
DEFINITION AU054169 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLK852, mRNA sequence.
ACCESSION AU054169
VERSION AU054169.1 GI:4702650
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 265)
AUTHORS Yoshino.R., Morio.T. and Tanaka.Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1. .265
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLK852"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 108 a 48 c 42 g 67 t
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 265;
Best Local Similarity 86.4%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||| ||||| |||||
Db 134 TGACCGTAACCTTTAGAGATGA 113

RESULT 5
AU053754/c 270 bp mRNA EST 28-APR-1999
LOCUS AU053754 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
DEFINITION AU053754 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLJ617, mRNA sequence.
ACCESSION AU053754
VERSION AU053754.1 GI:4702236
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum.
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 270)
AUTHORS Yoshino.R., Morio.T. and Tanaka.Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1. .270
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLJ617"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 111 a 48 c 43 g 68 t
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 270;
Best Local Similarity 86.4%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||||| ||||| |||||
Db 138 TGACCGTAACCTTTAGAGATGA 117

RESULT 6
AU040059/c 340 bp mRNA EST 29-MAR-1999
LOCUS AU040059 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
DEFINITION AU040059 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLA335, mRNA sequence.
ACCESSION AU040059
VERSION AU040059.1 GI:4009299

```

KEYWORDS`
SOURCE Dictyostellium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

REFERENCE
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
        Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
        Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
TITLE The Dictyostellium developmental cDNA project: generation and
        analysis of expressed sequence tags from the first-finger stage of
        development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
        Institute of Biological Sciences
        University of Tsukuba
        3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
        Email: d402hu@sakura.cc.tsukuba.ac.jp
        PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.

FEATURES
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/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLA335"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 136 a 67 c 55 g 82 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 340;
Best Local Similarity 86.4%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 211 TGACCGTAACCTTTAGAGATGA 190

RESULT 7
LOCUS AU039239 371 bp mRNA EST 29-MAR-1999
DEFINITION AU039239 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
        discoideum cDNA clone SLH241, mRNA sequence.
ACCESSION AU039239
VERSION AU039239.1 GI:4008220
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
        Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
        Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
        The Dictyostellium developmental cDNA project: generation and
        analysis of expressed sequence tags from the first-finger stage of
        development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
        Institute of Biological Sciences
        University of Tsukuba
        3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
        Email: d402hu@sakura.cc.tsukuba.ac.jp
        PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.
        Location/Qualifiers
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/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLH241"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"

KEYWORDS`
SOURCE Dictyostellium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

REFERENCE
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
        Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
        Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
TITLE The Dictyostellium developmental cDNA project: generation and
        analysis of expressed sequence tags from the first-finger stage of
        development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT Contact: Hideko Urushihara
        Institute of Biological Sciences
        University of Tsukuba
        3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
        Email: d402hu@sakura.cc.tsukuba.ac.jp
        PROJECT = 'Dictyostellium discoideum cDNA project in Japan'.
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/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLH241"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"

FEATURES
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SLC303"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 209 a 77 c 70 g 101 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 457;
Best Local Similarity 86.4%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 282 TGACCGTAACCTTTAGAGATGA 261

RESULT 9
LOCUS AU052381 474 bp mRNA EST 28-APR-1999
DEFINITION AU052381 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
        discoideum cDNA clone SLD225, mRNA sequence.
ACCESSION AU052381
VERSION AU052381.1 GI:4700865
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

```


COMMENT

Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
Location/Qualifiers

FEATURES

source
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLG510"
/clone_lib="dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
211 a 101 c 90 g 118 t

BASE COUNT
ORIGIN

Query Match 78.2%; Score 17.2; DB 107; Length 520;
Best Local Similarity 86.4%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 393 TGACCGTAACTTTAGAGATGA 372

RESULT 13

C22959/c
LOCUS C22959 669 bp mRNA EST 02-APR-1997
DEFINITION Dictyostelium discoideum FC (H.Urushihara) Dictyostelium
discoideum cDNA clone FC-AG10, mRNA sequence.

ACCESSION

C22959

VERSION

C22959.1

KEYWORDS

EST

SOURCE

Dictyostelium discoideum.

ORGANISM

Dictyostelium discoideum.

REFERENCE

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

AUTHORS

1 (bases 1 to 669)

TITLE

Shimizu, H. and Urushihara, H.

JOURNAL

Sexual-cDNA in CSM

COMMENT

Unpublished (1997)

Contact: Hideko Urushihara

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University of Tsukuba

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Email: d402huesakura.cc.tsukuba.ac.jp.

FEATURES

source

1..669

/organism="Dictyostelium discoideum"

/strain="KAX3"

/db_xref="taxon:44689"

/clone="FC-AG10"

/clone_lib="Dictyostelium discoideum FC (H.Urushihara)"

270 a 131 c 114 g 154 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 78.2%; Score 17.2; DB 156; Length 669;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 522 TGACCGTAACTTTAGAGATGA 501

RESULT 14

BG138405/c
LOCUS BG138405 697 bp mRNA EST 31-JAN-2001
DEFINITION ES7478847 wild tomato pollen Lycopersicon pennellii cDNA clone
CLPP9118 5' sequence, mRNA sequence.

ACCESSION

BG138405

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon pennellii.

Lycopersicon pennellii.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 697)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,

Hansen, C., Ronning, C. and Tanksley, S.

Generation of ESTs from wild tomato (L. pennellii) pollen

Unpublished (2001)

Contact: CUCI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES

source

1..697

/organism="Lycopersicon pennellii"

/cultivar="TA56"

/db_xref="taxon:28526"

/clone="clpp9118"

/clone_lib="wild tomato pollen"

/tissue_type="pollen"

/dev_stage="pollen collected from open flowers"

/lab_host="SOLR"

/note="vector: paluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Pollen was collected from open flowers from

L.pennellii TA56, and stored at -80 C until library

construction."

240 a 134 c 168 g 155 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 78.2%; Score 17.2; DB 174; Length 697;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
||||| ||| || |||||
Db 627 TGACGTGAAAGTTTGAGATGA 606

RESULT 15

AU034932/c
LOCUS AU034932 699 bp mRNA EST 28-APR-1999
DEFINITION AU034932 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLE359, mRNA sequence.

ACCESSION

AU034932

VERSION

AU034932.1

KEYWORDS

EST

SOURCE

Dictyostelium discoideum.

Dictyostelium discoideum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

1 (bases 1 to 699)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,

Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

The Dictyostelium developmental cDNA project: generation and

analysis of expressed sequence tags from the first-finger stage of

development

DNA Res. 5 (6), 335-340 (1998)

99156227

Contact: Hideko Urushihara

Institute of Biological Sciences

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3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan

Email: d402huesakura.cc.tsukuba.ac.jp

PROJECT = 'Dictyostelium discoideum cDNA project in Japan'

POLYA=No.

Location/Qualifiers


```

source      1. .699
            /organism="Dictyostellium discoideum"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="SLE359"
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            /dev_stage="slug"
BASE COUNT  267 a 145 c 120 g 167 t
ORIGIN

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Query Match      78.2%; Score 17.2; DB 107; Length 699;
Best Local Similarity 86.4%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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    ||||| ||||| |||||
Db  567 TGACCGTAACCTTAGAGATGA 546

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Search completed: October 9, 2001, 18:20:13
Job time: 9783 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:47 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-2
Perfect score: 22
Sequence: 1 tgaccggaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SID8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID8/gcgdata/geneseq/geneseq/NA1985.DAT.*
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8: /SID8/gcgdata/geneseq/geneseq/NA1987.DAT.*
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14: /SID8/gcgdata/geneseq/geneseq/NA1993.DAT.*
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16: /SID8/gcgdata/geneseq/geneseq/NA1995.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	22	100.0	22	AAV80105	Oligo used in expe
2	22	100.0	22	AAV80096	Immunomodulatory o
3	22	100.0	22	AAA38066	Immunostimulatory
4	22	100.0	22	AAV77041	Immunostimulatory
5	20.4	92.7	22	AAV32079	Nucleotide sequenc
6	20.4	92.7	22	AAV36624	ISS-ODN DY1018 nuc
7	20.4	92.7	22	AAV80097	Immunomodulatory o
8	20.4	92.7	22	AAV80102	Immunomodulatory o
9	20.4	92.7	22	AAV80103	Immunomodulatory o
10	20.4	92.7	22	AAC64051	Immunostimulatory
11	20.4	92.7	22	AAA96253	Sequence of a stab

12	20.4	92.7	22	AAA90458	CpG adjuvant oligo
13	20.4	92.7	22	AAV14467	Immunostimulatory
14	20.4	92.7	22	AAA38065	Immunostimulatory
15	20.4	92.7	22	AAA38071	Immunostimulatory
16	20.4	92.7	22	AAA38072	Immunostimulatory
17	20.4	92.7	22	AZ55876	Immunomodulatory o
18	20.4	92.7	22	AAV77040	Immunomodulatory o
19	20.4	92.7	22	AAV29800	Cholera toxin immu
20	20.4	92.7	22	AAC82107	Oligonucleotide OD
21	20.4	92.7	22	AAV2377	CG motif and CFA c
22	19.6	89.1	22	AAV77046	Immunostimulatory
23	19.4	88.2	22	AZ55880	Immunomodulatory o
24	18.8	85.5	22	AAV80099	Immunomodulatory o
25	18.8	85.5	22	AAV80101	Immunomodulatory o
26	18.8	85.5	22	AAV6254	Sequence of a stab
27	18.8	85.5	22	AAA38068	Immunostimulatory
28	18.8	85.5	22	AAA38070	Immunostimulatory
29	18.8	85.5	22	AAV77043	Immunostimulatory
30	18.8	85.5	22	AAV77047	Immunostimulatory
31	18.4	83.6	22	AZ55881	Immunomodulatory o
32	18	81.8	22	AAV77045	Immunostimulatory
33	17.8	80.9	22	AZ55877	Immunomodulatory o
34	17.2	78.2	22	AAV32080	Nucleotide sequenc
35	17.2	78.2	22	AAV36625	ISS-ODN mutant DY1
36	17.2	78.2	22	AAV55790	Immunostimulatory
37	17.2	78.2	22	AAV55797	Immunostimulatory
38	17.2	78.2	22	AAV55788	Immunostimulatory
39	17.2	78.2	22	AAV80106	Oligo used in expe
40	17.2	78.2	22	AAV80104	Oligo used in expe
41	17.2	78.2	22	AAC64052	Non-CpG control ph
42	17.2	78.2	22	AAV6252	Sequence of a stab
43	17.2	78.2	22	AAV6260	Sequence of a stab
44	17.2	78.2	22	AAA90459	CpG adjuvant oligo
45	17.2	78.2	22	AAA92378	CG motif and CFA c

ALIGNMENTS

RESULT 1
AAV80105/c
ID AAV80105 standard; DNA; 22 BP.
XX
XX AAV80105;
XX
XX 12-MAR-1999 (first entry)
XX
XX Oligo used in experiments for stimulation of cytokine production.
XX
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.
XX
XX Synthetic.
XX
XX W09855495-A2.
XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-US11578.
XX
XX 06-JUN-1997; 97US-0048793.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Dina D, Roman M, Schwartz D;
XX
XX WPI; 1999-059898/05.
XX
XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX
PS

Example 1; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AAGTTCC, AAGTTCCG,
 CC GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
 CC oligonucleotides that were tested for immunostimulatory activity. These
 CC were used in experiments for the stimulation of cytokine production and
 CC were found to lack immunostimulatory activity. The invention provides
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22

|||||

Db 22 TGACCGTGAACGTTCCGAGATGA 1

RESULT 2

AAV80096

ID AAV80096 standard; DNA; 22 BP.

XX AAV80096;

XX

DT 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX

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CC GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22

|||||

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 3

AAA38066

ID AAA38066 standard; DNA; 22 BP.

XX AAA38066;

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XX

XX Anti-HIV composition comprises immunostimulatory polynucleotides and
 CC HIV glycoprotein gp120 useful for modulating, stimulating an immune
 CC response against HIV in an HIV infected individual
 CC Disclosure: Page 16; 65pp; English.
 CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunostimulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies of gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual

CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 4

AAAF77041

ID AAF77041 standard; DNA; 22 BP.

XX

AC AAF77041;

XX

DT 15-MAY-2001 (first entry)

XX Immunostimulatory DNA #1.

DE Modulate; immune; antigen; immunostimulatory; ds.

KW Synthetic.

OS

XX WO200112223-A2.

PN

XX

XX

PD 22-FEB-2001.

XX

PF 18-AUG-2000; 2000WO-US22835.

XX

PR 19-AUG-1999; 99US-0149768.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

PI Van Nest G;

XX

DR WPI; 2001-211136/21.

XX

PT Modulating immune response to a second antigen in humans involves administering an immunostimulatory polynucleotide comprising an immunostimulatory sequence and a first antigen -

XX

PS Disclosure; Page 15; 63pp; English.

XX

CC The present invention relates to modulating an immune response to a second antigen in an individual, involving administering to the individual an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 22; DB 22; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 5

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX

DT 09-SEP-1998 (first entry)

XX

DE Nucleotide sequence of DY1018.

XX DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody; immunisation; anaphylaxis; IgE; retinopathies; ss.

OS synthetic.

FX Key Location/Qualifiers

FT modified_base 1..22

FT /*tag= a

PN /note= "phosphothioate backbone"

XX

PN WO9816247-A1.

XX

PD 23-APR-1998.

XX

PF 09-OCT-1997; 97WO-US19004.

XX

PR 11-OCT-1996; 96US-0028118.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Carson DA, Raz E, Roman M;

XX

DR WPI; 1998-261028/23.

XX

PT New immunomodulatory compositions - comprising an antigen conjugated to a polynucleotide that contains an immunostimulatory sequence

XX

PS Example 1; Page 36; 69pp; English.

XX

CC This is the nucleotide sequence of DY1018, which is conjugated to beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM), which comprises an antigen conjugated to a polynucleotide (PN) that contains at least one immunostimulatory nucleotide sequence (ISS). The conjugate synergistically boost the magnitude of the host immune response against an antigen to a level greater than the host immune response to either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM conjugates are particularly acute during the important early phase of the host immune response to an antigen. The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular (Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE production in response to the antigen challenge. The conjugates can also be used to combat pathogenic infection and to stimulate CC therapeutic angiogenesis to treat conditions in which localised blood flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match

Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgaccgtgaacgttcgagatga 22

RESULT 6

AAAX36624

ID AAX36624 standard; DNA; 22 BP.

XX

AC AAX36624;

XX

DT 09-JUL-1999 (first entry)

XX

DE ISS-ODN DY1018 nucleotide sequence.

XX

KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;

KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

PN 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DV1018 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypersensitivity, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgaccgtgaacgttcgagatga 22

||||| ||||||| |||||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 7

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX Synthetic.

PN WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D. Roman M. Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AAGGTTC, AAGGTTCG,
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgaccgtgaacgttcgagatga 22

||||| ||||||| |||||||

Db 1 tgactgtgaacgttcgagatga 22

RESULT 8

AAV80102

ID AAV80102 standard; DNA; 22 BP.

XX AAV80102;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 11

FT /*tag= a

FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX

PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Dina D, Roman M, Schwartz D;
 XX
 DR WPI; 1999-059898/05.
 XX

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX

PS Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.21;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgacgtgaacgttcgagatga 22
 |||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 9
 AAV80103
 ID AAV80103 standard; DNA; 22 BP.

AC AAV80103;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT modified_base 11

FT /*tag= a
 FT /note= *5-bromocytosine*

XX W09B55495-A2.

PN 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

PR 06-JUN-1997; 97US-0048793.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

DR WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX

PS Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.21;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgacgtgaacgttcgagatga 22
 |||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 10

AAC64051
 ID AAC64051 standard; DNA; 22 BP.

AC AAC64051;

XX 15-FEB-2001 (first entry)

XX Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
 KW enhanced antigen presentation; antigen-presenting cell; APC;
 KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
 KW vaccine; ss.

OS Synthetic.

XX WO2000062787-A1.

XX 26-OCT-2000.

XX 11-APR-2000; 2000WO-US09664.

XX 15-APR-1999; 99US-0292278.

XX (REGC) UNIV CALIFORNIA.

PI Raz E, Martin-Orozco E;

XX WPI; 2000-679548/66.

XX Enhancing antigen-presentation capabilities of T-cells for cancer
 PT immunotherapy, by contacting cells with an immunostimulatory
 PT oligonucleotide

XX PS Example 1; Page 18; 42pp; English.

XX CC The invention relates to a method of inducing activation of T-cells

CC to respond to an antigen, comprising contacting antigen-presenting cells

CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs

CC thus treated have enhanced antigen presenting capabilities compared to

CC antigen-activated APCs. APCs with enhanced antigen-presentation

CC capabilities then present the antigen to T-cells. The method is useful

CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour

CC antigen presenting capacity of tumour cells, thereby inducing T-cell

CC activation, and is therefore useful for treating tumours. Additionally,

CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.

CC ISS-ODN treated APCs are induced to take up antigen through upregulation

CC of Fc-receptor expression, to present antigen through upregulation of

CC major histocompatibility complex (MHC) Class I and II expression and

CC CD4 expression, to produce co-stimulatory factors (B7 and CD40), to

CC provide cell-to-cell adhesion through upregulation of intercellular

CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory

CC cytokine production, all at levels greater than that achieved through

CC contact of APC with antigen alone. The present sequence represents

CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the

XX CC invention.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAA96253

ID AAA96253 standard; DNA; 22 BP.

XX AC AAA96253;

XX 08-FEB-2001 (first entry)

XX Sequence of a stabilised oligonucleotide with antitumour activity.

DE Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;

KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.

XX Synthetic.

XX WO200056342-A2.

XX 28-SEP-2000.

XX 17-MAR-2000; 2000WO-FR00676.

XX 19-MAR-1999; 99FR-0003433.

XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX Carpentier A;

XX WPI; 2000-602192/57.

XX Use of stabilised oligonucleotides as antitumor agents, particularly

PT against nervous system tumors, have optimal activity and are not toxic

PT -

XX Example 2; Page 16; 57pp; French.

XX The present sequence represents a stabilised oligonucleotide which has

CC antitumour activity. The oligonucleotide comprises an octamer motif

CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where

CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are

CC immunostimulatory, and are not toxic. They may be adapted for use in

CC animals or humans. The stabilised oligonucleotides are used for

CC treating tumours, of any type and any degree of anaplasia, particularly

CC human tumours in the peripheral or central nervous systems, specifically

CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.21;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAA90458

ID AAA90458 standard; DNA; 22 BP.

XX AC AAA90458;

XX 10-JAN-2001 (first entry)

XX CpG adjuvant oligonucleotide, SEQ ID NO:19.

DE CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;

KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;

KW viral infection; bacterial infection; parasitic infection; HCV; HBV;

KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;

KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;

KW rabies virus; cholera; diphtheria; tetanus; pertussis;

KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.

XX Synthetic.

XX WO200050006-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-US03331.

XX 26-FEB-1999; 99US-0121858.

XX 29-JUL-1999; 99US-0146391.

XX 28-OCT-1999; 99US-0161997.

XX (CHIR) CHIRON CORP.

XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Ugoczoli M, Singh M;

PI Barackman J;

XX WPI; 2000-587123/55.

XX Microemulsion having an adsorbent surface comprising a microdroplet

PT emulsion consisting of a metabolizable oil and an emulsifying agent

PT which is a detergent, useful as a vaccine to treat bacterial, viral,

PT and parasitic infection

XX Claim 17; Page 40; 95pp; English.

XX The invention relates to a microdroplet emulsion (microemulsion) with an

CC adsorbent surface, and which comprises a metabolizable oil and an

CC emulsifying agent (a detergent). It also relates to a composition

CC comprising the microemulsion and a microparticle with an adsorbent

CC surface, where the microparticle comprises a polymer selected from a

CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a

CC polycaprolactone, a polyorthoester, a polyanhydride, and a

CC polycyanoacrylate, and a second detergent. The surface of the

CC microparticles efficiently adsorb biologically active macromolecules such
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,
 CC mediators of transcription or translation, metabolic intermediates and
 CC adjuvants. Additionally, a second biologically active molecule may be
 CC encapsulated within the microparticle. The microemulsion can be used in
 CC methods of immunising a host animal, particularly a human, against a
 CC viral, bacterial or parasitic infection, and in methods of increasing a
 CC Th1 immune response. The microemulsions (having the appropriate antigens
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif
 CC which are claimed for use as adjuvants in the compositions of the
 CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.21;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 13

AAA14467
 ID AAA14467 standard; DNA; 22 BP.

XX AAA14467;

XX 21-AUG-2000 (first entry)

XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.

XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
 KW secretory immunoglobulin A production; siGa: Th1 phenotype; ds.

XX Synthetic.

XX WO200020039-A1.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-US21203.

XX 05-OCT-1998; 98US-0167039.

XX (RECC) UNIV CALIFORNIA.

XX Raz E, Horner AA, Carson DA;

XX WPI; 2000-303647/26.

XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
 PT an antigen in a mammalian host through production of secretory
 PT immunoglobulin A.

XX Claim 8; Page 21; 64pp; English.

XX The invention relates to a method of inducing mucosal immunity to an
 CC antigen in a mammalian host, including the production of secretory
 CC immunoglobulin A (siGa). Immune protection in the mucosa (the principal
 CC site of entry of most foreign antigens) is mediated by mucosa-associated
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
 CC cell sub-populations. The primary immune response which characterises
 CC the induction of mucosal immunity to an antigen is siGa production by
 CC activated B-cells. The method comprises introducing an immunostimulatory

CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
 CC ISS-ODN includes a core nucleotide sequence. The core nucleotide
 CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A
 CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The
 CC level of siGa production induced in the host is at least 3 times the
 CC magnitude of siGa production achievable in response to introduction of
 CC antigen alone into the mucosal tissue and is equivalent or greater than
 CC the magnitude of siGa production achievable in response to introduction
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The
 CC host immune response is stimulated to antigen specific IgA production,
 CC biased towards the Th1 phenotype while antigen-induced IgE production is
 CC avoided. The adjuvant has little or no known toxicity in mammals and its
 CC efficacy is comparable to that of cholera toxin which is used as a
 CC mucosal adjuvant. The present sequence represents the immunostimulatory
 CC oligonucleotide DY1018.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.21;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 14

AAA38065
 ID AAA38065 standard; DNA; 22 BP.

XX AAA38065;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #1.

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KW development; ss.

XX Synthetic.

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual.

XX Claim 3; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or
CC stimulating a specific immune response against gp120 in an individual by
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC is also used for suppressing or delaying development of HIV infection in
CC an individual infected with HIV or an individual at risk of infection
CC with HIV, respectively. It is also used for treating an individual
CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.21;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
DB 1 tgactgtgaacgttcgagatga 22

RESULT 15

AAA38071
ID AAA38071 standard; DNA; 22 BP.

XX AC AAA38071;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX Immunostimulatory sequence: ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 11
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-Bromocytosine"

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT response against HIV in an HIV infected individual -
XX Disclosure; Page 17; 65pp; English.

XX The present invention relates to an immunostimulatory composition
CC comprising a human immunodeficiency virus (HIV) antigen, and an
CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC (ISS). This sequence represents an ISS that can be used in the
CC composition. An immunostimulatory composition which comprises a gp120
CC conjugated to an immunomodulatory polynucleotide, or is proximately
CC associated to it and not conjugated, is used for modulating or
CC stimulating a specific immune response against gp120 in an individual by
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection
CC with HIV, respectively. It is also used for treating an individual
CC infected with HIV in need of immune modulation.
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
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Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.21;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 tgactgtgaacgttcgagatga 22

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27	20.4	92.7	22	25	US-09-642-492-1
28	20.4	92.7	22	28	US-09-700-354-1
29	20.4	92.7	22	28	US-09-713-136-1
30	20.4	92.7	22	29	US-09-746-130-1
31	20.4	92.7	22	30	US-09-774-403-1
32	20.4	92.7	22	30	US-09-791-500-1
33	20.4	92.7	22	31	US-09-820-484-1
34	20.4	92.7	22	31	US-09-820-484-3
35	20.4	92.7	22	31	US-09-828-505-1
36	19.6	89.1	22	18	US-09-415-186-7
37	19.4	88.2	22	16	US-09-296-477-15
38	19.4	88.2	22	17	US-09-324-191A-5
39	19.4	88.2	22	25	US-09-642-492-7
40	19.4	88.2	22	28	US-09-713-136-7
41	18.8	85.5	22	1	PCT-US00-35064-2
42	18.8	85.5	22	1	PCT-US01-03029-2
43	18.8	85.5	22	1	PCT-US01-06034-4
44	18.8	85.5	22	1	PCT-US01-06034-5
45	18.8	85.5	22	31	US-09-828-505-2

Query Match 100.0%; Score 22; DB 25; Length 22;
Best Local Similarity 100.0%; Pred No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels

APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 8
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 9
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO

US-09-713-136-2
; Sequence 2, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 37782001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-2

Query Match 100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
DB 1 tgaccgtgaacgttcgagatga 22

RESULT 6
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
|||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 7
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal

; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 10
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE REFERENCE: 06510-18WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 11
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas

; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE REFERENCE: 06510-18WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
PCT-US01-11290-1
; Sequence 1, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
PCT-US01-14508-1
; Sequence 1, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji

;; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
;; TITLE OF INVENTION: Methods of Use Thereof
;; FILE REFERENCE: 06510/168WO1
;; CURRENT APPLICATION NUMBER: PCT/US01/14508
;; CURRENT FILING DATE: 2000-05-04
;; PRIOR FILING DATE: 60/262,321
;; PRIOR FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 60/202,274
;; PRIOR FILING DATE: 2000-05-05
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 22
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14
PCT-US99-21203-19
;; Sequence 19, Application PC/TUS9921203
;; GENERAL INFORMATION:
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
;; TITLE OF INVENTION: MUCOSAL IMMUNITY
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski L.L.P.
;; STREET: 865 S. Figueroa Street, 29th Floor
;; CITY: Los Angeles
;; STATE: CA
;; COUNTRY: US
;; ZIP: 90017
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US99/21203
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/927,120
;; FILING DATE: 05 September 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Berliner, Robert
;; REGISTRATION NUMBER: 20,121
;; REFERENCE/DOCKET NUMBER: 5555-188
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 213-892-9200
;; TELEFAX: 213-680-4518
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: non-coding oligonucleotides
PCT-US99-21203-19

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22
RESULT 15
US-08-927-120-19
;; Sequence 19, Application US/08927120
;; GENERAL INFORMATION:
;; APPLICANT: Raz, Eyal
;; TITLE OF INVENTION: IMMUNIZATION-FREE METHODS
;; TITLE OF INVENTION: FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING
;; TITLE OF INVENTION: INFLAMMATION IN A HOST
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: US
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,120
;; FILING DATE: 22-AUG-1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Taylor, Stacy L.
;; REGISTRATION NUMBER: 34,842
;; REFERENCE/DOCKET NUMBER: 07340/054001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-678-5070
;; TELEFAX: 619-678-5099
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: non-coding oligonucleotides
US-08-927-120-19

Query Match 92.7%; Score 20.4; DB 13; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
||||| ||||||| ||||||| |||||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

Search completed: October 9, 2001, 21:12:35
Job time: 20060 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:35:59 ; Search time 1391.6 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-713-136-2
Perfect score: 22
Sequence: 1 tgaccgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA, New: *
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
8: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	7 US-09-802-518-2	Sequence 2, Appli
2	22	100.0	22	7 US-09-802-359-2	Sequence 2, Appli
3	22	100.0	22	7 US-09-802-376-2	Sequence 2, Appli
4	20.4	92.7	22	7 US-09-802-518-1	Sequence 1, Appli
5	20.4	92.7	22	7 US-09-802-359-1	Sequence 1, Appli
6	20.4	92.7	22	7 US-09-802-376-1	Sequence 1, Appli
7	19.4	88.2	22	7 US-09-802-518-7	Sequence 7, Appli
8	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appli
9	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appli
10	18.8	85.5	22	6 US-09-770-943-2	Sequence 2, Appli
11	18.8	85.5	22	7 US-09-802-518-4	Sequence 4, Appli
12	18.8	85.5	22	7 US-09-802-359-4	Sequence 4, Appli
13	18.8	85.5	22	7 US-09-802-376-4	Sequence 4, Appli
14	18.4	83.6	22	7 US-09-802-518-8	Sequence 8, Appli
15	18.4	83.6	22	7 US-09-802-359-8	Sequence 8, Appli
16	18.4	83.6	22	7 US-09-802-376-8	Sequence 8, Appli
17	17.8	80.9	22	7 US-09-802-518-6	Sequence 6, Appli
18	17.8	80.9	22	7 US-09-802-359-6	Sequence 6, Appli
19	17.8	80.9	22	7 US-09-802-376-6	Sequence 6, Appli
20	17.2	78.2	22	6 US-09-770-943-1	Sequence 1, Appli
21	17.2	78.2	22	6 US-09-770-943-3	Sequence 3, Appli
22	17.2	78.2	22	6 US-09-770-943-10	Sequence 10, Appl
23	17.2	78.2	22	7 US-09-802-518-10	Sequence 10, Appl
24	17.2	78.2	22	7 US-09-802-518-11	Sequence 11, Appl
25	17.2	78.2	22	7 US-09-802-359-9	Sequence 9, Appli

26	17.2	78.2	22	7 US-09-802-359-10	Sequence 10, Appli
27	17.2	78.2	22	7 US-09-802-376-9	Sequence 9, Appli
28	17.2	78.2	22	7 US-09-802-376-10	Sequence 10, Appli
29	15.8	71.8	1407	6 US-09-894-844-35	Sequence 35, Appli
30	15.6	70.9	22	6 US-09-770-943-4	Sequence 4, Appli
31	15.6	70.9	189	8 US-60-253-652-21559	Sequence 21559, A
32	15.6	70.9	252	5 US-09-825-790-331	Sequence 331, App
33	15.6	70.9	333	6 US-09-803-110-7440	Sequence 7440, Ap
34	15.6	70.9	550	6 US-09-803-110-2557	Sequence 2557, Ap
35	15.6	70.9	768	5 US-09-543-681A-2526	Sequence 2526, Ap
36	15.6	70.9	813	1 PCT-US01-08656-2544	Sequence 1899, Ap
37	15.6	70.9	813	7 US-09-861-478-1899	Sequence 1899, Ap
38	15.6	70.9	821	7 US-09-861-478-1379	Sequence 1379, Ap
39	15.6	70.9	110684	6 US-09-803-736-1100	Sequence 1100, Ap
40	15.4	70.0	341	7 US-09-840-145-1568	Sequence 1568, Ap
41	15.4	70.0	207674	6 US-09-803-736-588	Sequence 588, App
42	15.2	69.1	252	7 US-09-540-213-28028	Sequence 28028, A
43	15.2	69.1	272	5 US-09-534-840-3533	Sequence 3533, Ap
44	15.2	69.1	285	7 US-09-540-213-47271	Sequence 47271, A
45	15.2	69.1	330	8 US-60-253-652-9623	Sequence 9623, Ap

ALIGNMENTS

RESULT 1

US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 37782001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match 100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 2

US-09-802-359-2
; Sequence 2, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

```
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-2

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
US-09-802-376-2
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-2

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| ||||| |||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 4
US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match      92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match      92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match      92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
    ||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22
```



```
RESULT 7
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
DB 1 tgactgtgaangttcgagatga 22

RESULT 8
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
DB 1 tgactgtgaangttcgagatga 22

RESULT 9
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
DB 1 tgactgtgaangttcgagatga 22

RESULT 10
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   |||| |||| |||| |||| ||||
DB 1 tgactgtgaacgttagagatga 22

RESULT 11
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
```

```
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 12
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 13
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4
```

```
Query Match      85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 14
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8
```

```
Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttngagatga 22
```

```
RESULT 15
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match 83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatga 22
||| |||| ||| |||||
Db 1 tgactgtgaangtngagatga 22

Search completed: October 9, 2001, 21:36:00
Job time: 21220 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:41:58 ; Search time 217.64 Seconds
(without alignments)
19,136 Million cell updates/sec

Title: US-09-713-136-2
Perfect score: 22
Sequence: 1 tgaccgtgaacgttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	22	4	US-09-092-314-2
2	17.2	78.2	22	4	US-09-092-314-1
3	17.2	78.2	22	4	US-09-092-314-3
4	17.2	78.2	22	4	US-09-092-314-10
5	15.6	70.9	22	4	US-09-092-314-4
6	15.6	70.9	77	1	US-08-399-412A-58
7	14.6	66.4	440	1	US-07-998-003A-37
8	14.6	66.4	440	1	US-08-453-274B-37
9	14.6	66.4	440	1	US-08-453-695A-37
10	14.6	66.4	440	1	US-08-453-702A-37
11	14.6	66.4	440	2	US-08-268-161A-37
12	14.6	66.4	440	5	PCT-US93-12588-37
13	14.6	66.4	440	5	PCT-US95-08071-37
14	14.6	66.4	1553	4	US-09-217-490-1
15	14.6	66.4	1560	1	US-08-344-536-3
16	14.6	66.4	1560	3	US-08-920-562-3
17	14.6	65.5	31	4	US-09-070-408-110
18	14.2	64.5	906	6	5204252-3
19	14	63.6	22	4	US-09-092-314-5
20	14	63.6	22	4	US-09-092-314-7
21	14	63.6	22	4	US-09-092-314-8
22	14	63.6	73	1	US-08-434-001-33
23	14	63.6	73	1	US-08-433-585-33
24	14	63.6	73	1	US-08-434-425-33
25	14	63.6	73	2	US-08-437-667-33
26	14	63.6	73	3	US-08-906-955-33
27	14	63.6	73	3	US-08-945-909-33

28	14	63.6	73	5	PCT-US96-06060-33	Sequence 33, Appl
29	14	63.6	76	1	US-08-442-572-42	Sequence 42, Appl
30	14	63.6	76	1	US-08-361-795-42	Sequence 42, Appl
31	14	63.6	76	5	PCT-US95-05600-125	Sequence 125, App
32	14	63.6	538	1	US-08-840-683-5	Sequence 5, Appl
33	14	63.6	538	2	US-08-555-722-5	Sequence 5, Appl
34	14	63.6	1179	4	US-09-147-926-1	Sequence 1, Appl
35	14	63.6	1352	1	US-07-714-819-1	Sequence 1, Appl
36	14	63.6	1352	1	US-08-246-978A-1	Sequence 1, Appl
37	14	63.6	1352	1	US-08-440-814A-1	Sequence 1, Appl
38	14	63.6	1418	1	US-08-391-615-7	Sequence 7, Appl
39	14	63.6	1484	1	US-08-485-618-102	Sequence 102, App
40	14	63.6	1484	1	US-08-605-672-102	Sequence 102, App
41	14	63.6	1484	2	US-08-482-293A-102	Sequence 102, App
42	14	63.6	1484	2	US-08-943-363-102	Sequence 102, App
43	14	63.6	1484	4	US-09-193-043-102	Sequence 102, App
44	14	63.6	1635	4	US-09-178-252-10	Sequence 10, Appl
45	14	63.6	1830	4	US-09-019-931-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 2
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match      78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||| ||||| ||| |||||
Db 1 tgactgtgaagttagagatga 22

RESULT 3
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match      78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||| ||||| ||| |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 4
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||| ||||| ||| |||||
Db 1 tgactgtgaagttagagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgaccgtgaacgttcgagatga 22
   ||| ||||| ||| |||||
Db 1 tgactgtgaagcttagagatga 22

RESULT 6
US-08-399-412A-58
; Sequence 58, Application US/08399412A
; Patent No. 5622828
; GENERAL INFORMATION:
; APPLICANT: Parma, David
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High-Affinity Oligonucleotide
; TITLE OF INVENTION: Ligands To Secretory Phospholipase
; TITLE OF INVENTION: A2 (sPLA2)
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
```

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,412A
FILING DATE: 6-MARCH-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Julie L. Bernard
REGISTRATION NUMBER: 36,450
REFERENCE/DOCKET NUMBER: NEX27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-399-412A-58

Query Match 70.9%; Score 15.6; DB 1; Length 77;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatga 22
: || |||||:|||||:|
Db 42 UGCCACGACGACGUCCAGCAUGA 63

RESULT 7
US-07-998-003A-37
Sequence 37, Application US/07998003A
Patent No. 5643781
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESSER: Bicknell
STREET: 20 South Clark Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,003A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5643781and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 30903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEFAX: 312/984-9740

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-998-003A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatg 21
||||| ||| | ||| |||||
Db 83 TGACCCCTGACCCCTTCAAGATG 103

RESULT 8
US-08-453-274B-37
Sequence 37, Application US/08453274B
Patent No. 5663300
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,274B
FILING DATE: 30-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5663300and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32660
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-453-274B-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgaccgtgaacgttcgagatg 21
||||| ||| | ||| |||||
Db 83 TGACCCCTGACCCCTTCAAGATG 103

RESULT 9
US-08-453-695A-37
Sequence 37, Application US/08453695A

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; Patent No. 5708143
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,695A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5708143and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32658
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-453-695A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| ||| |||
Db 83 TGACCCTGACCCCTCAAGATG 103

RESULT 10
US-08-268-161A-37
; Sequence 37, Application US/08268161A
; Patent No. 5798224
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,161A
; FILING DATE: June 27, 1994
```

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Young J. Suh
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-268-161A-37

Query Match 66.4%; Score 14.6; DB 1; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| ||| |||
Db 83 TGACCCTGACCCCTCAAGATG 103

RESULT 11
US-08-453-702A-37
; Sequence 37, Application US/08453702A
; Patent No. 5891706
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,702A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5891706and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32657
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-453-702A-37

Query Match 66.4%; Score 14.6; DB 2; Length 440;
Best Local Similarity 81.0%; Pred. No. 62;
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Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| |||||
Db 83 TGACCCGTGACCCCTTCAAGATG 103

RESULT. 12

PCT-US93-12588-37

; Sequence 37, Application PC/TUS9312588

; GENERAL INFORMATION:

; APPLICANT: Suzuki, Shintaro

; TITLE OF INVENTION: Protocadherin Materials and Methods

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 S. Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/12588

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/998,003

; FILING DATE: 29 DEC 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31811

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 440 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

PCT-US93-12588-37

Query Match 66.4%; Score 14.6; DB 5; Length 440;

Best Local Similarity 81.0%; Pred. No. 62;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21
||||| ||| ||| |||||
Db 83 TGACCCGTGACCCCTTCAAGATG 103

RESULT 13

PCT-US95-08071-37

; Sequence 37, Application PC/TUS9508071

; GENERAL INFORMATION:

; APPLICANT: Suzuki, Shintaro

; TITLE OF INVENTION: Protocadherin Materials and Methods

; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

; ADDRESSEE: Borun

; STREET: 6300 Sears Tower, 233 S. Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08071

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/12588

; FILING DATE: 23 DEC 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 32149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 440 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

PCT-US95-08071-37

Query Match 66.4%; Score 14.6; DB 5; Length 440;

Best Local Similarity 81.0%; Pred. No. 62;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgaccgtgaacgttcgagatg 21

||||| ||| ||| |||||

Db 83 TGACCCGTGACCCCTTCAAGATG 103

RESULT 14

US-09-217-490-1/c

; Sequence 1, Application US/09217490

; Patent No. 6165761

; GENERAL INFORMATION:

; APPLICANT: Schneider, Paile

; APPLICANT: Christensen, Soren

; APPLICANT: Dybdal, Lone

; APPLICANT: Fugisang, Claus Crone

; APPLICANT: Xu, Feng

; APPLICANT: Golightly, Elizabeth

; TITLE OF INVENTION: Carbohydrate Oxidase And use Thereof In

; FILE REFERENCE: 5421.200-US

; CURRENT APPLICATION NUMBER: US/09/217,490

; CURRENT FILING DATE: 1998-12-21

; EARLIER APPLICATION NUMBER: PA 1997 01505

; EARLIER FILING DATE: 1997-12-22

; EARLIER APPLICATION NUMBER: PA 1998 00763

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/068,717

; EARLIER FILING DATE: 1997-12-23

; EARLIER APPLICATION NUMBER: 60/088/725

; EARLIER FILING DATE: 1998-06-10

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1553

TYPE: DNA
ORGANISM: Microdochium nivale
FEATURE:
NAME/KEY: Intron
LOCATION: (1012)..(1076)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1011)
FEATURE:
NAME/KEY: CDS
LOCATION: (1077)..(1553)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (67)..(1550)
US-09-217-490-1

Query Match 66.4%; Score 14.6; DB 4; Length 1553;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 gaccgtgaacgttcgagatga 22
||||||| ||||| |||||
DB 529 GACCGTCATGTCGAGCTGA 509

RESULT 15
US-08-344-536-3
Sequence 3, Application US/08344536
Patent No. 5674735
GENERAL INFORMATION:
APPLICANT: Onions, David E.
APPLICANT: Nicolson, Lesley
TITLE OF INVENTION: EHV-4 GLYCOPROTEIN VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NO. 5674735th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,536
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,672
FILING DATE: 05-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 1749-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 52..1506
US-08-344-536-3

Query Match 66.4%; Score 14.6; DB 1; Length 1560;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 tgaccgtgaacgttcgagatg 21
||||||| ||||| |||||
DB 1088 TGCCGTAACGTTGAAGATG 1108

Search completed: October 9, 2001, 15:41:59
Job time: 289 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:29 ; Search time 2150.93 Seconds
(without alignments)
165.397 Million cell updates/sec

Title: US-09-713-136-3
Perfect score: 23
Sequence: 1 tcattcgaaacgtccacagtca 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba1:
2: gb_ba2:
3: gb_ba3:
4: gb_in1:
5: gb_in2:
6: gb_in3:
7: gb_om:
8: gb_ov:
9: gb_pat1:
10: gb_pat2:
11: gb_ph:
12: gb_pl1:
13: gb_pl2:
14: gb_pl3:
15: gb_pl4:
16: em_ba1:
17: em_ba2:
18: em_fun:
19: em_htgo_hum:
20: em_htgo_inv:
21: em_htgo_rod:
22: em_htg_hum1:
23: em_htg_hum2:
24: em_htg_hum3:
25: em_htg_hum4:
26: em_htg_hum5:
27: em_htg_hum6:
28: em_htg_hum7:
29: em_htg_hum8:
30: em_htg_inv1:
31: em_htg_inv2:
32: em_htg_other:
33: em_htg_rod:
34: em_hum1:
35: em_hum2:
36: em_hum3:
37: em_hum4:
38: em_hum5:
39: em_hum6:
40: em_hum7:
41: em_in:
42: em_om:
43: em_or:

44: em_ov:
45: em_pat:
46: em_ph:
47: em_pl:
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49: em_sts:
50: em_sv:
51: em_un:
52: em_vl:
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55: gb_sts3:
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57: gb_un:
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86: gb_pr2:
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88: gb_pr4:
89: gb_pr5:
90: gb_pr6:
91: gb_pr7:
92: gb_pr8:
93: gb_pr9:
94: gb_rol:
95: gb_ro2:
96: gb_in4:
97: gb_pr10:
98: em_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	23	10	AX083677
C 2	18.4	80.0	160974	90	AL139330 Human DNA
C 3	17.2	74.8	213	94	U26223 Mus musculus
C 4	17.2	74.8	992	53	AL43316 T3 end of
C 5	17.2	74.8	1158	7	M19680 Bovine mito
C 6	17.2	74.8	1718	95	J05266 Rat mitocho
7	17.2	74.8	7015	6	AF101304 Caenorhab
8	17.2	74.8	34348	6	AF067944 Caenorhab

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c 9 17.2 74.8 46057 88 AC073276 Homo sapi
c 10 17.2 74.8 71441 86 AC007042 Homo sapi
c 11 17.2 74.8 72265 86 AC006516 Homo sapi
c 12 17.2 74.8 83287 13 AP000603 Arabidops
c 13 17.2 74.8 128289 86 AC007972 Homo sapi
c 14 17.2 74.8 132060 78 AC090898 Homo sapi
c 15 17.2 74.8 138698 60 AC008454 Homo sapi
c 16 17.2 74.8 157965 72 AC053498 Homo sapi
c 17 17.2 74.8 192276 79 AL355353 Homo sapi
c 18 17.2 74.8 195247 81 AL390717 Homo sapi
c 19 17.2 74.8 208287 67 AC022532 Homo sapi
c 20 17 73.9 49323 12 AC007109 Arabidops
c 21 16.8 73.0 664 72 AC058348 Giardia i
c 22 16.8 73.0 811 71 AC039842 Giardia i
c 23 16.8 73.0 877 76 AC081149 Giardia i
c 24 16.8 73.0 882 71 AC040526 Giardia i
c 25 16.8 73.0 897 74 AC070300 Giardia i
c 26 16.8 73.0 924 72 AC065824 Giardia i
c 27 16.8 73.0 939 74 AC070334 Giardia i
c 28 16.8 73.0 993 77 AC085260 Giardia i
c 29 16.8 73.0 1022 72 AC061054 Giardia i
c 30 16.8 73.0 1033 72 AC065301 Giardia i
c 31 16.8 73.0 1058 75 AC077153 Giardia i
c 32 16.8 73.0 1140 72 AC054342 Giardia i
c 33 16.8 73.0 38392 65 AC019553 Drosophil
c 34 16.8 73.0 110000 79 AL355364-3 Continuation (4 of
c 35 16.8 73.0 150682 82 AL590378 Homo sapi
c 36 16.8 73.0 159103 59 AC025687 Homo sapi
c 37 16.8 73.0 177226 78 AC090496 Mus muscu
c 38 16.8 73.0 185054 77 AC090013 Homo sapi
c 39 16.8 73.0 309883 4 AE003479 Drosophil
c 40 16.6 72.2 1108 94 AF237817 Mus muscu
c 41 16.6 72.2 1731 13 AP000392 Oryza sat
c 42 16.6 72.2 2190 94 AF284380 Mus muscu
c 43 16.6 72.2 8355 94 AB047760 Mus muscu
c 44 16.6 72.2 31147 65 AC018318 Drosophil
c 45 16.6 72.2 31309 12 AB013387 Arabidops

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ALIGNMENTS

```

RESULT 1
LOCUS AX083677 23 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 3 from Patent WO0112223.
ACCESSION AX083677
VERSION AX083677.1 GI:13185409
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 23)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Patent: WO 011223-A 3 22-FEB-2001.
Dynamax Technologies Corporation (US)
FEATURES
source Location/Qualifiers
1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 8 c 3 g 6 t
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 100.0%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tcattctcgaaacgtttccacagtca 23
|||||

```

```

Db 1 TCATCTCGAAGCTTCCACAGTCA 23
RESULT 2
LOCUS AL139330/c
DEFINITION Human DNA sequence from clone RP11-266C7 on chromosome 6q25.2-26, complete sequence.
ACCESSION AL139330
VERSION AL139330.17
KEYWORDS GI:13398696
SOURCE HTG.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 160974)
REFERENCE Sycamore,N.
AUTHORS Direct Submission
TITLE Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
JOURNAL requests: clonerequest@sanger.ac.uk
COMMENT On Mar 21, 2001 this sequence version replaced gi:13274265. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C-elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-266C7 is from the library RPi-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-266C7 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-266C7 is at 1 in this sequence. The true left end of clone RP3-403L10 is at 160875 in this sequence. The true right end of clone RPI-257C19 is at 72466 in this sequence.
FEATURES
Source Location/Qualifiers
1..160974
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="q25.2-26"
/clone="RP11-266C7"
/clone_lib="RPI-11.1"
17..541
/note="match: GSS: Em:AQ488081"
repeat_region 143..456
/note="Alusg repeat: matches 1..310 of consensus"
591..1015
/note="match: STS: Em:C37401"
complement(689..1172)
/note="match: GSS: Em:AQ763085"
4594..4892
/note="Alusx repeat: matches 1..298 of consensus"

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repeat_region 5190..5524
/note="MER47A repeat: matches 1. .366 of consensus"
repeat_region 6295..6584
/note="AluSg repeat: matches 21. .308 of consensus"
repeat_region 6973..7265
/note="AluJb repeat: matches 1. .303 of consensus"
repeat_region 7266..7398
/note="AluJo repeat: matches 2. .138 of consensus"
repeat_region 7648..7985
/note="L1MB7 repeat: matches 5830. .6173 of consensus"
repeat_region 7986..8290
/note="AluY repeat: matches 2. .304 of consensus"
repeat_region 8291..8414
/note="L1MB7 repeat: matches 5718. .5830 of consensus"
repeat_region 8415..8722
/note="AluY repeat: matches 1. .309 of consensus"
repeat_region 8914..9225
/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 11473..11709
/note="AluJb repeat: matches 85. .312 of consensus"
repeat_region 11862..11885
/note="12 copies 2 mer aa 95% conserved"
misc_feature 12664..13070
/note="CpG island"
evidence-not_experimental
repeat_region 13947..14128
/note="MER5A repeat: matches 18. .189 of consensus"
repeat_region 14438..14733
/note="AluJb repeat: matches 1. .297 of consensus"
repeat_region 14926..15235
/note="AluSx repeat: matches 1. .303 of consensus"
repeat_region 16326..16818
/note="AluSx repeat: matches 1. .293 of consensus"
repeat_region 17079..17245
/note="AluSx repeat: matches 147. .302 of consensus"
repeat_region 17246..17550
/note="AluSg repeat: matches 2. .306 of consensus"
repeat_region 17551..17689
/note="AluSx repeat: matches 5. .147 of consensus"
repeat_region 17805..18138
/note="AluJo repeat: matches 1. .302 of consensus"
repeat_region 19067..19261
/note="L1MB3A repeat: matches 5556. .5743 of consensus"
repeat_region 19262..19564
/note="AluSg repeat: matches 1. .304 of consensus"
misc_feature 19527..19976
/note="match: STS: Em:HS355C7S"
repeat_region 19565..19661
/note="L1MB3A repeat: matches 5743. .5841 of consensus"
repeat_region 19836..19973
/note="L2 repeat: matches 2606. .2745 of consensus"
repeat_region 20097..20373
/note="AluSx repeat: matches 3. .298 of consensus"
repeat_region 20664..20969
/note="AluSx repeat: matches 1. .302 of consensus"
repeat_region 22067..22106
/note="20 copies 2 mer tt 82% conserved"
repeat_region 22465..22777
/note="AluSp repeat: matches 1. .312 of consensus"
repeat_region 23399..23521
/note="L2 repeat: matches 2582. .2708 of consensus"
repeat_region 23577..23800
/note="AluJb repeat: matches 50. .276 of consensus"
repeat_region 24106..24399
/note="AluSg repeat: matches 1. .296 of consensus"
repeat_region 24527..24834
/note="AluSx repeat: matches 1. .307 of consensus"
repeat_region 25811..25971
/note="MIR repeat: matches 6. .167 of consensus"
repeat_region 26053..26242
/note="MER3 repeat: matches 2. .203 of consensus"
repeat_region 26261..26562
/note="AluSx repeat: matches 1. .304 of consensus"
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repeat_region 26672..26970
/note="AluSx repeat: matches 1. .299 of consensus"
repeat_region 28552..28856
/note="AluSx repeat: matches 2. .303 of consensus"
repeat_region 32169..32208
/note="10 copies 4 mer caaa 80% conserved"
repeat_region 32440..32755
/note="AluSg repeat: matches 1. .313 of consensus"
repeat_region 36071..36364
/note="AluSg repeat: matches 16. .308 of consensus"
misc_feature complement(36336..36775)
/note="match: GSS: Em:AQ119669"
misc_feature complement(36340..36779)
/note="match: GSS: Em:B89745"
repeat_region 36519..36969
/note="MER82 repeat: matches 2. .441 of consensus"
repeat_region 37004..37094
/note="MER82 repeat: matches 556. .646 of consensus"
repeat_region 37503..37616
/note="2 copies 57 mer 87% conserved"
repeat_region 39904..40210
/note="AluSg repeat: matches 1. .307 of consensus"
repeat_region 40816..41111
/note="AluJo repeat: matches 3. .292 of consensus"
repeat_region 42185..42311
/note="MIR repeat: matches 89. .226 of consensus"
repeat_region 42393..42467
/note="3 copies 25 mer 90% conserved"
repeat_region 43657..43709
/note="Alu repeat: matches 254. .308 of consensus"
repeat_region 44222..44253
/note="16 copies 2 mer ac 100% conserved"
repeat_region 45307..45446
/note="L1MC4 repeat: matches 6867. .7005 of consensus"
repeat_region 45449..45692
/note="61 copies 4 mer gatg 82% conserved"
repeat_region 45479..45672
/note="97 copies 2 mer tg 55% conserved"
repeat_region 45693..45772
/note="20 copies 4 mer atgg 81% conserved"
repeat_region 45698..45937
/note="12 copies 20 mer 62% conserved"
repeat_region 45773..45944
/note="43 copies 4 mer ggat 77% conserved"
repeat_region 45945..46104
/note="8 copies 20 mer 80% conserved"
repeat_region 46099..46146
/note="12 copies 4 mer aggt 75% conserved"
repeat_region 46256..46972
/note="L1MC4 repeat: matches 7015. .7771 of consensus"
repeat_region 46973..47379
/note="MSTRB repeat: matches 1. .425 of consensus"
repeat_region 47415..47533
/note="L1MC4 repeat: matches 7853. .7974 of consensus"
repeat_region 47774..48093
/note="AluJb repeat: matches 1. .311 of consensus"
misc_feature 48660..49031
/note="match: GSS: Em:AQ032423"
repeat_region 49386..49555
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Query Match 80.0%; Score 18.4; DB 90; Length 160974;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcattctgaacgttcacag 20
|||||
DB 131791 TCATTCTAGACGTTCCACAG 131772

RESULT 3
MMU26223/c 213 bp RNA ROD 09-FEB-1996
LOCUS MMU26223
DEFINITION Mus musculus clone pmg7 nonsatellite RNA sequence.

11152876
3 (bases 1 to 992)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source
1..992
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA015F02"
/clone_lib="BB0AA"
/note="end : T3"
<1..>837
/note="similar to Saccharomyces cerevisiae ORF YNL101w [
similarity to YKL146w]"
/evidence=not_experimental

BASE COUNT 265 a 215 c 209 g 302 t 1 others
ORIGIN

Query Match 74.8%; Score 17.2; DB 53; Length 992;
Best Local Similarity 86.4%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattctgcgaactgtccacagtc 22
||||| ||||| ||||| ||||| |||||
Db 422 TGATCTTGAACTTCCACAGTC 443

RESULT 5
BOVATPSAS/c
LOCUS
BOVATPSAS 1158 bp mRNA MAM 26-APR-1993
DEFINITION
Bovine mitochondrial ATP synthase alpha-subunit mRNA, 5' end.
ACCESSION
M19680
VERSION
M19680.1 GI:162718
KEYWORDS
ATP synthase alpha subunit.
SOURCE
Bovine liver, cDNA to mRNA.
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1158)
Breen,G.A.M.
Bovine liver cDNA clones encoding a precursor of the alpha-subunit
of the mitochondrial ATP synthase complex
JOURNAL
Biochem. Biophys. Res. Commun. 152, 264-269 (1988)
MEDLINE
88192643
COMMENT
Draft entry and computer-readable sequence for [1] kindly provided
by G.A.M.Breen, 12-JUL-1988.

FEATURES
source
1..1158
/organism="Bos taurus"
/db_xref="taxon:9913"
82..>210
/note="ATP synthase alpha subunit signal peptide"
82..>1158
/note="ATP synthase alpha subunit precursor"
/codon_start=1
/protein_id="AAA30399.1"
/db_xref="GI:162719"

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/translation="MLSVRIAAARALPRRAGLVSKNALGSSFVCTRNLHASNTRLQ
KGTAMSSILREILGADTSVDLESTGRVLSIGDGIARVHGLRNVAQAEVFESSGL
KGMSLNLEPDNVGVVFGNDKLIKEDIVKRTGAIVDPVPGDELGRVADALGNADIG
KGPVSKIRRIIRVGLKAPGIIPRISREPMOTGKAVDSLVPVIGRGORELIIGDROTKG
TSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGOKRSTVAQLVKRLTDADAMKTYIVVS
ATASDAAPLOYLAPYSGCSMGVEFRDNGKHALIYDLSKQAVAYROMSLLLRPPGR
EAYPGDVFVLSHRLERAAKMNDSF"
mat_peptide 211..1155
/note="ATP synthase alpha subunit"
BASE COUNT 259 a 296 c 329 g 274 t
ORIGIN 55 bp upstream of PstI site.

Query Match 74.8%; Score 17.2; DB 7; Length 1158;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcactcgaacgttccacagtc 22
Db 359 TCAGCTTGAACGTTCTCAGTC 338

RESULT 6
RATATPSB/c 1718 bp mRNA ROD 27-APR-1993
LOCUS Rat mitochondrial H+-ATP synthase alpha subunit mRNA, complete cds.
DEFINITION J05266
VERSION J05266.1 GI:203054
KEYWORDS ATP synthase; nucleotide-binding protein.
SOURCE Rat (Sprague-Dawley adult) liver, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1718)
AUTHORS Lee J.H., Garboczi D.N., Thomas P.J. and Pedersen P.L.
TITLE Mitochondrial ATP synthase: cDNA cloning, amino acid sequence,
overexpression, and properties of the rat liver alpha subunit
JOURNAL J. Biol. Chem. 265, 4664-4669 (1990)
MEDLINE 90170980
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by P.J.Thomas, 24-JAN-1990.
FEATURES
source location/Qualifiers
1..1718
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
<1..99
/note="ATP synthase alpha subunit signal peptide (put.)
(EC 3.6.1.3); putative"
<1..1632
/note="ATP synthase alpha subunit precursor (EC 3.6.1.3)"
/codon_start=1
/protein_id="AAA40784.1"
/db_xref="GI:203055"
/translation="RRALPRRAGLVSKNALGSSFVCTRNLHASNTRLQKGTAEISSI
LEIRIGADTSVDLESTGRVLSIGDGIARVHGLRNVAQAEVFESSGLKGMSLNLEPD
NVGVVFGNDKLIKEDIVKRTGAIVDPVPGDELGRVADALGNADIGKGPVSKIRR
RVGLKAPGIIPRISREPMOTGKAVDSLVPVIGRGORELIIGDROTKGTSIAIDTIIN
QKRFNDGTDEKKKLYCIYVAIGOKRSTVAQLVKRLTDADAMKTYIVVSATASDAAPLO
YLAPYSGCSMGVEFRDNGKHALIYDLSKQAVAYROMSLLLRPPGR EAYPGDVFVLSH
RLERAAKMNDSFGGGSGLTAPVETQAGDSAYIPTNVISITDGGIIFLETFLYK
HSRLERAAKMNDSFGGGSGLTAPVETQAGDSAYIPTNVISITDGGIIFLETFLYK
GIRPAIINVGLSVRSGAAQTRAMKQVAGTKLELAQYREVAAFAQFGSDLDATQQL
LSRGVRLTELLKQGYSPMAIEQVAVIYAGVIRGVLKLEPKSKITKPFSAFLSHVSG
<100..1629
HOSLLGNIRSDGKISEQSDAKLKEIVTNFLAGEP"
mat_peptide 399 a 414 c 470 g 435 t
/note="ATP synthase alpha subunit (EC 3.6.1.3)"
BASE COUNT 399 a 414 c 470 g 435 t
ORIGIN

Query Match 74.8%; Score 17.2; DB 95; Length 1718;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcactcgaacgttccacagtc 22
Db 359 TCAGCTTGAACGTTCTCAGTC 338

RESULT 7
CELCO2E11 7015 bp DNA INV 29-OCT-1998
LOCUS Caenorhabditis elegans cosmid C02E11.
DEFINITION AF101304
ACCESSION AF101304
VERSION AF101304.1 GI:3806125
KEYWORDS Caenorhabditis elegans.
SOURCE Caenorhabditis elegans.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 7015)
AUTHORS Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J.,
Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kersey J., Kirsten J., Lalster N.,
Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B.,
O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A.,
Saunders D., Showkeen R., Smaildon N., Smith A., Sonnenmet E.,
Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M.,
Vaughan K., Waterston R., Watson A., Weinstock L.,
Wilkinson-Sproat J. and Wohlman P.
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans 368 (6466), 32-38 (1994)
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 7015)
AUTHORS Pauley A. and Harper M.
TITLE The sequence of C. elegans cosmid C02E11
JOURNAL Unpublished (1998)
REFERENCE 3 (bases 1 to 7015)
AUTHORS Waterston R.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rw@nematoe.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is R09A1, 200 bp overlap; 3' cosmid is K10C9, 2700 bp
overlap. Actual start of this cosmid is not known. Last known
base of 5' overlap is at base position 11396 of CELR09A1; actual
end is at 4319 of CELC02E11.

NOTES:

```

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES

```

source
1. .7015
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="C02E11"
/chromosome="V"
/complement(1574..7000)
/gene="C02E11.1"
complement(join(1574..1666,2444..3467,3517..4088,
4579..5367,5417..5638,6124..6536,6892..7000))
/gene="C02E11.1"
/notes="contains similarity to human Pm5 protein; coded for
by C. elegans cDNA yk286h3.3; coded for by C. elegans cDNA
yk4b11.3; coded for by C. elegans cDNA yk21f6.3; coded for
by C. elegans cDNA yk7d11.3; coded for by C. elegans cDNA
yk28c8.3; coded for by C. elegans cDNA yk390g6.3; coded
for by C. elegans cDNA yk397a11.3; coded for by C. elegans
cDNA yk332e1.3; coded for by C. elegans cDNA yk503b8.3;
coded for by C. elegans cDNA yk395c7.3; coded for by C.
elegans cDNA yk431b6.3; coded for by C. elegans cDNA
yk395c7.5; coded for by C. elegans cDNA yk286h3.5; coded
for by C. elegans cDNA yk39a8.5; coded for by C. elegans
cDNA yk21f6.5; coded for by C. elegans cDNA yk4b11.5;
coded for by C. elegans cDNA yk431b6.5; coded for by C.
elegans cDNA yk7d11.5"
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/protein_id="AAC69200.1"
/db_xref="GI:3806126"
/translations="MKHEEVNPSNGYEMIPVYKNGHYTLKVSAPAGYVEPDSIERK
IDGKTDAISNEDLYHLTGSVGRVVDGAAAGLPLYLTENGKQIAETKTDGKMYEM
RAPPGKTEVSTAGASGECISKGKTSVEVNAPVVPVFNKISGQVLEHRTESMPFF
YLAAMTLTATSSLDINIKVCSGSESLNVPSTHVKCSIGKTDPRGLRSLVACVPSGEY
YLAASHVNGPSKINFSNPQKVVVQAASAREFAVQATGRVVRTSKDPLSLGSEVLY
NEKSGGKTSGQGLKLTENLKEDEHTITAKAPQTFSTHANYKFPKVEIDVTQVGF
DICGOVEKSPNGVLKLTFTFKDDKRSLEIQPKADGSCFQPSVGLFTIEPTDKTSL
TPRLLEVEVLKNAVTLNLFTHFTKTNANVHLSGICGACTATVSLFLGQTLVRVKGTD
VFTFENAGDKQTLGARDNDGRGCEKSEMTLVVEQSNTOPTIHFQNGFAAQLEISHP
AEIENSNADKQNLNGSTKGGVEISICVPTSGVYDVLGSCYKFERQKFLQIEIHPD
VHKEVAARISGTDIDLENDKAAVSIRIKSAGDNFISQVPAIDNGRFTPEELPSSG
EQLVIVPSKRLPEPTSKVSTVTKCIENAVKNSFRGIFLDGSKPAVEKAVKAV
LKQKQVIEAISNKGDAFKIGPKRVEDYDITLDGKFTPTSTPGHQSQVLSQ
SIRVDEVTNAPLDGVLVSGKAGSDYRSNNVLDETAHKNVVALAPGEYFVRALL
QEIFSPSTSTVYKGGQHNVLKGRVSFAYSAYGKMRSGDAMKDVIIEALSEGCD
HQSEATTREDGYTRINGLLPDCEYQVHAKSYADGSPAPHSFPRSTVSMTEADVKGL
EFMATITAKTIDIAVEIGMDTLPEIQSVRVITKNNNDHVQASVVAPOHLHYLVNLP
RDGVEAIRVEAEKPPQAFKTVRVVADQAMKVARVPLTSSKRANDVDISVCTFLSL
PFVTLALVFENQNRVLELLGTDFIDHARNTFAPTADNHHRRK"
repeat_region 5704..5892
/notes="C. elegans telomere-like hexamer repeat"
BASE COUNT 2109 a 1486 c 1442 g 1978 t
ORIGIN

Query Match 74.8%; Score 17.2; DB 6; Length 7015;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tcactcgacgcttccacagtc 22
||||||| ||||||| |||
Db 6339 TCATCTCGTACTTTCACCCGTC 6360

RESULT 8
CELK10C9 34348 bp DNA INV 28-MAY-1998
LOCUS
DEFINITION Caenorhabditis elegans cosmid K10C9.
ACCESSION AF067944
VERSION AF067944.1 GI:3165551
KEYWORDS

```

SOURCE

ORGANISM

Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE

1 (bases 1 to 34348)

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Ropra, A.,
Saunders, D., Showkneen, R., Smalton, N., Smith, A., Sonhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.

2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans

Nature 368 (6466), 32-38 (1994)

94150718

2 (bases 1 to 34348)

Du, Z. and Maggi, L.

The sequence of C. elegans cosmid K10C9

Unpublished (1998)

3 (bases 1 to 34348)

Waterston, R.

Direct Submission

Submitted (23-MAY-1998) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Submitted by:

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA, and

Sanger Centre, Hinxton Hall

Cambridge CB10 1RQ, England

e-mail: tw@nematode.wustl.edu and jes@sanger.ac.uk

COMMENT

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA, and

Sanger Centre, Hinxton Hall

Cambridge CB10 1RQ, England

e-mail: tw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.

It may be shorter because we only sequence overlapping sections

once, or longer because we provide a small overlap between

neighboring submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded or sequenced with an alternate

chemistry; an attempt was made to resolve all sequencing problems,

such as compressions and repeats; all regions were covered by

sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is C02E11, 2700 bp overlap; 3' cosmid is Y50D48.

Actual start of this cosmid is at base position 1 of CELK10C9;

actual end is at 34348 of CELK10C9

NOTES:

Coding sequences below are predicted from computer analysis, using

the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers

1. .34348

/organism="Caenorhabditis elegans"

/strain="Bristol N2"

/db_xref="taxon:6239"

/clone="K10C9"

/chromosome="V"

complement(4432..7320)

/gene="K10C9.4"

complement(join(4432..4599,5154..5405,5797..5995,

7226..7320))

/gene="K10C9.4"

FEATURES

source

gene

CDS

```
repeat_region
repeat_region
gene
CDS
complement(join(10854..10942,10995..11307,12060..12201,
12727..12831,12882..13048,13096..13293))
/gene="K10C9.8"
/translation="similar to C. elegans olfactory receptor ODR-10
(GB:U49449)"
/evidence-not_experimental
/protein_id="AAC17674.1"
/db_xref="GI:3165558"
/translation="MLGKQSDLLKLIQDVSAFSLIINTLLIFVILTKSPKOLGAYK
CLMIIYSVEIFSLDVLVLPQHYSHGSTFLVIVGKDKLFSPVLELFLSSCIWRCF
GASMAVFAHFVYRWLVYEAHLKKEGKWLWFSIPFYALTWTCTGYILSAEN
KEFELFEDYIVLGPPELYKKENGTLTYIMPFGILGIISSIISSIIIVLIGILC
YRLNLSVTYTMNSNLNRQLQFLVLIQTVPFVLMHIPAVIMEFAFLOIDLGV
YSAVVSTIIYIPAVDPITIVIVENRKTVLKFFGCFKTHQIGTWTIAPTQFASST
HVN"
15903..16372
/gene="K10C9.3"
join(15903..16186,16243..16372)
/gene="K10C9.3"
/translation="similar to ribonuclease; K10C9.3"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17668.1"
/db_xref="GI:3165552"
/translation="MKLLLLCISCIPLAYSHDGEPEFDYLMFTTIYPTACRADDSSV
PECEIPSGTPQNSIHGLWPNFENGSPQNCRTGPRHEDENLINKSIEDRLVWVWPNLY
PKTIQSPWKEVDKHGCTCAQSEKLFESLAYTE"
complement(16894..18897)
/gene="K10C9.6"
complement(join(16894..16964,17009..17457,18410..18897))
/gene="K10C9.6"
/translation="similar to C. elegans olfactory receptor ODR-10
(GB:U49449)"
/codon_start=1
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/db_xref="GI:3165557"
/translation="MRVDFSEICRKGVYFVASTNEVLWITVVFHAKLFGAYKKMI
IYISVLTSSGLEIMKPTTHYNGALLSNCELNIPKIRQIFILISQFVLVI
SFISQVYRILCVFNQKTKYDGLKTIWILYLVYVGTIFALSHLYCSDSEFTDS
YKRAIFENVALEYSPELVAMYPAAAGSIRAKGIIFLLFAIVLISFSCIIIFTCV
QMRHMKELKFKSTQNKLEYQFFALVMQTIQGTIFLIPTGPIMLTPIAIPFEL
EVNMQTNLSLVGFYFSDSIAPFMIVSEKIFLKKVICRMMKNNTAVPSAVAVST
19421..22162
/gene="K10C9.2"
join(19421..19570,19619..19774,22043..22162)
/gene="K10C9.2"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17670.1"
/db_xref="GI:3165554"
/translation="MKVFDSDIDVAGLKGVPSEKPIVTSDDLKNSLGSVTSKGTQFQH
CLRKTKQFLGLDILRLCNKDLTIRDCPTDGKHPNRVFRERSIGNRRRGPPLPSFO
PCPAEFLYLPMSSSISKSDSTSPSIFGRINSAIKNIGN"
complement(20003..21979)
/gene="K10C9.7"
complement(join(20003..20197,20409..20591,20635..20779,
21642..21750,21802..21979))
/gene="K10C9.7"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17671.1"
/db_xref="GI:3165555"
/translation="MKRGLNHPQNRKKIIFRPPRLTKLSEKNLFOICKTTLNERRK
MKSIQNTIDELRKLKLSAGKSEEVORLKEQKHSKMFGEIFGVYGVATVGPKPKEKVK
VPTKEMTFEKKLLLETFPNKVTGQARAKRETNFIANNPEIYATASPODPSKAK
TDPVSRPOLNIISFSWPITSGSDWSHGSEFNDLTAPRVCKLTPVQWSDMKKSSLK
LGTEDNFSKNSYDPAYSNTTQSQSVTTLYNSTSTPYVDDSDGLGFLPLTCVG"
29577..30095
/gene="K10C9.1"
join(29577..29667,29862..29905,30015..30095)
/gene="K10C9.1"
/codon_start=1
/evidence-not_experimental
/protein_id="AAC17669.1"
/db_xref="GI:3165553"
/translation="MRVLAVLLLLINIVGAVSSPYVLRSSQSGAAIVQILNDFEIP
VWLKFLNITNFQKNFFQVYSRKLTM"
BASE COUNT 11109 a 6038 c 5959 g 11242 t
ORIGIN
Query Match 74.8%; Score 17.2; DB 6; Length 34348;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 tcattctggaacgtttccacagtc 22
||||||| || ||||| |||
Db 2024 TCATCTCGTACTTCCACCGTC 2045
RESULT 9
AC073276/c
LOCUS AC073276 46057 bp DNA PRI 08-DEC-2000
DEFINITION Homo sapiens clone RP11-634P5, complete sequence.
ACCESSION AC073276
VERSION AC073276.5 GI:11597181
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 46057)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Dec 7, 2000 this sequence version replaced gi:10944507.
Center project name: H_NH0654P05.
FEATURES
source
1..46057
/organism="Homo sapiens"
```



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/db_xref="taxon:9606"
/clone="RP11-654P5"
BASE COUNT 15064 a 8714 c 8650 g 13629 t
ORIGIN

Query Match 74.8%; Score 17.2; DB 88; Length 46057;
Best Local Similarity 86.4%; Pred. NO. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgaacgttcacagtca 23
| ||||| ||| ||||| |||||
Db 33363 CTTCTCAAACTTTCACAGTCA 33342

RESULT 10
AC007042 71441 bp DNA PRI 30-SEP-2000
LOCUS Homo sapiens BAC clone RP11-399H17 from Y, complete sequence.
AC007042
DEFINITION Homo sapiens BAC clone RP11-399H17 from Y, complete sequence.
AC007042
VERSION AC007042.2 GI:7243920
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 71441)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 71441)
AUTHORS Nelson, D., Wohlmann, P. and Harris, A.
TITLE The sequence of Homo sapiens BAC clone RP11-399H17
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 7 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 8 (bases 1 to 71441)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 9 (bases 1 to 71441)
AUTHORS Waterston, R.

```

Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 15, 2000 this sequence version replaced gi:4371303.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.edu
----- Summary Statistics

Center project name: H_NH0399H17

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The position of this clone was established as part of a
collaboration between the Human Chromosome Y Mapping Project
(Tomoko Kawaguchi, Helen Skaletsky, Laura G. Brown, Steve Rozen,
and David C. Page at the Whitehead Institute for Biomedical
Research, Cambridge MA) and the Washington University Genome
Sequencing Center, St. Louis MO.

SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-462A19. Actual start of
this clone is at base position 51511 of RP11-462A19; actual end is
at base position 71441 of RP11-399H17.

The sequence RP11-399H17 contains a dinucleotide (GA) repeat from
base position 25628 to 25795, in which the exact sequence is
unknown. The size of the repeat is consistent with digest
information and PCR from clone DNA.

The clone sequenced to the left is RP11-462A19, 200 bp overlap.
Actual start of this clone is at base position 51511 of
RP11-462A19; actual end is at base position 71441 of RP11-399H17.

FEATURES
Location/Qualifiers
1. .71441
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="y"
/map="y"
/clone="RP11-399H17"
/clone_lib="RPC1-11"
232. .255
/rpt_family="AT-rich"
1617. .1655
/rpt_family="(CA)n"
1680. .2091
/rpt_family="MER2_type"
2102. .2140
/rpt_family="GA-rich"

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repeat_region 2138..2310
/rpt_family="(TAGA)n"
repeat_region 2946..3067
/rpt_family="Alu"
repeat_region 3439..3929
/rpt_family="MER1_type"
repeat_region 4207..4424
/rpt_family="MER21-group"
repeat_region 5307..6287
/rpt_family="L1"
repeat_region 6354..6518
/rpt_family="MIR"
repeat_region 6679..6972
/rpt_family="Alu"
repeat_region 6986..7168
/rpt_family="GA-rich"
repeat_region 7169..7198
/rpt_family="GA-rich"
repeat_region 7200..7245
/rpt_family="(GGGA)n"
repeat_region 7364..7563
/rpt_family="GA-rich"
repeat_region 7857..8093
/rpt_family="MaLR"
repeat_region 8094..8123
/rpt_family="MaLR"
repeat_region 8124..8197
/rpt_family="MaLR"
repeat_region 8237..8300
/rpt_family="Alu"
repeat_region 10527..10644
/rpt_family="MIR"
repeat_region 10645..10676
/rpt_family="Alu"
repeat_region 10913..11162
/rpt_family="(TAA)n"
repeat_region 11338..11754
/rpt_family="CT-rich"
repeat_region 12042..18127
/rpt_family="L1"
repeat_region 18128..18164
/rpt_family="AT-rich"
repeat_region 19474..19775
/rpt_family="Alu"
repeat_region 19836..20116
/rpt_family="Alu"
repeat_region 20117..20144
/rpt_family="(CAAA)n"
repeat_region 21022..21053
/rpt_family="AT-rich"
repeat_region 21667..22969
/rpt_family="L1"
repeat_region 22971..24502
/rpt_family="L1"
repeat_region 24527..24602
/rpt_family="LTR52"
repeat_region 24603..24640
/rpt_family="(CA)n"
repeat_region 24641..24911
/rpt_family="LTR52"
repeat_region 24915..25177
/rpt_family="Alu"
repeat_region 25202..25362
/rpt_family="(GAAA)n"
repeat_region 25390..25567
/rpt_family="GA-rich"
repeat_region 25588..25768
/rpt_family="GA-rich"
repeat_region 25769..25824
/rpt_family="(GAAA)n"
repeat_region 25825..26383

```

Query Match

74.8%; Score 17.2; DB 86; Length 71441;

```

Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgacgttccacagtca 23
||||| ||| |||||
DB 60643 CATCTCCAAAGTTTCACAGTCA 60664

RESULT 11
AC006516/C
LOCUS Homo sapiens Xq28 BAC GSHB-557D6 (Genome Systems Human BAC Library)
DEFINITION complete sequence.
ACCESSION AC006516
VERSION AC006516.10 GI:5649182
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 72265)
AUTHORS Muzny,D., Arenson,A.D., Bouck,J., Brundage,E., Bunac,C., Chen,Z.,
Di,W., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C.,
Gorrell,J.H., Gorrell,L.L., Hernandez,J., Jackson,L.,
Kondejewski,N., Leal,B., Lichtarge,O., Liu,W., Logan,L.,
Martinez,C., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Simon,M., Vo,Q.,
Williamson,A., Worley,K.C., Yu,W., Zhou,X., Nelson,D. and
Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 72265)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 72265)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 72265)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jul 29, 1999 this sequence version replaced gi:4584315.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3399-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

RESULT 12

AP000603 LOCUS 83287 bp DNA PLN 27-DEC-2000
 Arabidopsis thaliana genomic DNA, chromosome 3, p1 clone: MRP15.
 AP000603 BA000014
 AP000603.1 GI:6045158
 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui p1
 clone:MRP15.
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiphyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 1 (sites)
 Kaneko,T., Kato,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
 Structural analysis of Arabidopsis thaliana chromosome 3. II.
 Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
 and BAC clones
 DNA Res. 7 (3), 217-221 (2000)
 20363099
 2 (bases 1 to 83287)
 Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
 Direct Submission
 Submitted (13-OCT-1999) Yasukazu Nakamura, Kazusa DNA Research
 Institute, Department of Plant Gene Research; 1532-3, Yana,
 Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
 Tel:81-438-52-3935, Fax:81-438-52-3934)
 Address for correspondence: kaos@kazusa.or.jp
 http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MRP15
 For the latest information on annotation of this clone, please see
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
 http://compbio.ornl.gov/grail-1.3/),
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplicePredictor (Volker Brendel, Stanford University,
 http://gremlini.zool.tastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SE/).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is MD011 and the 3' clone is K20M4.
 FEATURES
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 1. 83287
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
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 /clone="MRP15"
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 1170. 4664
 /note="gene_id:MRP15.1"
 /codon_start=1
 /evidence=not_experimental
 /product="receptor protein kinase"
 /protein_id="BAB01743.1"
 /db_xref="GI:9280288"
 /translation="MKQWQFLICLLVLTVDSSRRRLSSDDVNDTALLTAFKQTS
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 LRLYLQGNFSSGSDSSSGCSLEVLDSLNSLTDSSIVDYVFSTCLNLYSVNFHN
 KLAGKSSPSANRKTITVDLSNNRSEDEIPETFIADFPNSLAKHLDSLNNTGDS
 RLSPFCNENITVFSQNSIGDRFPVSLNCKLLETNLNRSNLKIPGDDYWGNF
 QNLKLSLAHLNIPPELSLICRTLEVLDSGLTQGLPQSFSCGSLQSLNIG
 NKLSGDFTSVYSKSLRITNLYLPFNISGSPISLTNCSNLRLVLDLSNNEFTGEVP
 SGCSLSSSVLKLILANNVLSCTVPVGLKCKSLKATIDLSFNALDLPKEITLIP
 KSLDLYVWNNLTGKIPESICVCGNLETILNLLNLTGSPESISKCTNKLWLISLS
 NLLTGEIPVGIKLEKLAIIQLQGNNSLTGNIPISELGNCKNLIMLDLNSNLTGPNLGE

LASOAGLVMPGSVSGKQFAFVRNEGTDGCRAGGLVEFEGIRAEIRLEHFFPMVHSCPKT
 RIYSGMTWYFSSNGSMIVLDLSYNAVSGSIPGLGYGAMGYQLVNLGLHLLTGTIDPS
 EGGKAIQVLDLSDNDLQGLFPGSLGCLSPSLDLSNNLTCPIPGGOLTFPLTR
 YANNSGLCVPLPSCSGSRPTRSHAKPKQSIATGNSAGIVSFHCTIYMLINALYA
 RKVKKKREKRYIESLPTSGSSSSSVHSEPLSINATFEPKPLKLTFAHLELATN
 GFSADSMIGSGGFGDYVAKADGDSYVAINKKLIQVTGGDRFEMAEKTIKTKHRL
 VPLGYCKIGEERLVEYMKYGLSTVLEKTKKGIFLDWQSAKTIATCAAKGLAF
 LHSCIPHIIRDMKSNVLLDQDFVARVSDFGMARVLSALDTHLSVSTLAGTPGYVP
 PEYQSFRCTAKGDVYSYVILLESLLSKKPIDPEEGEDNNLVGNAKOLYREKRAE
 ILDPVELTDRSGDVELHLYLKIASQCLDDRRFRKPTHIQVMTFKELVQVDTNDSLD
 EFLKETPLVEESRDKEP"
 complement(join(5331. 5634,5771. 6880,6969. 7219))
 /note="gene_id:MRP15.2"
 /codon_start=1
 /evidence=not_experimental
 /product="l-ascorbate oxidase; pectinesterase-like
 protein; pollen-specific protein-like"
 /protein_id="BAB01744.1"
 /db_xref="GI:9280289"
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VLLIFVSGKIVITGAKMRDITYKAFENIVPVSFRKIQQ"
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* runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 2356: contig of 2356 bp in length
* 2357 2456: gap of unknown length
* 2457 4774: contig of 2318 bp in length
* 4775 4874: gap of unknown length
* 4875 7061: contig of 2187 bp in length
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* 12919 13018: gap of unknown length
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* 24406 24505: gap of unknown length
* 24506 27588: contig of 3083 bp in length
* 27589 27688: gap of unknown length
* 27689 30161: contig of 2473 bp in length
* 30162 30261: gap of unknown length
* 30262 33203: contig of 2942 bp in length
* 33204 35661: contig of 2358 bp in length
* 35662 35761: gap of unknown length
* 35762 40312: contig of 4551 bp in length
* 40313 40412: gap of unknown length
* 40413 46185: contig of 5773 bp in length
* 46186 46285: gap of unknown length
* 46286 51511: contig of 5226 bp in length
* 51512 51611: gap of unknown length
* 51612 57825: contig of 6215 bp in length
* 57826 57925: gap of unknown length
* 57927 59345: contig of 1419 bp in length
* 59346 59445: gap of unknown length
* 59446 60782: contig of 1337 bp in length
* 60783 60882: gap of unknown length
* 60883 62260: contig of 1378 bp in length
* 62261 62360: gap of unknown length
* 62361 63527: contig of 1167 bp in length
* 63528 63627: gap of unknown length
* 63628 64971: contig of 1344 bp in length
* 64972 65071: gap of unknown length
* 65072 66277: contig of 1206 bp in length
* 66278 66377: gap of unknown length
* 66378 67704: contig of 1327 bp in length
* 67705 67804: gap of unknown length
* 67805 68968: contig of 1164 bp in length
* 68969 69068: gap of unknown length
* 69069 70477: contig of 1409 bp in length
* 70478 70577: gap of unknown length
* 70578 71753: contig of 1176 bp in length
* 71754 71853: gap of unknown length
* 71854 73684: contig of 1831 bp in length
* 73685 75145: contig of 1365 bp in length
* 75146 75245: gap of unknown length
* 75246 77192: contig of 1943 bp in length
* 77193 77292: gap of unknown length
* 77293 78985: contig of 1693 bp in length
* 78986 79085: gap of unknown length
* 79086 80573: contig of 1488 bp in length
* 80574 81992: gap of unknown length
* 81993 82092: contig of 1319 bp in length
* 82093 83653: contig of 1561 bp in length
* 83654 83753: gap of unknown length
* 83754 83828: contig of 1575 bp in length

```

```

* 85329 85428: gap of unknown length
* 85429 87021: contig of 1599 bp in length
* 87022 87121: gap of unknown length
* 87122 88426: contig of 1299 bp in length
* 88427 88526: gap of unknown length
* 88527 89898: contig of 1372 bp in length
* 89899 91567: gap of unknown length
* 91568 91667: contig of 1569 bp in length
* 91668 93050: contig of 1383 bp in length
* 93051 93150: gap of unknown length
* 93151 94283: contig of 1133 bp in length
* 94284 94383: gap of unknown length
* 94384 96054: contig of 1671 bp in length
* 96055 96154: gap of unknown length
* 96155 97637: contig of 1483 bp in length
* 97638 99299: contig of 1562 bp in length
* 99300 99399: gap of unknown length
* 99400 101166: contig of 1767 bp in length
* 101167 101266: gap of unknown length
* 101267 103151: contig of 1885 bp in length
* 103152 103251: gap of unknown length
* 103252 105319: contig of 2068 bp in length
* 105320 105419: gap of unknown length
* 105420 108102: contig of 2683 bp in length
* 108103 108202: gap of unknown length
* 108203 110341: contig of 2139 bp in length
* 110342 110441: gap of unknown length
* 110442 112323: contig of 1882 bp in length
* 112324 112423: gap of unknown length
* 112424 114236: contig of 1813 bp in length
* 114237 114336: gap of unknown length
* 114337 116297: contig of 1961 bp in length
* 116298 116397: gap of unknown length
* 116398 118448: contig of 2051 bp in length
* 118449 118548: gap of unknown length
* 118549 121185: contig of 2637 bp in length
* 121186 121285: gap of unknown length
* 121286 123030: contig of 1745 bp in length
* 123031 123130: gap of unknown length
* 123131 125712: contig of 2582 bp in length
* 125713 125812: gap of unknown length
* 125813 127531: contig of 1719 bp in length
* 127532 127631: gap of unknown length
* 127632 129750: contig of 2119 bp in length
* 129751 129850: gap of unknown length
* 129851 132060: contig of 2210 bp in length.

```

FEATURES

```

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="UNK"
/clone="RP11-522A4"

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/note="assembly_name:Contig100"

misc_feature
2457..4774
/note="assembly_name:Contig101"

misc_feature
4875..7061
/note="assembly_name:Contig102"

misc_feature
7162..9430
/note="assembly_name:Contig103"

misc_feature
9531..12918
/note="assembly_name:Contig104"

misc_feature
13019..15420
/note="assembly_name:Contig105"

misc_feature
15521..18397
/note="assembly_name:Contig106"

misc_feature
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/note="assembly_name:Contig107"

misc_feature
21227..24405
/note="assembly_name:Contig108"

misc_feature
24506..27588

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/note="assembly_name:Contig109"
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/note="assembly_name:Contig110"
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/note="assembly_name:Contig111"
33304..33561
/note="assembly_name:Contig112"
35762..40312
/note="assembly_name:Contig113"
40413..46185
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46286..51511
/note="assembly_name:Contig115"
51612..57826
/note="assembly_name:Contig116"
57927..59345
/note="assembly_name:Contig139"
59446..60782
/note="assembly_name:Contig140"
60883..62260
/note="assembly_name:Contig149"
62361..63527
/note="assembly_name:Contig151"
63628..64971

Query Match      74.88; Score 17.2; DB 78; Length 132060;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctcgaaacttcacagtcac 23
||||| ||||| ||||| |||||
Db 96281 CATCTCCAAAGTTTCACAGTCA 96260

RESULT 15
AC008454
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTC-345M13, WORKING DRAFT SEQUENCE,
16 unordered pieces.
AC008454
VERSION AC008454.3 GI:7708872
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 138698)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
REFERENCE 2 (bases 1 to 138698).
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On May 5, 2000 this sequence version replaced gi:6601060.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 317959
Center clone name: CIT-HSPC_345M13
-----
Summary Statistics
Consensus quality: 114452 bases at least Q40
Consensus quality: 128842 bases at least Q30
Consensus quality: 131746 bases at least Q20
Estimated insert size: 142000; pulse field gel estimation
Estimated insert size: 137198; sum-of-contigs estimation
Quality coverage: 4.16 in Q20 bases; pulse field gel estimation
Quality coverage: 4.31 in Q20 bases; sum-of-contigs estimation.

```

* NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence recorded is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

* 1 2234: contig of 2234 bp in length
* 2235: gap of unknown length
* 2335: contig of 2347 bp in length
* 4681: gap of unknown length
* 4782: contig of 3053 bp in length
* 7835: gap of unknown length
* 7935: contig of 2331 bp in length
* 10265: gap of unknown length
* 10365: contig of 2309 bp in length
* 10366: gap of unknown length
* 12674: contig of 2001 bp in length
* 12675: gap of unknown length
* 14775: contig of 3446 bp in length
* 14776: gap of unknown length
* 18321: contig of 2779 bp in length
* 18322: gap of unknown length
* 18422: contig of 4473 bp in length
* 21300: gap of unknown length
* 21301: contig of 4465 bp in length
* 25774: gap of unknown length
* 25773: contig of 4465 bp in length
* 30338: gap of unknown length
* 30339: contig of 4465 bp in length
* 30438: gap of unknown length
* 36382: contig of 5944 bp in length
* 36383: gap of unknown length
* 47292: contig of 10810 bp in length
* 47293: gap of unknown length
* 47392: contig of 11962 bp in length
* 47393: gap of unknown length
* 59454: contig of 14919 bp in length
* 59455: gap of unknown length
* 74373: contig of 14919 bp in length
* 74374: gap of unknown length
* 74474: contig of 24441 bp in length
* 98915: gap of unknown length
* 99015: contig of 39684 bp in length.

```

FEATURES

```

source
1..138698
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-345M13"
/clone_lib="Caltech human BAC library C"
BASE COUNT 35193 a 28953 c 30941 g 42070 t 1541 others
ORIGIN

```

```

Query Match      74.88; Score 17.2; DB 60; Length 138698;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```
Qy 1 tcactcgaaacttcacagtcac 22
||||| ||||| ||||| |||||

```

```
Db 46730 TCCTCTAGAACGTCCTCCACAGTC 46751

```

```

Search completed: October 9, 2001, 16:18:53
Job time: 2503 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:13 ; Search time 6788.49 Seconds
(without alignments)
32.027 Million cell updates/sec

Title: US-09-713-136-3
Perfect score: 23
Sequence: 1 tcattcgaacgttcacagtgca 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*
12: gb_est12.*
13: gb_est13.*
14: gb_est14.*
15: gb_est15.*
16: gb_est16.*
17: gb_est17.*
18: gb_est18.*
19: gb_est19.*
20: gb_est20.*
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22: gb_est22.*
23: gb_est23.*
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26: gb_est26.*
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110: gb_est33.*
111: gb_est34.*
112: gb_est35.*
113: gb_est36.*
114: gb_est37.*
115: gb_est38.*
116: gb_est39.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19.4	84.3	848	137	BE570879	601329225
C 2	17.2	74.8	245	161	BB591857	BB591857
C 3	17.2	74.8	307	158	H34259	EST111000 R
C 4	17.2	74.8	360	26	AV193020	AV193020
C 5	17.2	74.8	360	26	AV193064	AV193064
C 6	17.2	74.8	545	122	AW914126	EST345430
C 7	17.2	74.8	567	138	BE665364	154341 MA
C 8	17.2	74.8	678	240	AZ240360	RPCI-23-3
C 9	17.2	74.8	879	247	AZ669229	ENTN42TR
C 10	17.2	74.8	1471	233	AQ750993	HS_5574_B
C 11	16.8	73.0	239	164	BE198167	ug75e03_Y
C 12	16.8	73.0	269	162	BE031712	130355 MA
C 13	16.8	73.0	306	116	AW436470	76707 MAR
C 14	16.8	73.0	334	116	AW486759	76713 MAR
C 15	16.8	73.0	416	164	BE198756	ug82b12_Y
C 16	16.8	73.0	417	111	AW119653	sd50e05_Y
C 17	16.8	73.0	470	164	BE197776	ug75e03_X
C 18	16.8	73.0	559	224	AQ073038	EP(3)3586
C 19	16.8	73.0	623	18	AI292915	GH15946.5
C 20	16.6	72.2	181	239	AZ193981	SP_1025_A
C 21	16.6	72.2	214	137	BE556613	sq07d11_Y
C 22	16.6	72.2	271	22	AI616514	zehno187_Y
C 23	16.6	72.2	283	132	BB368590	BB368590
C 24	16.6	72.2	305	127	BB162497	BB162497
C 25	16.6	72.2	316	161	BB558391	BB558391
C 26	16.6	72.2	346	174	BG226875	kp99b04_Y
C 27	16.6	72.2	360	153	BG404581	602420727
C 28	16.6	72.2	369	147	BF328053	QV3-BN015
C 29	16.6	72.2	369	234	AQ847354	LMJFV1.1
C 30	16.6	72.2	384	168	BF703470	MI-P-H1-a
C 31	16.6	72.2	399	223	AQ030039	RPCI111-37
C 32	16.6	72.2	418	237	AZ022893	RPCI-23-2
C 33	16.6	72.2	489	111	AW060925	UI-M-BH1
C 34	16.6	72.2	528	229	AQ494321	HS_5146_B
C 35	16.6	72.2	566	232	AQ699515	HS_5569_A
C 36	16.6	72.2	591	149	BF478532	WHE2009_G
C 37	16.6	72.2	613	111	AW069158	Cr43b10.X
C 38	16.6	72.2	683	32	AW714759	AV714759
C 39	16.6	72.2	717	229	AQ489343	RPCI-11-2
C 40	16.6	72.2	779	251	AZ903022	RPCI-24-1
C 41	16.6	72.2	807	233	AQ740875	HS_2274_A
C 42	16.6	72.2	811	168	BF670945	602150746
C 43	16.6	72.2	890	137	BE603743	HVSMEH008
C 44	16.6	72.2	1186	144	BF099637	601751660
C 45	16.4	71.3	357	224	AQ085892	HS_2164_B

ALIGNMENTS

RESULT 1
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LOCUS BE570879 848 bp mRNA EST 15-AUG-2000
DEFINITION 601329225F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3602983 5', mRNA sequence.
ACCESSION BE570879
VERSION BE570879.1 GI:9814599
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 848)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabps-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM8791 row: b column: 08
 High quality sequence stop: 651.
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 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3602983"
 /clone.lib="NCI_CGAP_Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
 BASE COUNT 202 a 210 c 238 g 198 t
 ORIGIN
 Query Match 84.3%; Score 19.4; DB 137; Length 848;
 Best Local Similarity 95.2%; Pred. NO. 20;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 tcattctgaacgttccacagt 21
 ||||| ||||| ||||| |||||
 Db 149 TCATCTCGAATGTTCCACAGT 129
RESULT 2
BB591857
LOCUS BB591857 245 bp mRNA EST 30-NOV-2000
DEFINITION BB591857 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA clone B020004B03 5', mRNA sequence.
ACCESSION BB591857
VERSION BB591857.1 GI:11488459
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 245)
AUTHORS Alizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiroaka, T., Hirozane, T., Hodozawa, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Saka, C., Sakai, K., Sakai, D., Sato, K., Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Tova, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Alizawa, K. et al. 2000)
 Unpublished (2000)
TITLE Yoshihide Hayashizaki
JOURNAL Contact: Yoshihide Hayashizaki
COMMENT Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-res@tc.riken.go.jp,
 URL: <http://genome.rtc.riken.go.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki

ORIGIN

```

Query Match      74.8%; Score 17.2; DB 26; Length 360;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||| ||| |||
Db 215 TCATCTCGTACTTCCACCGTC 194

RESULT 5
AV193064/c 360 bp mRNA EST 22-JUL-1999
LOCUS AV193064 Yujii Kohara unpublished cDNA:Strain N2 hermaphrodite
DEFINITION embryo Caenorhabditis elegans cDNA clone yk612h9 5', mRNA sequence.
ACCESSION AV193064
VERSION AV193064.1 GI:5575216
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Shin-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Mochizuki,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yujii Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk612h9"
/clone_lib="Yujii Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 95 a 83 c 108 g 73 t 1 others
ORIGIN

Query Match      74.8%; Score 17.2; DB 26; Length 360;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||| ||| |||
Db 197 TCATCTCGTACTTCCACCGTC 176

RESULT 6
AW914126/c 545 bp mRNA EST 25-MAY-2000
LOCUS AW914126 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
DEFINITION RGI1A76 5' end, mRNA sequence.
ACCESSION AW914126
VERSION AW914126.1 GI:8079799
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 545)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
FEATURES
source
1..545
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGI1A76"
/clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 129 a 116 c 176 g 124 t
ORIGIN

Query Match      74.8%; Score 17.2; DB 122; Length 545;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgtttccacagtc 22
||||| ||| ||| ||| |||
Db 165 TCAGCTTGAACGTTCTCAGTC 144

RESULT 7
BE665364 567 bp mRNA EST 08-SEP-2000
LOCUS BE665364 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE665364
ACCESSION BE665364.1 GI:10025864
VERSION BE665364.1
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 567)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
JOURNAL EST discovery in cattle
COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred 18
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 71 row: P column: 4
Seq primer: ATTAGTGACACTATAG.
FEATURES
source
1..567
/organism="Bos taurus"
/db_xref="taxon:9913"

```

```

/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="Dh108"
/notes="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT      121 a   180 c   97 g   168 t   1 others
ORIGIN

Query Match      74.8%; Score 17.2; DB 138; Length 567;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 332 CATCTGGAAGGTTCCAGTAGTCA 353

RESULT 8
A2240360 A2240360 678 bp DNA GSS 15-JUN-2000
LOCUS
DEFINITION RPCI-23-32H8.TVB RPCI-23 Mus musculus genomic clone RPCI-23-32H8,
DNA sequence.
ACCESSION A2240360
VERSION A2240360.1 GI:8553470
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 678)
Zhao S., Niernan W., Feldblyum T., Malek J., Shatsman S., Akinret
B., Levins M., McGann S., Isegaye G., Geer K., Kroi M., de Jong P.,
and Fraser C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-32H8.TJB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac.ends/mouse/bac\_end\_intro.html
Plate: 32 row; H column: 8
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .678
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-32H8"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="Dh108"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      189 a   163 c   136 g   190 t
ORIGIN

```

```

Query Match      74.8%; Score 17.2; DB 240; Length 678;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 381 CATCTGGTACCTTCCACAGTCA 402

```

```

RESULT 9
A2669229/c
LOCUS
DEFINITION A2669229 879 bp DNA GSS 14-DEC-2000
ENTH421R Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, DNA sequence.
ACCESSION A2669229
VERSION A2669229.1 GI:11806375
KEYWORDS GSS.
SOURCE Entamoeba histolytica.
ORGANISM Entamoeba histolytica
REFERENCE Eukaryota; Entamoebidae; Entamoeba.
AUTHORS 1 (bases 1 to 879)
Loftus B., Van Aken S. and Fraser C.
TITLE Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 50
High quality sequence stop: 721.
Location/Qualifiers
1. .879
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: PHOSI; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
BASE COUNT      325 a   101 c   158 g   295 t
ORIGIN

```

```

FEATURES
source
1. .879
/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: PHOSI; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
BASE COUNT      325 a   101 c   158 g   295 t
ORIGIN

```

```

Query Match      74.8%; Score 17.2; DB 247; Length 879;
Best Local Similarity 86.4%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctgaacgttccacagtca 23
||||| ||| ||||| |||||
Db 862 CATCTGACGTTCACAGTCA 841

RESULT 10
AQ750993/c

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LOCUS      AQ750993      1471 bp      DNA      GSS      19-JUL-1999
DEFINITION HS_5574_B1_G10_SP6_RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate-1150 Col-19 Row-N, DNA sequence.
ACCESSION  AQ750993
VERSION    AQ750993.1 GI:5538151
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 1471)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pje@redjones.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1150 row: N column: 19
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 1471.
FEATURES   source
            1..1471
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="plate-1150 Col-19 Row=N"
                /clone_lib="RPCI-11 Human Male BAC Library"
                /sex="male"
            /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
            Male blood DNA was isolated from one randomly chosen donor
            and partially digested with a combination of EcoRI and
            EcoRI Methylase. Size selected DNA was cloned into the
            pBACE3.6 vector at EcoRI sites"
BASE COUNT 385 a 366 c 374 g 324 t 22 others
ORIGIN
Query Match 74.8%; Score 17.2; DB 233; Length 1471;
Best Local Similarity 86.4%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 catctgaacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 520 CATCTGGATGTTCCACATTCA 499

RESULT 11
BE198167/c
LOCUS      BE198167      239 bp      mRNA      EST      26-JUN-2000
DEFINITION uq75e03.y1 Soares_mammary_gland_NMLMG Mus musculus
            IMAGE:1548220 5' similar to qb-M37104 ATP SYNTHASE COUPLING FACTOR
            6 MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  BE198167
VERSION    BE198167.1 GI:8710336
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE  1 (bases 1 to 239)
AUTHORS   NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgaaps-remail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:953568
            Seq primer: -40RP from Gibco
            High quality sequence stop: 230.
FEATURES   Location/Qualifiers
            1..239
                /organism="Mus musculus"
                /db_xref="taxon:10090"
                /clone="IMAGE:1548220"
                /clone_lib="Soares_mammary_gland_NMLMG"
                /sex="female (lactating)"
                /tissue_type="mammary gland"
                /lab_host="DH10B"
            /note="Vector: pT73D-Pac (Pharmacia) with a modified
            polylinker; 1st strand cDNA was prepared from mammary
            gland tissue from a lactating female, and was then primed
            with a Not I - oligo(dT) primer. Double-stranded cDNA was
            ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the
            modified pT73 vector. Library is normalized. Library
            was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 63 a 47 c 66 g 63 t
ORIGIN
Query Match 73.0%; Score 16.8; DB 164; Length 239;
Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgacgtttccacagtca 23
||||| ||||| ||||| |||||
Db 77 TCTCTAACATTCCACAGTCA 58

RESULT 12
BE031712/c
LOCUS      BE031712      269 bp      mRNA      EST      09-JUL-2000
DEFINITION 130355 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  BE031712
VERSION    BE031712.1 GI:8326721
KEYWORDS   EST.
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 269)
AUTHORS   Fahrénkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
TITLE      Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
JOURNAL    Unpublished (2000)
COMMENT    Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt.trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTCCTCAGTCACGACG
            Plate: 60 row: H column: 12

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Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers

source

1. .269
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2P1G"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."

BASE COUNT

134 a 47 c 53 g 34 t 1 others

ORIGIN

Query Match

73.0%; Score 16.8; DB 162; Length 269;

Best Local Similarity

90.0%; Pred. No. 3.6e+02;

Matches 18; Conservative

0; Mismatches 2; Indels 0; Gaps 0;

Qy

4 tctcgaaacgttccacagtca 23

Db

70 TCTCGAACCTTCCAGAGTCA 51

RESULT 13

AW436470/c

LOCUS

AW436470 306 bp mRNA EST 09-JUL-2000

DEFINITION

76707 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION

AW436470

VERSION

AW436470.1 GI:6971776

KEYWORDS

EST.

SOURCE

pig.

ORGANISM

Sus scrofa

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

TITLE

1 (bases 1 to 306)

JOURNAL

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

COMMENT

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.

and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

EST discovery in swine

Unpublished (2000)

Unpublished (2000)

Contact: Smith TPL

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Tel: 402 762 4366

Fax: 402 762 4390

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -minmatch 12 options.

and -minmatch 12 options.

PCR Primers

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

BACKWARD: GTTTCCAGTCACGACG

Plate: 31 row: M column: 10

Plate: 31 row: M column: 10

Seq primer: ATTTAGGTGACACTATAG.

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

Location/Qualifiers

1. .306

1. .306

/organism="Sus scrofa"

/organism="Sus scrofa"

/db_xref="taxon:9823"

/db_xref="taxon:9823"

/clone_lib="MARC 2P1G"

/clone_lib="MARC 2P1G"

/tissue_type="pooled"

/tissue_type="pooled"

/lab_host="DH10B"

/lab_host="DH10B"

/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;

/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from testis, ovary,

Library made from pooled tissue from testis, ovary,

endometrium, hypothalamus, pituitary, and placenta."

endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT

70 a 99 c 66 g 71 t

ORIGIN

Query Match

73.0%; Score 16.8; DB 116; Length 306;

Best Local Similarity

90.0%; Pred. No. 3.6e+02;

Matches 18; Conservative

0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgaaacgttccacagtca 23

Db 222 TCTCGAACCTTCCAGAGTCA 203

RESULT 14

AW486759/c

LOCUS

AW486759 334 bp mRNA EST 09-JUL-2000

DEFINITION

76713 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION

AW486759

VERSION

AW486759.1 GI:7056865

KEYWORDS

EST.

SOURCE

pig.

ORGANISM

Sus scrofa

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

TITLE

1 (bases 1 to 334)

JOURNAL

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

COMMENT

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.

and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

EST discovery in swine

Unpublished (2000)

Unpublished (2000)

Contact: Smith TPL

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Tel: 402 762 4366

Fax: 402 762 4390

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 20

v0.980904.e. Vector identified by cross_match with the -minscore 20

and -minmatch 12 options.

and -minmatch 12 options.

PCR Primers

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

BACKWARD: GTTTCCAGTCACGACG

Plate: 31 row: N column: 10

Plate: 31 row: N column: 10

Seq primer: ATTTAGGTGACACTATAG.

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

Location/Qualifiers

1. .334

1. .334

/organism="Sus scrofa"

/organism="Sus scrofa"

/db_xref="taxon:9823"

/db_xref="taxon:9823"

/clone_lib="MARC 2P1G"

/clone_lib="MARC 2P1G"

/tissue_type="pooled"

/tissue_type="pooled"

/lab_host="DH10B"

/lab_host="DH10B"

/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;

/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from testis, ovary,

Library made from pooled tissue from testis, ovary,

endometrium, hypothalamus, pituitary, and placenta."

endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT

86 a 102 c 68 g 74 t

ORIGIN

0; Mismatches 2; Indels 0; Gaps 0;

Query Match

73.0%; Score 16.8; DB 116; Length 334;

Best Local Similarity

90.0%; Pred. No. 3.7e+02;

Matches 18; Conservative

0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctcgaaacgttccacagtca 23

Db 222 TCTCGAACCTTCCAGAGTCA 203

RESULT 15

BE198756/c

LOCUS

BE198756 416 bp mRNA EST 26-JUN-2000

DEFINITION

u82B12.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone

IMAGE:1548863 5', similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR

6, MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

BE198756

VERSION

BE198756.1 GI:8710925

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 416)
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:954211
Seq primer: -40RP from Gibco
High quality sequence stop: 380.
Location/Qualifiers
1..416
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:154863"
/clone_lib="Soares.mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia); digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 122 a 81 C 105 G 107 T 1 others
ORIGIN
Query Match 73.0%; Score 16.8; DB 164; Length 416;
Best Local Similarity 90.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 tctcgaacgttccacagtca 23
|||||
Db 78 TCTCTAACATTCCACAGTCA 59

Search completed: October 9, 2001, 18:20:16
Job time: 9786 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:47 ; Search time 515.84 Seconds
(without alignments)
27.997 Million cell updates/sec

Title: US-09-713-136-3
Perfect score: 23
Sequence: 1 tcactcgaacgttcacagtcac 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
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3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAV80098	Immunomodulatory o
2	23	100.0	23	AAA38067	Immunostimulatory
3	23	100.0	23	AAF77042	Immunostimulatory
C 4	17.4	75.7	3491	AAV74428	Staphylococcus aur
C 5	17.2	74.8	1192	AAV37952	Arabidopsis thalia
C 6	17.2	74.8	2021	AAC51260	Arabidopsis thalia
C 7	16.6	72.2	23	AAV80109	Oligo used in expe
C 8	16.2	70.4	932	AAV53340	DNA encoding a p11
C 9	16.2	70.4	1735	AAV53340	Arabidopsis thalia
C 10	16.2	70.4	6623	AAV75251	Nucleotide sequenc
C 11	15.8	68.7	508	AAA44452	Human secreted exp

C 12	15.8	68.7	3365	11	ARO05751	RNA 1 gene of CMV.
C 13	15.6	67.8	928	21	AAV42372	Arabidopsis thalia
C 14	15.6	67.8	2972	20	AAV24415	Human bladder tumor
C 15	15.6	67.8	3641	11	AAQ05752	Microspore-specific
C 16	15.6	67.8	3641	18	AAV48866	Brassica napus mic
C 17	15.6	67.8	6199	21	AAV75562	Human ORFX ORF117
C 18	15.6	67.8	9179	20	AAV13246	Enterococcus faeca
C 19	15.6	67.8	49999	20	AAV23904	Human LOBO homolog
C 20	15.2	66.1	611590	21	AAV22303	Arabidopsis thalia
C 21	15	65.2	22	19	AAV32079	Nucleotide sequenc
C 22	15	65.2	22	20	AAV36624	ISS-ODN DY1018 nuc
C 23	15	65.2	22	20	AAV80105	Oligo used in expe
C 24	15	65.2	22	20	AAV80096	Immunomodulatory o
C 25	15	65.2	22	20	AAV80097	Immunomodulatory o
C 26	15	65.2	22	20	AAV80102	Immunomodulatory o
C 27	15	65.2	22	20	AAV80103	Immunomodulatory o
C 28	15	65.2	22	21	AAV64051	Immunostimulatory
C 29	15	65.2	22	21	AAV96253	Sequence of a stab
C 30	15	65.2	22	21	AAV90458	CpG adjuvant oligo
C 31	15	65.2	22	21	AAV14467	Immunostimulatory
C 32	15	65.2	22	21	AAA38065	Immunostimulatory
C 33	15	65.2	22	21	AAA38066	Immunostimulatory
C 34	15	65.2	22	21	AAA38071	Immunostimulatory
C 35	15	65.2	22	21	AAA38072	Immunostimulatory
C 36	15	65.2	22	21	AAV55876	Immunomodulatory o
C 37	15	65.2	22	22	AAV77040	Immunomodulatory o
C 38	15	65.2	22	22	AAV77041	Immunostimulatory
C 39	15	65.2	22	22	AAV29800	Cholera toxin immu
C 40	15	65.2	22	22	AAV82107	Oligonucleotide OD
C 41	15	65.2	22	22	AAV92377	CG motif and CFA c
C 42	15	65.2	187	16	AAV20195	Human gene signatu
C 43	15	65.2	518	21	AAV77543	Human ORFX ORF3098
C 44	15	65.2	910	21	AAV51128	Arabidopsis thalia
C 45	15	65.2	913	21	AAV32622	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAV80098
ID AAV80098 standard; DNA; 23 BP.

XX AAV80098;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX Claim 6; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AAGTTTC, AACGTTTCG,

CC GACGTTTC, and GACGTTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

SQ

Query Match 100.0%; Score 23; DB 20; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcattctcgaacggttcacagctca 23

|||||

Db 1 tcattctcgaacggttcacagctca 23

RESULT 2

AAA38067

ID AAA38067 standard; DNA; 23 BP.

AC AAA38067;

XX

XX 24-AUG-2000 (first entry)

XX

XX Immunostimulatory sequence (ISS) #3.

XX

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

KW gp120; human immunodeficiency virus; HIV; immune response; infection;

KW development; ss.

XX

XX Synthetic.

XX

XX WO200021556-A1.

XX

XX 20-APR-2000.

XX

XX 08-OCT-1999; 99WO-US23677.

XX

XX 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

XX

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX

XX WPI; 2000-317846/27.

XX

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

PT HIV glycoprotein gp120 useful for modulating, stimulating an immune

PT response against HIV in an HIV infected individual

XX

XX Disclosure; Page 16; 65pp; English.

XX

XX The present invention relates to an immunostimulatory composition

CC comprising a human immunodeficiency virus (HIV) antigen, and an

CC immunomodulatory polynucleotide comprising an immunostimulatory sequence

CC (ISS). This sequence represents an ISS that can be used in the

CC composition. An immunostimulatory composition which comprises a gp120

CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or

CC stimulating a specific immune response against gp120 in an individual by

CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection in

CC with HIV, respectively. It is also used for treating an individual

CC infected with HIV in need of immune modulation.

XX

SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 23; DB 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcattctcgaacggttcacagctca 23

|||||

Db 1 tcattctcgaacggttcacagctca 23

RESULT 3

AAF77042

ID AAF77042 standard; DNA; 23 BP.

XX

XX AAF77042;

XX

XX 15-MAY-2001 (first entry)

DT

XX

XX Immunostimulatory DNA #2.

DE

XX

XX Modulate; Immune; antigen; immunostimulatory; ds.

XX

XX Synthetic.

XX

XX WO200112223-A2.

PN

XX

XX 22-FEB-2001.

PD

XX

XX 18-AUG-2000; 2000WO-US22835.

PF

XX

XX 19-AUG-1999; 99US-0149768.

PR

XX

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PA

XX

XX Van Nest G;

PI

XX

XX WPI; 2001-211136/21.

DR

XX

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen

XX

XX Disclosure; Page 15; 63pp; English.

PS

XX The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 23; DB 22; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcattctcgaacggttcacagctca 23

|||||

Db 1 tcattctcgaacggttcacagctca 23

RESULT 4

AAV74428/c

ID AAV74428 standard; DNA; 3491 BP.
 AC AAV74428;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE Staphylococcus aureus contig SEQ ID #117.
 XX
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH misc_feature 1741..1800
 FT /*tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence".
 XX
 XX EP786519-A2.
 XX
 PD 30-JUL-1997.
 XX
 XX 07-JAN-1997; 97EP-0100117.
 PF
 XX 05-JAN-1996; 96US-0009861.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 PI Rosen CA;
 PI
 XX WPI: 1997-374922/35.
 DR
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus
 XX stored on computer readable medium and used in the production of
 PT anti-S.aureus vaccines
 PT
 XX Claim 1: Page 665-666; 327lpp; English.
 PS
 XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the
 CC computer readable medium.
 XX
 SQ Sequence 3491 BP; 1321 A; 457 C; 679 G; 964 T; 70 other;
 Query Match 75.7%; Score 17.4; DB 18; Length 3491;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 atctcgaaacgtttccacagcta 23
 Db 1264 ATTTCCGACGTTCAACAGTCA 1244

RESULT 5
 AAC37952/C
 ID AAC37952 standard; DNA; 1192 BP.
 XX
 AC AAC37952;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19256.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
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 PR 28-MAY-1999; 99US-0136782.
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 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
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 PR 14-JUN-1999; 99US-0139119.
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PR 18-AUG-1999; 99US-0149426.

PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.8%; Score 17.2; DB 21: Length 1192;
Best Local Similarity 86.4%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcatctcgaacgtttccacgctc 22
||| ||||| ||||| |||
Db 683 TCAGATCGAACGTTCCACATTC 662

RESULT 6
AAC51260/C
ID AAC51260 standard; DNA; 2021 BP.
XX
AC AAC51260;


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PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161404.
PR 23-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.8%; Score 17.2; DB 21; Length 2021;
Best Local Similarity 86.4%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgttccacagtc 22
DB 1511 TCAGATCGAACGTTCCACATTC 1490

RESULT 7
AAV80109/c
ID AAV80109 standard; DNA: 23 BP.
AC AAV80109;
XX
XX
DT 12-MAR-1999 (first entry)
XX
DE Oligo used in experiments for stimulation of cytokine production.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
Synthetic.
XX WO9855495-A2.
XX 10-DEC-1998.
XX 05-JUN-1998; 98WO-US11578.
XX 06-JUN-1997; 97US-0048793.
(DYNA-) DYNAVAX TECHNOLOGIES CORP.
PI Dina D, Roman M, Schwartz D;
XX WPI; 1999-059898/05.
XX
XX Immunostimulatory oligonucleotides regulate the immune system - and
XX contain an immune-stimulating octanucleotide sequence; for treating
XX cancer, allergic and infectious diseases
XX
XX Example 1; Page 29; 63pp; English.
XX
XX The invention relates to immunomodulatory oligonucleotides that comprise
XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX sequences are selected from the group consisting of AAGTTCC, AACGTTCC,
XX GAGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
XX patients needing immune regulation, such as those suffering from cancer,
XX an allergic disease and asthma. They are also used to prevent infectious
XX diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and
XX Schistosoma. The immunomodulatory sequences are used to screen for human
XX immunostimulatory activity by incubating macrophage cells and the
XX oligonucleotide; and determining the relative amount of Th1-biased
XX cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
XX oligonucleotides that were tested for immunostimulatory activity. These
XX were used in experiments for the stimulation of cytokine production and
XX were found to lack immunostimulatory activity. The invention provides
XX specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX
XX Sequence 23 BP; 7 A; 3 C; 7 G; 6 T; 0 other;

Query Match 72.2%; Score 16.6; DB 20; Length 23;
Best Local Similarity 82.6%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattcgaacgttccacagtc 23
DB 23 TCATCTCTAACGTTCCAGAGTCA 1

RESULT 8
AAV53540/c
ID AAV53540 standard; DNA: 932 BP.
XX
XX AAV53540;
XX
XX 30-OCT-1998 (first entry)
XX
XX DNA encoding a p115 protein.
XX
XX Staphylococcus aureus protein; Immune response induction; eye infection;
XX antibody production; T-cell immune response; gastrointestinal infection;
XX respiratory infection; inhibitor; bacterial infection; cardiac infection;
XX central nervous system; kidney infection; urinary tract infection;
XX antimicrobial compound identification; broad spectrum antibiotic;
XX therapy; ss.
XX
XX Staphylococcus aureus.
XX
OS

```

XX PN EP841394-A2. 99US-0121825.
 XX PR 05-MAR-1999; 99US-0123180.
 XX PD 13-MAY-1998. 99US-0123548.
 XX PR 23-MAR-1999; 99US-0125788.
 XX PF 24-SEP-1997; 97EP-0307485. 99US-0126264.
 XX PR 29-MAR-1999; 99US-0126785.
 XX PR 01-APR-1999; 99US-0127462.
 XX PR 06-APR-1999; 99US-0128234.
 XX PR 08-APR-1999; 99US-0128714.
 XX PR 16-APR-1999; 99US-0129845.
 XX PR 19-APR-1999; 99US-0130077.
 XX PR 21-APR-1999; 99US-0130449.
 XX PR 23-APR-1999; 99US-0130510.
 XX PR 28-APR-1999; 99US-0130891.
 XX PR 30-APR-1999; 99US-0131449.
 XX PR 30-APR-1999; 99US-0132048.
 XX PR 04-MAY-1999; 99US-0132407.
 XX PR 05-MAY-1999; 99US-0132485.
 XX PR 06-MAY-1999; 99US-0132486.
 XX PR 07-MAY-1999; 99US-0132487.
 XX PR 11-MAY-1999; 99US-0132863.
 XX PR 14-MAY-1999; 99US-0134256.
 XX PR 14-MAY-1999; 99US-0134218.
 XX PR 14-MAY-1999; 99US-0134219.
 XX PR 14-MAY-1999; 99US-0134221.
 XX PR 18-MAY-1999; 99US-0134370.
 XX PR 18-MAY-1999; 99US-0134376.
 XX PR 19-MAY-1999; 99US-0134941.
 XX PR 20-MAY-1999; 99US-0135124.
 XX PR 21-MAY-1999; 99US-0135353.
 XX PR 24-MAY-1999; 99US-0135629.
 XX PR 25-MAY-1999; 99US-0136021.
 XX PR 27-MAY-1999; 99US-0136392.
 XX PR 28-MAY-1999; 99US-0136782.
 XX PR 01-JUN-1999; 99US-0137222.
 XX PR 03-JUN-1999; 99US-0137528.
 XX PR 04-JUN-1999; 99US-0137502.
 XX PR 07-JUN-1999; 99US-0137724.
 XX PR 08-JUN-1999; 99US-0138094.
 XX PR 10-JUN-1999; 99US-0138540.
 XX PR 10-JUN-1999; 99US-0138847.
 XX PR 14-JUN-1999; 99US-0139119.
 XX PR 16-JUN-1999; 99US-0139452.
 XX PR 16-JUN-1999; 99US-0139453.
 XX PR 17-JUN-1999; 99US-0139492.
 XX PR 18-JUN-1999; 99US-0139454.
 XX PR 18-JUN-1999; 99US-0139455.
 XX PR 18-JUN-1999; 99US-0139456.
 XX PR 18-JUN-1999; 99US-0139457.
 XX PR 18-JUN-1999; 99US-0139458.
 XX PR 18-JUN-1999; 99US-0139459.
 XX PR 18-JUN-1999; 99US-0139460.
 XX PR 18-JUN-1999; 99US-0139461.
 XX PR 18-JUN-1999; 99US-0139462.
 XX PR 18-JUN-1999; 99US-0139463.
 XX PR 18-JUN-1999; 99US-0139750.
 XX PR 18-JUN-1999; 99US-0139763.
 XX PR 21-JUN-1999; 99US-0139817.
 XX PR 22-JUN-1999; 99US-0139899.
 XX PR 23-JUN-1999; 99US-0140353.
 XX PR 23-JUN-1999; 99US-0140354.
 XX PR 24-JUN-1999; 99US-0140695.
 XX PR 28-JUN-1999; 99US-0140823.
 XX PR 29-JUN-1999; 99US-0140991.
 XX PR 30-JUN-1999; 99US-0141287.
 XX PR 01-JUL-1999; 99US-0141842.
 XX PR 01-JUL-1999; 99US-0142154.
 XX PR 02-JUL-1999; 99US-0142055.
 XX PR 06-JUL-1999; 99US-0142390.
 XX PR 08-JUL-1999; 99US-0142803.
 XX PR 09-JUL-1999; 99US-0142920.

XX 25-FEB-1999; 99US-0121825.
 XX PR 05-MAR-1999; 99US-0123180.
 XX PR 23-MAR-1999; 99US-0125788.
 XX PR 25-MAR-1999; 99US-0126264.
 XX PR 29-MAR-1999; 99US-0126785.
 XX PR 01-APR-1999; 99US-0127462.
 XX PR 06-APR-1999; 99US-0128234.
 XX PR 08-APR-1999; 99US-0128714.
 XX PR 16-APR-1999; 99US-0129845.
 XX PR 19-APR-1999; 99US-0130077.
 XX PR 21-APR-1999; 99US-0130449.
 XX PR 23-APR-1999; 99US-0130510.
 XX PR 28-APR-1999; 99US-0130891.
 XX PR 30-APR-1999; 99US-0131449.
 XX PR 30-APR-1999; 99US-0132048.
 XX PR 04-MAY-1999; 99US-0132407.
 XX PR 05-MAY-1999; 99US-0132485.
 XX PR 06-MAY-1999; 99US-0132486.
 XX PR 07-MAY-1999; 99US-0132487.
 XX PR 11-MAY-1999; 99US-0132863.
 XX PR 14-MAY-1999; 99US-0134256.
 XX PR 14-MAY-1999; 99US-0134218.
 XX PR 14-MAY-1999; 99US-0134219.
 XX PR 14-MAY-1999; 99US-0134221.
 XX PR 18-MAY-1999; 99US-0134370.
 XX PR 18-MAY-1999; 99US-0134376.
 XX PR 19-MAY-1999; 99US-0134941.
 XX PR 20-MAY-1999; 99US-0135124.
 XX PR 21-MAY-1999; 99US-0135353.
 XX PR 24-MAY-1999; 99US-0135629.
 XX PR 25-MAY-1999; 99US-0136021.
 XX PR 27-MAY-1999; 99US-0136392.
 XX PR 28-MAY-1999; 99US-0136782.
 XX PR 01-JUN-1999; 99US-0137222.
 XX PR 03-JUN-1999; 99US-0137528.
 XX PR 04-JUN-1999; 99US-0137502.
 XX PR 07-JUN-1999; 99US-0137724.
 XX PR 08-JUN-1999; 99US-0138094.
 XX PR 10-JUN-1999; 99US-0138540.
 XX PR 10-JUN-1999; 99US-0138847.
 XX PR 14-JUN-1999; 99US-0139119.
 XX PR 16-JUN-1999; 99US-0139452.
 XX PR 16-JUN-1999; 99US-0139453.
 XX PR 17-JUN-1999; 99US-0139492.
 XX PR 18-JUN-1999; 99US-0139454.
 XX PR 18-JUN-1999; 99US-0139455.
 XX PR 18-JUN-1999; 99US-0139456.
 XX PR 18-JUN-1999; 99US-0139457.
 XX PR 18-JUN-1999; 99US-0139458.
 XX PR 18-JUN-1999; 99US-0139459.
 XX PR 18-JUN-1999; 99US-0139460.
 XX PR 18-JUN-1999; 99US-0139461.
 XX PR 18-JUN-1999; 99US-0139462.
 XX PR 18-JUN-1999; 99US-0139463.
 XX PR 18-JUN-1999; 99US-0139750.
 XX PR 18-JUN-1999; 99US-0139763.
 XX PR 21-JUN-1999; 99US-0139817.
 XX PR 22-JUN-1999; 99US-0139899.
 XX PR 23-JUN-1999; 99US-0140353.
 XX PR 23-JUN-1999; 99US-0140354.
 XX PR 24-JUN-1999; 99US-0140695.
 XX PR 28-JUN-1999; 99US-0140823.
 XX PR 29-JUN-1999; 99US-0140991.
 XX PR 30-JUN-1999; 99US-0141287.
 XX PR 01-JUL-1999; 99US-0141842.
 XX PR 01-JUL-1999; 99US-0142154.
 XX PR 02-JUL-1999; 99US-0142055.
 XX PR 06-JUL-1999; 99US-0142390.
 XX PR 08-JUL-1999; 99US-0142803.
 XX PR 09-JUL-1999; 99US-0142920.

Query Match 70.48; Score 16.2; DB 19; Length 932;
 Best Local Similarity 85.74; Pred. No. 40;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 atctcgaacgtccacagtcga 23
 ||||| ||||| ||||| |||||
 Db 214 ATTTCGCACGTTCAACAGTCA 194

RESULT 9
 AAC46985/c
 ID AAC46985 standard; DNA: 1735 BP.
 XX AC AAC46985;
 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52135.
 XX KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-0301439.

This sequence encodes a Staphylococcus aureus protein that (based on homology with a Mycoplasma hyorhinis protein) is a Pil5 protein, and represents a DNA sequence of the invention.
 The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides.
 Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.

Claim 1: Page 199; 390pp; English.

New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful in vaccines and for treatment of bacterial infections of e.g. respiratory tract and central nervous system

Black MT, Burnham MKR, Hodgson JE, Knowles DJC;
 Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M;
 Ward JM;
 WPI; 1998-252940/23.
 P-PSDB; AAW7752.

PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 26-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.

PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 70.4%; Score 16.2; DB 21: Length 1735;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcattctcgacagcttcacagt 21
| ||| ||||| |||||
Db 402 TTATCTAGACGCTCCACACT 382

RESULT 10

AAT75251
ID AAT75251 standard; DNA: 6623-BP.

XX AC AAT75251;

XX DT 21-DEC-1998 (first entry)

XX DE Nucleotide sequence encoding human RAD50 intron 5, 3' end.

XX KW ds; human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;
central nervous system.

XX OS Homo sapiens.

XX PN W09727284-A2.

XX XX 31-JUL-1997.

XX PF 24-JAN-1997; 97WO-US01299.

XX PR 17-JUL-1996; 96US-0687080.

XX PR 26-JAN-1996; 96US-0592126.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Dolganov G;

XX XX

DR WP: 1997-393672/36.
 XX Human tumour suppressor gene RAD50 - useful to detect
 PT predisposition to, decrease risk of and treat cancer, also Septin-2
 PT homologues
 XX
 PS Claim 1: Page 103-106; 195pp; English.
 XX
 CC The human RAD50 (hRAD50) is involved in DNA repair and has tumour
 CC suppression activity, can be used to detect predisposition to, decrease
 CC the risk of or treat cancers, e.g. acute myeloid leukaemia,
 CC myelodysplastic syndrome, therapy related myelodysplastic syndrome,
 CC therapy related acute myeloid leukaemia, refractory anaemia or refractory
 CC anaemia with excess blasts. Also disclosed in this invention is Human
 CC Septin-2 homologues of which may be used as targets for cancer therapies
 CC and central nervous system directed treatment methods, and to measure the
 CC proliferative potential of selected cell types.
 XX
 SQ Sequence 6623 BP; 1823 A; 1242 C; 1314 G; 2244 T; 0 other;

Query Match 70.4%; Score 16.2; DB 18; Length 6623;
 Best Local Similarity 85.7%; Pred. No. 51;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tcatctcgaacgttcacagt 21
 ||||| ||| ||||| |||
 DB 587 tcatctcgaacgttcacagt 607

RESULT 11
 AAA44452/c
 ID AAA44452 standard; cDNA; 508 BP.
 XX
 AC AAA44452;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human secreted expressed sequence tag SEQ ID NO:1027.

XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
 KW expressed sequence tag; EST; probe; chemotactic; proliferative;
 KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
 KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
 KW antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
 KW antitumor; osteoprotective; neuroprotective; nootropic; antipsoriatic;
 KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
 KW vaccine; autolimmune diabetes; multiple sclerosis; allergic condition;
 KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KW central nervous system disorder; Alzheimer's disease; stroke;
 KW Parkinson's disease; Huntington's disease; coagulation disorder;
 KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
 KW tumour; infection; depression; psoriasis; ss.

XX Homo sapiens.
 OS
 XX WO200021991-A1.
 PN
 XX 20-APR-2000.
 PD
 XX 15-OCT-1999; 99WO-US24206.
 PF
 XX 15-OCT-1998; 98US-0104436.
 PR
 XX (GENY) GENETICS INST INC.
 PA
 XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR;
 PI
 XX WPI: 2000-317938/27.
 DR
 XX Isolated polynucleotides, and encoded proteins, comprising secreted

PT expressed sequence tags (seSTs), useful for treating various disorders
 XX such as autoimmune, infectious, and central nervous system disorders -
 PS Claim 1: Page 466; 803pp; English.
 XX
 CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
 CC sequence tags (seSTs), isolated from human, mouse, chicken and rat
 CC tissue sources. The seSTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
 CC antiasthmatic; vulnerary; antitumor; osteopathic; neuroprotective;
 CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The seSTs can be used for gene
 CC therapy and in vaccines. The seSTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the seSTs. Proteins encoded by the seSTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 508 BP; 178 A; 102 C; 126 G; 102 T; 0 other;

Query Match 68.7%; Score 15.8; DB 21; Length 508;
 Best Local Similarity 89.5%; Pred. No. 59;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 ctggaacgttcacagtca 23
 ||||| ||||| ||||| |||||
 DB 232 CTCGAAGGTTCCACAGTCA 214

RESULT 12
 AAQ05751
 ID AAQ05751 standard; cDNA; 3365 BP.
 XX
 AC AAQ05751;
 XX
 DT 19-DEC-1990 (first entry)
 XX
 DE RNA 1 gene of CMV.
 XX
 KW CMV; RNA 1; ss.
 XX
 OS Cucurbit mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..3075
 FT /*tag= a
 XX
 PN JP02167080-A.
 XX
 PD 27-JUN-1990.
 XX
 PF 19-DEC-1988; 88JP-0320015.
 XX
 PR 19-DEC-1988; 88JP-0320015.
 XX
 PA (NOGY-) NOGYO SEIBUTSU IDEN.
 XX
 DR WPI: 1990-241950/32.
 DR P-PSDB; AAR96531.
 XX
 PT Genome RNA 1 gene for prepn. of cucumber mosaic virus - codes

PT protein contg. specified sequence of 994 amino acids used in prepn.
PT of resistant plants.

XX PS Claim 2; Page 2; 10pp; Japanese.

XX CC The gene can be used to prepare plants which are resistant to
CC cucumber mosaic virus. The DNA was prep'd. from RNA isolated from
CC CMV-O virus.

XX SQ Sequence 3365 BP; 850 A; 734 C; 810 G; 971 T; 0 other;

Query Match 68.7%; Score 15.8; DB 11; Length 3365;
Best Local Similarity 89.5%; Pred. NO. 76;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tcattctggaacgttcaca 19
||||| ||||| |||||

Db 548 tcattctggaacgttcaca 566

RESULT 13

AAC42372/c
ID AAC42372 standard; DNA; 928 BP.

XX AC AAC42372;

XX DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35303.

XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;

XX KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

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PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 19-MAY-1999; 99US-0134768.

PR 20-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

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PR 01-JUN-1999; 99US-0137222.
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PR 22-JUN-1999; 99US-0139899.
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PR 27-JUL-1999; 99US-0145918.
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PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.

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PR 27-AUG-1999; 99US-0151065.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.8%; Score 15.6; DB 21; Length 938;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tcattcgaacgttccacagtc 22
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Db 894 TCATCTCTAGCTTCAACAGTC 873

RESULT 14
AAZ24415
ID AAZ24415 standard; cDNA; 2972 BP.
XX
AC AAZ24415;
XX
DT 14-FEB-2000 (first entry)
XX
DE Human bladder tumour cDNA library derived EST 27.
XX
KW Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
KW treatment; gene therapy; EST; ss.
XX
OS Homo sapiens.
XX
PN DE19818619-A1.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1998; 98DE-1018619.
XX
PR 21-APR-1998; 98DE-1018619.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX WPI; 1999-612028/53.
XX
PT New nucleic acid sequences expressed in bladder tumor tissue, and
PT derived polypeptides, for treatment of bladder tumor and identification
PT of therapeutic agents -
XX
PS Claim 3; Page 81-82; 132pp; German.
XX
CC This invention describes novel polypeptide fragments (I) and the
CC polynucleotides (II) that encode them that are highly expressed in a
CC human bladder tumour and which have cytostatic activity. (II) are used
CC for recombinant expression of (I) and to isolate complete genes. (I) are
CC used to identify agents suitable for treatment of bladder cancer, to
CC directly treat this form of cancer (including expression from gene
CC therapy vectors) or are used in a preparation for cancer treatment. (I)
CC is also used for the generation of specific antibodies. (II) are
CC identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of expression patterns. This
CC allows a significantly longer fragment of the gene to be revealed, and
CC therefore reduces the number of failures associated with the fact that
CC ESTs from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AA243260-243309 represent expressed sequence tag (EST)
CC fragments isolated from a human bladder tumour cDNA library which encode
CC the proteins represented in AA243260-243309.
XX
SQ Sequence 2972 BP; 710 A; 820 C; 773 G; 669 T; 0 other;

Query Match 67.8%; Score 15.6; DB 20; Length 2972;
Best Local Similarity 81.8%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 2 catctgaacgttcacagtc 23
||| || ||||| ||||| ||
Db 2171 catatcaaacgttcacagaca 2192
RESULT 15
AAQ05752/c
ID AAQ05752 standard; DNA; 3641 BP.
XX AAQ05752;
XX
DT 02-JAN-1991 (first entry)
DE Microspore-specific clone L10 from Brassica napus.
XX
KW microspore; controllable male sterility; blocking pollen formation;
KW anti-sense DNA; ss;
XX Brassica napus spp. oleifera Westar.
XX
FH Key Location/Qualifiers
FT TATA_signal 759..762
FT FT /*tag= a
FT prim_transcript 790..2780
FT FT /*tag= b
FT FT /note="includes 2 introns"
FT FT /note="precise position of end not determined"
FT FT 854..1104
FT FT /*tag= c
FT FT /number=1
FT FT 1105..1264
FT FT /*tag= d
FT FT /number=1
FT FT 1265..2374
FT FT /*tag= e
FT FT 2375..2461
FT FT /*tag= f
FT FT /number=2
FT FT 2462..2780
FT FT /*tag= g
FT FT /number=3
FT FT promoter 1..726
FT FT /*tag= h
XX
PN W09008828-A.
XX
XX
PD 09-AUG-1990.
XX
PF 02-FEB-1990; 90WO-CA00037.
XX
PR 03-FEB-1989; 89EP-0301053.
PR 02-FEB-1989; 89NZ-0227835.
PR 03-FEB-1989; 89US-0306438.
XX
PA (PALA-) PALADIN HYBRIDS INC.
XX
PI Fabijanski S, Albani D, Robert LS, Arnison PG;
XX
XX WPI: 1990-260937/34.
DR P-PSDB; AAR06518.
XX
XX Hybrid seed prodn. from plants with controllable male sterility -
PT induced by insertion of anti-sense DNA which blocks formation of
PT pollen.
XX
XX Claim 108; Page 159; 207pp; English.
PS
XX
XX Clone L10 was identified as microspore-specific and critical to
CC pollen formation and function. The promoter sequence may be cloned
CC into a plasmid carrying a pollen-specific gene in the anti-sense
CC orientation with respect to the promoter. The construct is

CC used to transform Brassica sp.
CC In addition the plasmid carries a resistance gene to a chemical
CC agent or stress. The sense and anti-sense genes are regulated such
CC that they are expressed at about the same time as each other.
CC Transfected plants are pollinated and selected according to
CC presence of the resistance gene. The promoter is inducible so that
CC plants are male-sterile only in the presence of the appropriate
CC inducer.
CC See also AAQ05749 and AAQ05753-Q05758.
XX
XX Sequence 3641 BP; 1094 A; 852 C; 673 G; 1012 T; 10 other;
SQ

Query Match 67.8%; Score 15.6; DB 11; Length 3641;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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||| ||||| ||||| ||
Db 2611 TCAGACGACGACGTTCCACATTC 2590

Search completed: October 9, 2001, 16:26:49
Job time: 2979 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:35 ; Search time 10334.3 Seconds
(without alignments)
32.887 Million cell updates/sec

Title: US-09-713-136-3

Perfect score: 23

Sequence: 1 tcatctgaacgttcacagtcacgta 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	23	16	US-09-296-477-4
2	23	100.0	23	18	US-09-415-186-3
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4	23	100.0	23	28	US-09-713-136-3
5	18.8	81.7	278	17	US-09-391-630-10240
6	18.8	81.7	278	25	US-09-654-617-60059
7	18.8	81.7	278	27	US-09-684-016-60059
8	18.8	81.7	278	46	US-60-144-084-9026
9	18.8	81.7	284	15	US-09-126-377-1868
10	17.8	77.4	1088	48	US-60-167-217-22953
11	17.8	77.4	3437	48	US-60-167-217-22952
12	17.4	75.7	612	16	US-09-270-849B-84639
13	17.4	75.7	3491	11	US-08-781-986A-117
14	17.4	75.7	3491	13	US-08-956-171-117
15	17.4	75.7	3491	13	US-08-956-171B-117
16	17.4	75.7	3491	13	US-08-956-171C-117
17	17.2	74.8	173	17	US-09-313-294A-3045
18	17.2	74.8	173	40	US-60-086-722-3045
19	17.2	74.8	310	45	US-60-138-103-17744
20	17.2	74.8	383	28	US-09-704-424-11573
21	17.2	74.8	395	19	US-09-521-640-8055
22	17.2	74.8	395	22	US-09-552-087-6707
23	17.2	74.8	407	28	US-09-704-424-13172
24	17.2	74.8	478	45	US-60-135-951-3244
25	17.2	74.8	506	25	US-09-654-617-409239
26	17.2	74.8	506	27	US-09-684-016-409239
27	17.2	74.8	516	28	US-09-704-424-10764
28	17.2	74.8	548	18	US-09-401-645-2094
29	17.2	74.8	571	17	US-09-371-508-3743
30	17.2	74.8	571	17	US-09-371-508-3743
31	17.2	74.8	571	29	US-09-747-508-3743
32	17.2	74.8	589	22	US-09-565-309A-34989
33	17.2	74.8	693	25	US-09-654-617-133602
34	17.2	74.8	693	27	US-09-684-016-133602
35	17.2	74.8	1509	16	US-09-270-849B-157528
36	17.2	74.8	1509	25	US-09-654-617-385350
37	17.2	74.8	1509	27	US-09-684-016-385350
38	17.2	74.8	10734	56	US-60-242-679-145
39	17.2	74.8	13205	31	US-09-835-811-3
40	17.2	74.8	18471	24	US-09-620-392-52694
41	17.2	74.8	26773	24	US-09-620-392-10511
42	17.2	74.8	26773	28	US-09-702-134-28340
43	17.2	74.8	29666	24	US-09-620-392-17397
44	17.2	74.8	32417	53	US-60-212-413-106
45	17.2	74.8	32768	53	US-60-212-356-108

ALIGNMENTS

RESULT 1
US-09-296-477-4
; Sequence 4, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296.477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092.329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048.793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-4

Query Match 100.0%; Score 23; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcattctgaaacgtttccacagtca 23
|||||
Db 1 tcattctgaaacgtttccacagtca 23

RESULT 2
US-09-415-186-3
; Sequence 3, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415.186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103.733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-3

Query Match 100.0%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcattctgaaacgtttccacagtca 23

Db 1 tcattctgaaacgtttccacagtca 23
|||||

RESULT 3
US-09-642-492-3
; Sequence 3, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642.492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149.768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-642-492-3

Query Match 100.0%; Score 23; DB 25; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcattctgaaacgtttccacagtca 23
|||||
Db 1 tcattctgaaacgtttccacagtca 23

RESULT 4
US-09-713-136-3
; Sequence 3, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713.136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165.467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-3

Query Match 100.0%; Score 23; DB 28; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcattctgaaacgtttccacagtca 23
|||||
Db 1 tcattctgaaacgtttccacagtca 23

RESULT 5
US-09-391-630-10240

```
; Sequence 10240, Application US/09391630
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Shukla, Hridayabhiramjam
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(15441)B
; CURRENT APPLICATION NUMBER: US/09/391,630
; CURRENT FILING DATE: 1999-09-08
; NUMBER OF SEQ ID NOS: 18889
; SEQ ID NO 10240
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-022-Q1-E1-A8
US-09-391-630-10240

Query Match      81.7%; Score 18.8; DB 17; Length 278;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 catctcgaaagcttccacagtca 23
    ||||| | ||||| |||||
Db  140 catctctaccgttccacagtca 161

RESULT 6
US-09-654-617-60059
; Sequence 60059, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong Annotated Plant Genes
; TITLE OF INVENTION: 38-21(15097)D
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 60059
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-654-617-60059

Query Match      81.7%; Score 18.8; DB 25; Length 278;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 catctcgaaagcttccacagtca 23
    ||||| | ||||| |||||
Db  140 catctctaccgttccacagtca 161

RESULT 7
US-09-684-016-60059
; Sequence 60059, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong Annotated Plant Genes
; TITLE OF INVENTION: 38-21(15097)D
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 60059
; LENGTH: 278
```

```
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-60059

Query Match      81.7%; Score 18.8; DB 27; Length 278;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 catctcgaaagcttccacagtca 23
    ||||| | ||||| |||||
Db  140 catctctaccgttccacagtca 161

RESULT 8
US-60-144-084-9026
; Sequence 9026, Application US/60144084
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Nelson, Donald E.
; APPLICANT: Shukla, Hridayabhiramjam
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(15444)B
; CURRENT APPLICATION NUMBER: US/60/144,084
; CURRENT FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 47776
; SEQ ID NO 9026
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-022-Q1-E1-A8
US-60-144-084-9026

Query Match      81.7%; Score 18.8; DB 46; Length 278;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 catctcgaaagcttccacagtca 23
    ||||| | ||||| |||||
Db  140 catctctaccgttccacagtca 161

RESULT 9
US-09-126-377-18668
; Sequence 1868, Application US/09126377
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Mullahy, Sara J.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT ADRENAL GL
; FILE REFERENCE: P2-0011 US
; CURRENT APPLICATION NUMBER: US/09/126,377
; CURRENT FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/054,913
; EARLIER FILING DATE: 97-06-08
; EARLIER APPLICATION NUMBER: 60/061,784
; EARLIER FILING DATE: 97-07-10
; NUMBER OF SEQ ID NOS: 2301
; SOFTWARE: PERL Program
; SEQ ID NO 1868
; LENGTH: 284
; TYPE: DNA
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-117
```


Query Match 75.7%; Score 17.4; DB 11; Length 3491;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23
11:111 11111 1111111

Db 1264 ATYTCGCACGTTCAACAGTCA 1244

RESULT 14
US-08-956-171-117/c
; Sequence 117, Application US/08956171
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-956-171-117

Query Match 75.7%; Score 17.4; DB 13; Length 3491;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23
11:111 11111 1111111

Db 1264 ATYTCGCACGTTCAACAGTCA 1244

RESULT 15
US-08-956-171B-117/c
; Sequence 117, Application US/08956171B
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171B
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 610-5790
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 3491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-08-956-171B-117

Query Match 75.7%; Score 17.4; DB 13; Length 3491;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 atctcgacggttcacagtcga 23
11:111 11111 1111111

Db 1264 ATYTCGCACGTTCAACAGTCA 1244

Search completed: October 9, 2001, 21:12:37
Job time: 20062 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:00 ; Search time 1391.6 Seconds
(without alignments)
37.721 Million cell updates/sec

Title: US-09-713-136-3
Perfect score: 23
Sequence: 1 tcattcgaacgttccacagtca 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.1.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	23	7	US-09-802-518-3
2	23	100.0	23	7	US-09-802-359-3
3	23	100.0	23	7	US-09-802-376-3
4	18.8	81.7	284	5	US-09-534-852-4062
5	17.2	74.8	83287	6	US-09-803-736-413
6	17	73.9	52784	6	US-09-803-736-255
7	16.6	72.2	219	6	US-09-804-730-2192
8	16.6	72.2	348	7	US-09-540-213-6759
9	16.6	72.2	1699	8	US-60-278-561-11368
10	16.6	72.2	6058	6	US-09-764-891-5493
11	16.6	72.2	31309	6	US-09-803-736-895
12	16.6	72.2	60476	6	US-09-803-736-823
13	16.6	72.2	116149	6	US-09-803-736-163
14	16.6	72.2	138181	6	US-09-803-736-184
15	16.2	70.4	136	8	US-60-253-378-24945
16	16.2	70.4	305	8	US-60-253-456-28528
17	16.2	70.4	434	6	US-09-904-809-7140
18	16.2	70.4	437	5	US-09-921-378-13959
19	16.2	70.4	441	5	US-09-921-378-13608
20	16.2	70.4	443	5	US-09-921-378-13607
21	16.2	70.4	459	6	US-09-904-809-6627
22	16.2	70.4	537	6	US-09-796-692-8874
23	16.2	70.4	581	6	US-09-796-692-7189
24	16.2	70.4	648	6	US-09-757-031-676
25	16.2	70.4	700	7	US-09-735-271-526

C 26	16.2	70.4	700	7	US-09-735-271-527	Sequence 527, App
C 27	16.2	70.4	1089	1	PCT-US01-04928A-44	Sequence 44, Appl
C 28	16.2	70.4	1091	1	PCT-US01-04928A-388	Sequence 388, App
C 29	16.2	70.4	1441	6	US-09-764-872-875	Sequence 875, App
C 30	16.2	70.4	78369	6	US-09-803-736-817	Sequence 817, App
C 31	15.8	68.7	97	7	US-09-853-369-1419	Sequence 1419, Ap
C 32	15.8	68.7	361	6	US-09-823-301-1400	Sequence 1400, Ap
C 33	15.8	68.7	476	7	US-09-834-366-2692	Sequence 2692, Ap
C 34	15.8	68.7	727	6	US-09-758-456-112	Sequence 112, App
C 35	15.8	68.7	1982	8	US-60-278-561-10217	Sequence 10217, A
C 36	15.8	68.7	2978	1	PCT-US01-14827-4939	Sequence 4939, Ap
C 37	15.8	68.7	97798	6	US-09-803-736-1079	Sequence 1079, Ap
C 38	15.6	67.8	214	8	US-60-253-654-11535	Sequence 11535, A
C 39	15.6	67.8	214	8	US-60-255-592-11535	Sequence 11535, A
C 40	15.6	67.8	240	7	US-09-912-292-25501	Sequence 25501, A
C 41	15.6	67.8	240	7	US-09-540-213-12400	Sequence 12400, A
C 42	15.6	67.8	240	7	US-09-773-518-160	Sequence 160, App
C 43	15.6	67.8	251	7	US-09-855-807-5902	Sequence 5902, Ap
C 44	15.6	67.8	297	8	US-60-253-654-11282	Sequence 11282, A
C 45	15.6	67.8	297	8	US-60-255-592-11282	Sequence 11282, A

ALIGNMENTS

RESULT 1
US-09-802-518-3
; Sequence 3, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-3

Query Match 100.0%; Score 23; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcattcgaacgttccacagtca 23
|||||
Db 1 tcattcgaacgttccacagtca 23

RESULT 2

US-09-802-359-3
; Sequence 3, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

```

; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-3

```

Query Match	100.0%	Score 23;	DB 7;	Length 23;
Best Local Similarity	100.0%	Pred. No.	0.016;	

Qy 1 tcattctgaacggttcacagtca 23
|||||

Db 1 tcattctgaacggttcacagtca 23

```

RESULT      3
US-09-802-376-3
; Sequence 3, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-3

```

Query Match	100.0%	Score 23;	DB 7;	Length 23;
Best Local Similarity	100.0%	Pred. NO.	0.016;	
Matches 23; Conservative	0;	Mismatches	0;	Indels

Qy 1 tcattctgaacggttccacagtca 23
|||||

Db 1 tcattctgaacggttccacagtca 23

```

RESULT      4
US-09-534-852-4062
; Sequence 4062, Application US/09534852
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ORGANELLE MOLECULES
; FILE REFERENCE: PD-1019 CJP
; CURRENT APPLICATION NUMBER: US/09/534, 852
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 21207
; SOFTWARE: PERL Program
; SEQ ID NO 4062
; LENGTH: 284
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: rat00055003

```

; NAME/KEY: unsure
 ; LOCATION: 108, 180, 204, 208, 216, 231, 252
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-534-852-4062

Query Match 81.7%; Score 18.8; DB 5; Length 284;
 • Best Local Similarity 90.9%; Pred. NO. 3.8;
 Matches 20; Conservative 0; Mismatches 2; Indels

Oy 2 catctcgaacggttcacagtc 23
| | | | | | | | | |
Db 123 cqtctcgaacgttccacagtc 144

RESULT 5
US-09-803-736-413
; Sequence 413, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 413
; LENGTH: 83287
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-413

Query Match 74.8%; Score 17.2; DB 6; Length 83287;
Best Local Similarity 86.4%; Pred. NO. 58;
Matches 19; Conservative 0; Mismatches 3; Indels 0;

Qy 1 tcattctcgaacgttccacagtc 22
||| ||||| ||||| ||
Db 5485 tcagatcgaacgttccacattc 5506

RESULT 6
US-09-803-736-255/c
; Sequence 255, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ. ID. NO 255
; LENGTH: 52784
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-255

Query Match 73.9%; Score 17; DB 6; Length 52784;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 tctcgacgcttccacag 20
|||||
Db 43475 TCTCGACGTTCCACAG 43459

RESULT 7
US-09-804-730-2192
; Sequence 2192, Application US/09804730
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Hammond-Kosack, Kim
; APPLICANT: Masucci, James D.
; APPLICANT: Urban, Martin
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51838)B
; CURRENT APPLICATION NUMBER: US/09/804,730
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,657
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 22828
; SEQ ID NO 2192
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Triticum aestivum
; OTHER INFORMATION: Clone ID: LIB3350-034-P1-K1-D4
US-09-804-730-2192

Query Match 72.2%; Score 16.6; DB 6; Length 219;
Best Local Similarity 82.6%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgacgcttccacagtc 23
|||||
Db 126 tcaactcgacgcttccacagca 148

RESULT 8
US-09-540-213-6759
; Sequence 6759, Application US/09540213
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF LIVER AND PANCREAS
; FILE REFERENCE: PD-1031 CIP
; CURRENT APPLICATION NUMBER: US/09/540,213
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53844
; SEQ ID NO 6759
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00312093
; NAME/KEY: unsure
; LOCATION: 23, 239, 283
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-213-6759

Query Match 72.2%; Score 16.6; DB 7; Length 348;

Best Local Similarity 82.6%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgacgcttccacagtc 23
|||||
Db 25 tcatatcaacgcttgacagaca 47

RESULT 9
US-60-278-561-11368/c
; Sequence 11368, Application US/60278561
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0012-1 P
; CURRENT APPLICATION NUMBER: US/60/278,561
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 15598
; SOFTWARE: PERL Program
; SEQ ID NO 11368
; LENGTH: 1699
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 404459.1
; NAME/KEY: unsure
; LOCATION: 1105-1155
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-561-11368

Query Match 72.2%; Score 16.6; DB 8; Length 1699;
Best Local Similarity 82.6%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgacgcttccacagtc 23
|||||
Db 192 TCTTCTCGAAGGTTCTCGAGTCA 170

RESULT 10
US-09-764-891-5493
; Sequence 5493, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5493
; LENGTH: 6058
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-5493

Query Match 72.2%; Score 16.6; DB 6; Length 6058;
Best Local Similarity 82.6%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tcatctcgacgcttccacagtc 23
|||||
Db 3334 tcatgtcaagtgcttccacagtc 3356

```
RESULT 11
US-09-803-736-895/c
; Sequence 895, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 895
; LENGTH: 31309
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-895

Query Match 72.2%; Score 16.6; DB 6; Length 31309;
Best Local Similarity 82.6%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23
||||| ||||||| |||||||
Db 31244 TCCTCTCGAACCTTCCACAGTCA 31222

RESULT 12
US-09-803-736-823
; Sequence 823, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 823
; LENGTH: 60476
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-823

Query Match 72.2%; Score 16.6; DB 6; Length 60476;
Best Local Similarity 82.6%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23
||||| ||||||| |||||||
Db 45102 tcattctgaaagcttccacagtca 45124

RESULT 13
US-09-803-736-163
; Sequence 163, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 163
; LENGTH: 116149
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-163

Query Match 72.2%; Score 16.6; DB 6; Length 116149;
Best Local Similarity 82.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23
||||| ||||||| |||||||
Db 25124 tcattctgaaagcttccacagtca 25146

RESULT 14
US-09-803-736-184/c
; Sequence 184, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 184
; LENGTH: 138181
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-184

Query Match 72.2%; Score 16.6; DB 6; Length 138181;
Best Local Similarity 82.6%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattctgaaagcttccacagtca 23
||||| ||||||| |||||||
Db 91835 TAATCTCGAACCTTCCGAAAGTCA 91813

RESULT 15
US-60-253-378-24945
; Sequence 24945, Application US/60253378
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; TITLE OF INVENTION: Polynucleotides isolated from plants
; FILE REFERENCE: 1054P3
; CURRENT APPLICATION NUMBER: US/60/253,378
; CURRENT FILING DATE: 2000-11-27
```

; NUMBER OF SEQ ID NOS: 40367
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24945
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-378-24945

Query Match 70.4%; Score 16.2; DB 8; Length 136;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 catctcgaaagttccacagtc 22
||| ||||| |||||
Db 2 catttgaacgttccaaagtc 22

Search completed: October 9, 2001, 21:36:13
Job time: 21233 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:41:59 ; Search time 217.64 Seconds
(without alignments)
20,006 Million cell updates/sec

Title: US-09-713-136-3

Perfect score: 23

Sequence: 1 tcatctcgacgtttccacagtca 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	70.4	6623	2	US-08-687-080-68
2	15.8	68.7	719	4	US-08-998-416-626
3	15.6	67.8	3641	1	US-08-030-098-5
C 4	15.2	66.1	321	4	US-09-060-758-260
5	15	65.2	2265	3	US-08-906-865-2
C 6	15	65.2	3383	3	US-08-884-324-12
C 7	15	65.2	11464	3	US-08-884-324-13
C 8	15	65.2	28994	3	US-08-884-324-14
9	14.6	63.5	836	4	US-08-998-416-316
10	14.6	63.5	1041	1	US-08-842-540-1
11	14.6	63.5	1041	1	US-08-842-540-3
12	14.6	63.5	1041	1	US-08-690-413-1
13	14.6	63.5	1041	1	US-08-690-413-3
14	14.6	63.5	1853	1	US-08-553-110-2
15	14.6	63.5	4279	4	US-09-041-888-22
C 16	14.4	62.6	2350	1	US-08-843-521-1
C 17	14.4	62.6	2350	1	US-09-012-871-1
18	14.2	61.7	816	3	US-08-776-251-10
C 19	14.2	61.7	816	3	US-08-776-251-10
C 20	14.2	61.7	1596	6	5180813-1
C 21	14.2	61.7	1893	3	US-08-878-474-10
C 22	14.2	61.7	2039	3	US-09-276-531-45
C 23	14	60.9	76	1	US-08-447-169A-90
C 24	14	60.9	76	1	US-08-447-169A-100
C 25	14	60.9	76	2	US-08-233-012C-90
C 26	14	60.9	76	2	US-08-233-012C-100
C 27	14	60.9	836	2	US-08-967-364-4

28	14	60.9	836	3	US-09-368-408-4	Sequence 4, Appl
C 29	14	60.9	1229	2	US-08-790-572-2	Sequence 2, Appl
C 30	14	60.9	1229	2	US-09-213-398-2	Sequence 2, Appl
31	14	60.9	1613	2	US-08-812-204-1	Sequence 1, Appl
C 32	14	60.9	3182	2	US-08-595-559-6	Sequence 6, Appl
33	14	60.9	4118	1	US-08-119-125A-3	Sequence 3, Appl
34	14	60.9	4615	2	US-08-674-351-3	Sequence 3, Appl
35	14	60.9	12847	1	US-08-550-715-1	Sequence 1, Appl
C 36	14	60.9	13146	2	US-08-724-354D-3	Sequence 3, Appl
C 37	14	60.9	13146	3	US-09-270-984A-3	Sequence 3, Appl
C 38	13.8	60.0	361	6	5304466-1	Patent No. 5304466
C 39	13.8	60.0	4649	6	5183745-1	Patent No. 5183745
C 40	13.8	60.0	6443	6	5183745-5	Patent No. 5183745
41	13.8	60.0	11561	1	US-08-450-332-1	Sequence 1, Appl
42	13.8	60.0	11561	2	US-08-637-640-1	Sequence 1, Appl
43	13.8	60.0	11561	4	US-09-004-406C-1	Sequence 1, Appl
44	13.6	59.1	63	3	US-07-921-104D-36	Sequence 36, Appl
C 45	13.6	59.1	77	1	US-08-447-169A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-687-080-68
; Sequence 68, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3' END OF INTRON 5 OF RAD50 GENOMIC
; INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-68

Query Match 70.4% Score 16.2; DB 2; Length 6623;

```
Best Local Similarity 85.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacagt 21
    ||||| ||| ||||| |||
Db 587 TCATCTTAACCTCCAGAGT 607

RESULT 2
US-08-998-416-626
; Sequence 626, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippson, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 626:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1423UP
; US-08-998-416-626

Query Match 68.7%; Score 15.8; DB 4; Length 719;
Best Local Similarity 89.5%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacac 19
    ||||| ||| ||||| |||
Db 498 TCATCCGCACAGTTCACCA 516

RESULT 3
US-08-030-096-5/c
; Sequence 5, Application US/08030096
; Patent No. 5426041
; GENERAL INFORMATION:
; APPLICANT: Fabijanski, Steven F.
; APPLICANT: Arnison, Paul G.
; TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
; TITLE OF INVENTION: SEED PRODUCTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,096
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/556,917
; FILING DATE: 20-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA91/00255
; FILING DATE: 22-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/164/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(854...1105, 1266...2375, 2463...2779)
; US-08-030-096-5

Query Match 67.8%; Score 15.6; DB 1; Length 3641;
Best Local Similarity 81.8%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tcattcgaacgttcacagtc 22
    ||| ||||| ||||| |||
Db 2611 TCAGACGAACGTTCCACATTC 2590

RESULT 4
US-09-060-756-260/c
; Sequence 260, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
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NUMBER OF SEQ ID NOS: 743
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 260
LENGTH: 321
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: unsure
LOCATION: (various positions within the sequence)
OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-260

Query Match 66.18; Score 15.2; DB 4; Length 321;
Best Local Similarity 85.08; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tcattcgaacgttccacag 20
|||||
Db 87 TCATCTCGAAGCTCGCGAG 68

RESULT 5
US-08-906-865-2
Sequence 2, Application US/08906865
Patent No. 6040168
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906.865
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-202
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2265 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: /desc = "Synapsin III"
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-906-865-2

Query Match 65.2%; Score 15; DB 3; Length 2265;
Best Local Similarity 78.3%; Pred. No. 51;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 tcattcgaacgttccacagtca 23
|||||
Db 15 TCATCTGCATCCATCCACAGCCA 37

RESULT 6
US-08-884-324-12/c
Sequence 12, Application US/08884324
Patent No. 6060283
GENERAL INFORMATION:
APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahito KURIMOTO
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA-1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3383 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
FEATURE:
NAME/KEY: intron
LOCATION: 1..3383
IDENTIFICATION METHOD: E
US-08-884-324-12

Query Match 65.2%; Score 15; DB 3; Length 3383;
Best Local Similarity 78.3%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tcattcgaacgttccacagtca 23
|||||
Db 1499 TCCACTAGGACGTTCCACAGACA 1477

RESULT 7
US-08-884-324-13/c
Sequence 13, Application US/08884324

```

: LOCATION: 6452..11224
: IDENTIFICATION METHOD: E
: NAME/KEY: mat peptide
: LOCATION: 11225..11443
: IDENTIFICATION METHOD: S
: NAME/KEY: 3'UTR
: LOCATION: 11444..11464
: IDENTIFICATION METHOD: E
:
: US-08-884-324-13
:
: Query Match 65.2%; Score 15; DB 3; Length 11464;
: Best Local Similarity 78.3%; Pred. No. 66;
: Matches 18; Conservative 0; Mismatches 5; Indels 0;
:
Qy 1 tcactcgaacgtccacagcta 23
   ||| ||||| ||||| ||
Db 2964 TCCACTAGGACGTCCACACACA 2942
:
RESULT 8
US-08-884-324-14/c
: Sequence 14, Application US/08884324
: Patent No. 6060283
: GENERAL INFORMATION:
: APPLICANT: Takanoiri OKURA
: APPLICANT: kakuji TORIGOE
: APPLICANT: Masahi KURIMOTO
: TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
: TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/884,324
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 185,305/96
: FILING DATE: 27-JUN-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: OKURA-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28994 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: ORIGINAL SOURCE:
: ORGANISM: human
: TISSUE TYPE: placenta
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..15606
: IDENTIFICATION METHOD: E
: NAME/KEY: leader peptide
: LOCATION: 15607..15685

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;
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-842-540-1

Query Match      63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaaacgttccacagtca 23
Db 92 ATTACGACCGTTTCACAGTCA 112

RESULT 11
US-08-842-540-3
; Sequence 3, Application US/08842540
; Patent No. 5776695
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; TITLE OF INVENTION: Biosynthetic Gene DDL From Streptococcus
; TITLE OF INVENTION: Pneumoniae
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842.540
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10556
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-842-540-3

Query Match      63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaaacgttccacagtca 23
Db 92 ATTACGACCGTTTCACAGTCA 112

RESULT 12
US-08-690-413-1
; Sequence 1, Application US/08690413
; Patent No. 5776733
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; TITLE OF INVENTION: Biosynthetic Gene DDL From Streptococcus
; TITLE OF INVENTION: Pneumoniae
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690.413
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10556
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-690-413-1

Query Match      63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 81.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 atctcgaaacgttccacagtca 23
Db 92 ATTACGACCGTTTCACAGTCA 112

RESULT 13
US-08-690-413-3
; Sequence 3, Application US/08690413
; Patent No. 5776733
; GENERAL INFORMATION:
; APPLICANT: Skatrud, Paul L.
; TITLE OF INVENTION: Biosynthetic Gene DDL From Streptococcus
; TITLE OF INVENTION: Pneumoniae
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690.413
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10556
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1041 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; NAME/KEY: CDS
; LOCATION: 1..1041
US-08-690-413-3
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/690,413
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Webster, Thomas D.
;; REGISTRATION NUMBER: 39,872
;; REFERENCE/DOCKET NUMBER: X-10556
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 317-276-3334
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1041 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-690-413-3

Query Match 63.5%; Score 14.6; DB 1; Length 1041;
Best Local Similarity 61.9%; Pred. No. 73;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 atctcgacgttcacagtc 23
I: ||| |||: |||||: ||
Db 92 AUUAGGACCGUUCACAGUCA 112

RESULT 14

US-08-553-110-2
; Sequence 2, Application US/08553110
; Patent No. 5723301

;; GENERAL INFORMATION:
;; APPLICANT: Burke, James R.
;; APPLICANT: Vance, Jeffrey M.
;; APPLICANT: Enghild, Jan
;; APPLICANT: Strittmatter, Warren J.
;; TITLE OF INVENTION: Therapeutics for Diseases Associated
;; TITLE OF INVENTION: with CAG Trinucleotide Repeat Expansion
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kenneth D. Sibley
;; STREET: P.O. Drawer 34009
;; CITY: Charlotte
;; STATE: No. 5723301th Carolina
;; COUNTRY: United States of America
;; ZIP: 28234

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION NUMBER: US/08/553,110
;; FILING DATE:

;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sibley, Kenneth D.
;; REGISTRATION NUMBER: 31,665
;; REFERENCE/DOCKET NUMBER: 5405-117
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-420-2200
;; TELEFAX: 919-881-3175

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1853 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide

US-08-553-110-2

Query Match 63.5%; Score 14.6; DB 1; Length 1853;
Best Local Similarity 81.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 catctcgacgttcacagtc 22
||||||| ||||| ||
Db 368 CATCTCGAATGTTCCAGGCTC 388

RESULT 15

US-09-041-886-22
; Sequence 22, Application US/09041886
; Patent No. 6235872

;; GENERAL INFORMATION:
;; APPLICANT: Bredesen, Dale E.
;; APPLICANT: Rabizadeh, Sharroz
;; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
;; TITLE OF INVENTION: Polypeptides and Methods of Use
;; NUMBER OF SEQUENCES: 72
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION NUMBER: US/09/041.886
;; FILING DATE:

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 2626
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001

;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4279 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 239..3794
US-09-041-886-22

Query Match 63.5%; Score 14.6; DB 4; Length 4279;
Best Local Similarity 81.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 catctcgacgttcacagtc 22
||||||| ||||| ||
Db 843 CATCTCGAATGTTCCAGGCTC 863

Search completed: October 9, 2001, 15:42:02
Job time: 292 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:18:53 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgtccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
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9: gb_pat1: *
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12: gb_pl1: *
13: gb_pl2: *
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22: em_htg_hum1: *
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89: gb_pr5: *
90: gb_pr6: *
91: gb_pr7: *
92: gb_pr8: *
93: gb_pr9: *
94: gb_roi: *
95: gb_ro2: *
96: gb_in4: *
97: gb_pr10: *
98: em_ba3: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	9 AX036946	AX036946 Sequence
2	22	100.0	22	10 AX083678	AX083678 Sequence
3	21	95.5	22	10 AX083680	AX083680 Sequence
4	20.4	92.7	22	9 AX036945	AX036945 Sequence
5	20.4	92.7	22	9 AX046993	AX046993 Sequence
6	20.4	92.7	22	10 AX083675	AX083675 Sequence
7	19.4	88.2	22	10 AX083681	AX083681 Sequence
8	19.4	88.2	145939	79 AL158143	AL158143 Homo sapi

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9 18.8 85.5 22 9 AX036952
10 18.8 85.5 22 10 AX03676 Sequence
11 18.4 83.6 22 10 AX03682 Sequence
12 17.8 80.9 4334 85 AB033099 Homo sapi
13 17.8 80.9 74992 74 AC069574
14 17.8 80.9 74992 74 AC069574
15 17.8 80.9 109120 79 AL157945
16 17.8 80.9 110762 81 AL391244
17 17.8 80.9 165010 93 HSD3839B4
18 17.8 80.9 186529 73 AC068363
19 17.8 80.9 197748 70 AC026283
20 17.8 80.9 197748 70 AC026283
21 17.4 79.1 108055 61 AC009521
22 17.4 79.1 168601 86 AC008123
23 17.4 79.1 169423 74 AC069309
24 17.4 79.1 169532 62 AC012513
25 17.2 78.2 22 9 AX036944
26 17.2 78.2 13302 1 AE001695
27 17.2 78.2 16854 1 AE001722
28 17.2 78.2 103785 13 ATE1116
29 17.2 78.2 146851 71 AC027697
30 17.2 78.2 152318 66 AC021766
31 17.2 78.2 158786 68 AC023337
32 17.2 78.2 166229 81 AL512601
33 17.2 78.2 190866 64 AC015954
34 17.2 78.2 193071 74 AC069535
35 17.2 78.2 193167 94 AC026767
36 17.7 77.3 7131 14 PPM5AS
37 16.8 76.4 1754 4 AB029058
38 16.8 76.4 102798 78 AL138730
39 16.8 76.4 111234 88 AC079157
40 16.8 76.4 135714 90 AL160037
41 16.8 76.4 142172 69 AC025957
42 16.8 76.4 151992 61 AC009939
43 16.8 76.4 153241 88 AC023510
44 16.8 76.4 157996 94 AC019026
45 16.8 76.4 159072 74 AC073123
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ALIGNMENTS

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RESULT 1
AX036946
LOCUS AX036946 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036946
VERSION AX036946.1 GI:11226374
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22
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```
RESULT 2
AX083678
LOCUS AX083678 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083678
VERSION AX083678.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
sequences and compositions for use therein
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g 6 t
BASE COUNT 6 a 4 c 6 g 6 t
ORIGIN
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22
```

```
RESULT 3
AX083680
LOCUS AX083680 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION AX083680
VERSION AX083680.1 GI:13185412
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
sequences and compositions for use therein
JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5-bromocytosine"
6 a 3 c 6 g 6 t 1 others
modified_base 11
BASE COUNT 6 a 3 c 6 g 6 t 1 others
ORIGIN
Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
Oy 1 tgactgtgaacgttcacatga 22
|||||
Db 1 TGACTGTGAANGTTCCAGATGA 22
```

```
RESULT 4
AX036945
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LOCUS AX036945 22 bp DNA PAT 16-NOV-2000
 DEFINITION Sequence 2 from Patent FR2790955.
 ACCESSION AX036945
 VERSION AX036945.1 GI:11226373
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Carpentier A.
 JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
 ASSIST PUBL HOPITAUX DE PARIS (FR)
 FEATURES Location/Qualifiers
 source 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="oligodeoxynucleotide"
 BASE COUNT 6 a 3 c 7 g 6 t
 ORIGIN
 Query Match 92.7%; Score 20.4; DB 9; Length 22;
 Best Local Similarity 95.5%; Pred. No. 5.1;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacggtccagatga 22
 |||||||
 Db 1 TGA CTGTGAACGTTTCGAGATGA 22
 RESULT 5
 AX046993
 LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
 DEFINITION Sequence 2 from Patent WO0067787.
 ACCESSION AX046993
 VERSION AX046993.1 GI:11876420
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Moss, R.B.
 TITLE HIV immunogenic compositions and methods
 JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
 THE IMMUNE RESPONSE CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="phosphorothioate-modified synthetic oligodeoxynucleotide"
 BASE COUNT 6 a 3 c 7 g 6 t
 ORIGIN
 Query Match 92.7%; Score 20.4; DB 9; Length 22;
 Best Local Similarity 95.5%; Pred. No. 5.1;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacggtccagatga 22
 |||||||
 Db 1 TGA CTGTGAACGTTTCGAGATGA 22
 RESULT 6
 AX083675
 LOCUS AX083675 22 bp DNA PAT 28-FEB-2001
 DEFINITION Sequence 1 from Patent WO0112223.
 ACCESSION AX083675
 VERSION AX083675.1 GI:13185407
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM

artificial sequence.
 1 (bases 1 to 22)
 AUTHORS van Nest, G.
 TITLE Methods of modulating an immune response using immunostimulatory sequences and compositions for use therein
 JOURNAL Patent: WO 0112223-A 1 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 FEATURES Location/Qualifiers
 source 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Synthetic construct"
 BASE COUNT 6 a 3 c 7 g 6 t
 ORIGIN
 Query Match 92.7%; Score 20.4; DB 10; Length 22;
 Best Local Similarity 95.5%; Pred. No. 5.1;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacggtccagatga 22
 |||||||
 Db 1 TGA CTGTGAACGTTTCGAGATGA 22
 RESULT 7
 AX083681
 LOCUS AX083681 22 bp DNA PAT 28-FEB-2001
 DEFINITION Sequence 7 from Patent WO0112223.
 ACCESSION AX083681
 VERSION AX083681.1 GI:13185413
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequence.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS van Nest, G.
 TITLE Methods of modulating an immune response using immunostimulatory sequences and compositions for use therein
 JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 FEATURES Location/Qualifiers
 source 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="5-bromocytosine"
 modified_base 11
 /mod_base=OTHER 7 g 6 t 1 others
 BASE COUNT 6 a 2 c 7 g 6 t 1 others
 ORIGIN
 Query Match 88.2%; Score 19.4; DB 10; Length 22;
 Best Local Similarity 90.9%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 tgactgtgaacggtccagatga 22
 |||||||
 Db 1 TGA CTGTGAACGTTTCGAGATGA 22
 RESULT 8
 AL158143
 LOCUS AL158143 145939 bp DNA HTG 08-APR-2001
 DEFINITION Homo sapiens chromosome X clone RP5-1074I8, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.
 ACCESSION AL158143
 VERSION AL158143.12 GI:13567909
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 145939)
Mclay, K.
Direct Submission
Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Apr 9, 2001 this sequence version replaced gi:9931672.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dj107418
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
Dye-terminator Big Dye; 92% of reads
Consensus quality: 137464 bases at least Q40
Consensus quality: 141229 bases at least Q30
Consensus quality: 143037 bases at least Q20
Insert size: 144339; sum-of-contigs
Insert size: 111741; 30.4% error; agarose-fp
Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.27x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
* 3025 3124: gap of 100 bp
* 3125 10834: contig of 7110 bp in length
* 10835 10934: gap of 100 bp
* 10935 13595: contig of 2661 bp in length
* 13596 13695: gap of 100 bp
* 13696 16092: contig of 2397 bp in length
* 16093 16192: gap of 100 bp
* 16193 22530: contig of 6338 bp in length
* 22531 22630: gap of 100 bp
* 22631 27253: contig of 4623 bp in length
* 27254 27353: gap of 100 bp
* 27354 30261: contig of 2908 bp in length
* 30262 30361: gap of 100 bp
* 30362 33611: contig of 3250 bp in length
* 33612 33711: gap of 100 bp
* 33712 38262: contig of 4551 bp in length
* 38263 38362: gap of 100 bp
* 38363 40615: contig of 2253 bp in length
* 40616 40715: gap of 100 bp
* 40716 44299: contig of 3584 bp in length
* 44300 44399: gap of 100 bp
* 44400 47229: contig of 2830 bp in length
* 47230 47329: gap of 100 bp
* 47330 52776: contig of 5447 bp in length
* 52777 52876: gap of 100 bp
* 52877 60226: contig of 7350 bp in length
* 60227 60326: gap of 100 bp
* 60327 62930: contig of 2604 bp in length
* 62931 63030: gap of 100 bp
* 63031 67418: contig of 4389 bp in length
* 67420 67519: gap of 100 bp
* 67520 145939: contig of 78420 bp in length.
Location/Qualifiers
1. 145939

FEATURES
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1. 145939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"

/clone="RP5-107418"
/clone_lib="RPci-5"
1. 3024
/note="assembly_fragment:00567
vector_end:SP6
vector_side:left"
3125. 10834
/note="assembly_fragment:00921
fragment_chain:1"
10935. 13595
/note="assembly_fragment:01789
fragment_chain:1"
13696. 16092
/note="assembly_fragment:01424
fragment_chain:2"
16193. 22530
/note="assembly_fragment:01022
fragment_chain:2"
22631. 27253
/note="assembly_fragment:00011"
27354. 30261
/note="assembly_fragment:00127"
30362. 33611
/note="assembly_fragment:00247"
33712. 38262
/note="assembly_fragment:00335"
38363. 40615
/note="assembly_fragment:00495"
40716. 44299
/note="assembly_fragment:00561"
44400. 47229
/note="assembly_fragment:00700"
47330. 52776
/note="assembly_fragment:00832"
52877. 60226
/note="assembly_fragment:00912"
60327. 62930
/note="assembly_fragment:01119"
63031. 67419
/note="assembly_fragment:01935"
67520. 145939
/note="assembly_fragment:02239"
BASE COUNT 45121 a 27951 c 28095 g 43161 t 1611 others
ORIGIN

Query Match 88.28; Score 19.4; DB 79; Length 145939;
Best Local Similarity 95.2%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttccagatga 22
||||||| |||||||
Db 37628 GACTGTGAATGTTCCAGATGA 37648

RESULT 9
LOCUS AX036952 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
KEYWORDS
SOURCE
ORGANISM synthetic construct.
synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier, A.
Patent: FR 2790955-A 9 22-SEP-2000;
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source
1. 22
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 7 a 2 c 6 g 7 t
 ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 22;
 Best Local Similarity 90.9%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22
 ||||| ||||| ||||| |||||
 Db 1 TGACTGTGAACGTTATAGATGA 22

RESULT 10

AX083676
 LOCUS AX083676 22 bp DNA PAT 28-FEB-2001
 DEFINITION Sequence 2 from Patent WO0112223.
 ACCESSION AX083676
 VERSION AX083676.1 GI:13185408
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE 1 (bases 1 to 22)
 AUTHORS van Nest,G.
 TITLE Methods of modulating an immune response using immunostimulatory s
 sequences and compositions for use therein
 JOURNAL Patent: WO 0112223-A 2 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 FEATURES
 source Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Synthetic construct" 5 t

BASE COUNT 6 a 4 c 7 g 5 t
 ORIGIN

Query Match 85.5%; Score 18.8; DB 10; Length 22;
 Best Local Similarity 90.9%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22
 ||||| ||||| ||||| |||||
 Db 1 TGACCGTGAACGTTTCGAGATGA 22

RESULT 11

AX083682
 LOCUS AX083682 22 bp DNA PAT 28-FEB-2001
 DEFINITION Sequence 8 from Patent WO0112223.
 ACCESSION AX083682
 VERSION AX083682.1 GI:13185414
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE 1 (bases 1 to 22)
 AUTHORS van Nest,G.
 TITLE Methods of modulating an immune response using immunostimulatory s
 sequences and compositions for use therein
 JOURNAL Patent: WO 0112223-A 8 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 FEATURES
 source Location/Qualifiers
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 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="5-bromocytosine" 11
 modified_base /mod_base=OTHER
 modified_base 15
 /note="5-bromocytosine"

BASE COUNT 6 a 1 c 7 g 6 t 2 others
 ORIGIN

Query Match 83.6%; Score 18.4; DB 10; Length 22;
 Best Local Similarity 86.4%; Pred. No. 57;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22
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 Db 1 TGACTGTGAANGTTNGAGATGA 22

RESULT 12

AB033099/c
 LOCUS AB033099 4334 bp mRNA PRI 11-NOV-1999
 DEFINITION Homo sapiens mRNA for KIAA1273 protein, partial cds.
 ACCESSION AB033099
 VERSION AB033099.1 GI:6382027
 KEYWORDS
 SOURCE Homo sapiens brain cDNA to mRNA, clone_llb:pBluescriptII SK plus
 clone:hk09394.
 ORGANISM
 REFERENCE 1 (sites)
 AUTHORS Ohara,O., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and
 Nagase,T.,
 TITLE Prediction of the coding sequences of unidentified human genes. XV.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro
 JOURNAL DNA Res. 6 (5), 337-345 (1999)
 MEDLINE 20039619
 REFERENCE 2 (bases 1 to 4334)
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE Direct Submission
 JOURNAL Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu
 Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology;
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:cdna@info.kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/,
 Tel:++81-438-52-3913, Fax:++81-438-52-3914)

FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="hk09394"
 /clone_llb="pBluescriptII SK plus"
 /tissue_type="brain"
 463..2283
 /gene="KIAA1273"
 <463..2283
 /gene="KIAA1273"
 /note="Start codon is not identified."
 /codon_start=1
 /product="KIAA1273 protein"
 /protein_id="BAA86587.1"
 /db_xref="GI:6382028"

gene

CDS

BASE COUNT 860 a 1275 c 1363 g 836 t
 ORIGIN

/translation="SWVMOLEALNLLTLWARSILCRAGAVOTQERLSGSGSPQVVP
 AGSCCALQVEAAVEOLKSEIQAASEBKTLSSETROHQAQYODKLARQYEDQ
 LKQQLLEENLRKQESVQKQEMRRATYEREMELRHKNEMLRVETEARAKAEH
 NADIIIEIRLKASEHQTVLESIRTAGTLFGEGRAFTVDROKVTATVAGTLTLAGV
 VYSAKNATAVTRFIEARLCKPSLVRETSLRTHLLYLPQPGTKTLFAKKLALHSGMDYAIM
 VLSPSLEARVDIAATRNKNGLYRHLLYLPQPGTKTLFAKKLALHSGMDYAIM
 TGGDVAPMGREGVTAMHKLFDWANTSRGLLPMDEADAFRLKRTATEISKDLRATLN
 AFLYHMGOSHNKFMVLASNLPEQFDCAINSRIDVMVFDLPQOEERLRLVRLHFDNC
 VLAPATEGKRRLKLAQFDYGRKSEVARLTGHSGRGIAQLAVNSQATAYASKDGLT
 EAMWDACVDAQVQYQKRMRLKAEGRGVGRVSGVQGETLFSNLSLADPSTPCLA
 GPCTFRICSMWGTGLCPGLSPRMSCGGFRFCPPGHPLL"

Query Match 80.9%; Score 17.8; DB 85; Length 4334;
 Best Local Similarity 90.5%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgcattgtgaacgttcagatg 21
 ||||| | |||||
 Db 3337 TGACTGTGCAGGTTCCAGATG 3317

RESULT 13

AC069574 74992 bp DNA HTG 03-JUN-2000
 LOCUS Homo sapiens chromosome 4 clone RP11-267H10 map 4, LOW-PASS
 DEFINITION SEQUENCE SAMPLING.
 AC069574
 ACCESSION AC069574.1 GI:8225556
 VERSION
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 74992)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
 Campoliano,A., Castie,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,K., Jones,C., Kann,L., Karatas,A.,
 Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczkzy,J.,
 Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tsefaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vesiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (03-JUN-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: W18R
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9895
 Center clone name: 267_H_10

 * NOTE: This record contains 86 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

* 1 784: contig of 784 bp in length
 * 785 884: gap of 100 bp
 * 885 1672: contig of 788 bp in length
 * 1673 1772: gap of 100 bp
 * 1773 2548: contig of 776 bp in length
 * 2549 2648: gap of 100 bp
 * 2649 3432: contig of 784 bp in length
 * 3433 3532: gap of 100 bp
 * 3533 4305: contig of 773 bp in length
 * 4306 4405: gap of 100 bp
 * 4406 5157: contig of 752 bp in length
 * 5158 5257: gap of 100 bp
 * 5258 6018: contig of 761 bp in length
 * 6019 6118: gap of 100 bp
 * 6119 6891: contig of 773 bp in length
 * 6892 6991: gap of 100 bp
 * 6992 7756: contig of 765 bp in length
 * 7757 7856: gap of 100 bp
 * 7857 8620: contig of 764 bp in length
 * 8621 8720: gap of 100 bp
 * 8721 9505: contig of 785 bp in length
 * 9506 9605: gap of 100 bp
 * 9606 10384: contig of 779 bp in length
 * 10385 10484: gap of 100 bp
 * 10485 11254: contig of 770 bp in length
 * 11255 11354: gap of 100 bp
 * 11355 12129: contig of 775 bp in length
 * 12130 12229: gap of 100 bp
 * 12230 13000: contig of 771 bp in length
 * 13001 13100: gap of 100 bp
 * 13101 13865: contig of 765 bp in length
 * 13866 13965: gap of 100 bp
 * 13966 14736: contig of 771 bp in length
 * 14737 14836: gap of 100 bp
 * 14837 15571: contig of 735 bp in length
 * 15572 15671: gap of 100 bp
 * 15672 16429: contig of 758 bp in length
 * 16430 16529: gap of 100 bp
 * 16530 17310: contig of 781 bp in length
 * 17311 17410: gap of 100 bp
 * 17411 18185: contig of 775 bp in length
 * 18186 18285: gap of 100 bp
 * 18286 19057: contig of 772 bp in length
 * 19058 19157: gap of 100 bp
 * 19158 19932: contig of 775 bp in length
 * 19933 20032: gap of 100 bp
 * 20033 20809: contig of 777 bp in length
 * 20810 20909: gap of 100 bp
 * 20910 21678: contig of 769 bp in length
 * 21679 21778: gap of 100 bp
 * 21779 22561: contig of 783 bp in length
 * 22562 22661: gap of 100 bp
 * 22662 23431: contig of 770 bp in length
 * 23432 23531: gap of 100 bp
 * 23532 24314: contig of 783 bp in length
 * 24315 24414: gap of 100 bp
 * 24415 25199: contig of 785 bp in length
 * 25200 25299: gap of 100 bp
 * 25300 26057: contig of 758 bp in length
 * 26058 26157: gap of 100 bp
 * 26158 26919: contig of 762 bp in length
 * 26920 27019: gap of 100 bp
 * 27020 27795: contig of 776 bp in length
 * 27796 27895: gap of 100 bp
 * 27896 28659: contig of 764 bp in length
 * 28660 28759: gap of 100 bp
 * 28760 29545: contig of 786 bp in length
 * 29546 29645: gap of 100 bp
 * 29646 30427: contig of 782 bp in length
 * 30428 30527: gap of 100 bp
 * 30528 31300: contig of 773 bp in length
 * 31301 31400: gap of 100 bp
 * 31401 32170: contig of 770 bp in length

* 32171 32270: gap of 100 bp
* 32271 33039: contig of 769 bp in length
* 33040 33139: gap of 100 bp
* 33140 33913: contig of 774 bp in length
* 33914 34013: gap of 100 bp
* 34014 34795: contig of 782 bp in length
* 34796 34895: gap of 100 bp
* 34896 35664: contig of 769 bp in length
* 35665 35764: gap of 100 bp
* 35765 36518: contig of 754 bp in length
* 36519 36618: gap of 100 bp
* 36619 37380: contig of 762 bp in length
* 37381 37480: gap of 100 bp
* 37481 38255: contig of 775 bp in length
* 38256 38355: gap of 100 bp
* 38356 39130: contig of 775 bp in length
* 39131 39230: gap of 100 bp
* 39231 40008: contig of 778 bp in length
* 40009 40108: gap of 100 bp
* 40109 40880: contig of 772 bp in length
* 40881 40980: gap of 100 bp
* 40981 41764: contig of 784 bp in length
* 41765 41864: gap of 100 bp
* 41865 42636: contig of 772 bp in length
* 42637 42736: gap of 100 bp
* 42737 43501: contig of 765 bp in length
* 43502 43601: gap of 100 bp
* 43602 44371: contig of 770 bp in length
* 44372 44471: gap of 100 bp
* 44472 45253: contig of 782 bp in length
* 45254 45353: gap of 100 bp
* 45354 46125: contig of 772 bp in length
* 46126 46225: gap of 100 bp
* 46226 46995: contig of 774 bp in length
* 47000 47099: gap of 100 bp
* 47100 47864: contig of 765 bp in length
* 47865 47964: gap of 100 bp
* 47965 48747: contig of 783 bp in length
* 48748 48847: gap of 100 bp
* 48848 49618: contig of 771 bp in length
* 49619 49718: gap of 100 bp
* 49719 50525: contig of 807 bp in length
* 50526 50625: gap of 100 bp
* 50626 51401: contig of 776 bp in length
* 51402 51501: gap of 100 bp
* 51502 52267: contig of 766 bp in length
* 52268 52367: gap of 100 bp
* 52368 53155: contig of 788 bp in length
* 53156 53255: gap of 100 bp
* 53256 54024: contig of 769 bp in length
* 54025 54124: gap of 100 bp
* 54125 54904: contig of 780 bp in length
* 54905 55004: gap of 100 bp
* 55005 55795: contig of 791 bp in length
* 55796 55895: gap of 100 bp
* 55896 56653: contig of 757 bp in length
* 56653 56752: gap of 100 bp
* 56753 57525: contig of 773 bp in length
* 57526 57625: gap of 100 bp
* 57626 58402: contig of 777 bp in length
* 58403 58502: gap of 100 bp
* 58503 59282: contig of 780 bp in length
* 59283 59382: gap of 100 bp
* 59383 60160: contig of 778 bp in length
* 60161 60260: gap of 100 bp

Query Match 80.98; Score 17.8; DB 74; Length 74992;
Best Local Similarity 90.58; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttccagatga 22
|||||||

Db 12039 GACTGTGAACATTCAGATAA 12059

RESULT 14 AC069574/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC069574 74992 bp DNA HTG 03-JUN-2000
Homo sapiens chromosome 4 clone RP11-267H10 map 4, LOW-PASS
SEQUENCE SAMPLING.
AC069574
AC069574.1 GI:8225556
HTG; HTGS_PHASE0.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74992)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-267H10
Unpublished
2 (bases 1 to 74992)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Glinde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, G., Locke, K., Macdonald, P., Marguis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9895
Center clone name: 267_H_10

* NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 784: contig of 784 bp in length
* 785 884: gap of 100 bp
* 885 1672: contig of 788 bp in length
* 1673 1772: gap of 100 bp
* 1773 2548: contig of 776 bp in length
* 2549 2648: gap of 100 bp
* 2649 3432: contig of 784 bp in length

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* 3433 3532: gap of 100 bp
* 3533 4305: contig of 773 bp in length
* 4306 4405: gap of 100 bp
* 4406 5157: contig of 752 bp in length
* 5158 5257: gap of 100 bp
* 5258 6018: contig of 761 bp in length
* 6019 6118: gap of 100 bp
* 6119 6891: contig of 773 bp in length
* 6892 6991: gap of 100 bp
* 6992 7756: contig of 765 bp in length
* 7757 7856: gap of 100 bp
* 7857 8620: contig of 764 bp in length
* 8621 8720: gap of 100 bp
* 8721 9505: contig of 785 bp in length
* 9506 9605: gap of 100 bp
* 9606 10384: contig of 779 bp in length
* 10385 10484: gap of 100 bp
* 10485 11254: contig of 770 bp in length
* 11255 11354: gap of 100 bp
* 11355 12129: contig of 775 bp in length
* 12130 12229: gap of 100 bp
* 12230 13000: contig of 771 bp in length
* 13001 13100: gap of 100 bp
* 13101 13865: contig of 765 bp in length
* 13866 13965: gap of 100 bp
* 13966 14736: contig of 771 bp in length
* 14737 14836: gap of 100 bp
* 14837 15571: contig of 735 bp in length
* 15572 15671: gap of 100 bp
* 15672 16429: contig of 758 bp in length
* 16430 16529: gap of 100 bp
* 16530 17310: contig of 781 bp in length
* 17311 17410: gap of 100 bp
* 17411 18185: contig of 775 bp in length
* 18186 18285: gap of 100 bp
* 18286 19057: contig of 772 bp in length
* 19058 19157: gap of 100 bp
* 19158 19932: contig of 775 bp in length
* 19933 20032: gap of 100 bp
* 20033 20809: contig of 777 bp in length
* 20810 20909: gap of 100 bp
* 20910 21678: contig of 769 bp in length
* 21679 21778: gap of 100 bp
* 21779 22561: contig of 783 bp in length
* 22562 22661: gap of 100 bp
* 22662 23431: contig of 770 bp in length
* 23432 23531: gap of 100 bp
* 23532 24314: contig of 783 bp in length
* 24315 24414: gap of 100 bp
* 24415 25199: contig of 785 bp in length
* 25200 25299: gap of 100 bp
* 25300 26057: contig of 758 bp in length
* 26058 26157: gap of 100 bp
* 26158 26919: contig of 762 bp in length
* 26920 27019: gap of 100 bp
* 27020 27795: contig of 776 bp in length
* 27796 27895: gap of 100 bp
* 27896 28659: contig of 764 bp in length
* 28660 28759: gap of 100 bp
* 28760 29545: contig of 786 bp in length
* 29546 29645: gap of 100 bp
* 29646 30427: contig of 782 bp in length
* 30428 30527: gap of 100 bp
* 30528 31300: contig of 773 bp in length
* 31301 31400: gap of 100 bp
* 31401 32170: contig of 770 bp in length
* 32171 32270: gap of 100 bp
* 32271 33039: contig of 769 bp in length
* 33040 33139: gap of 100 bp
* 33140 33913: contig of 774 bp in length
* 33914 34013: gap of 100 bp
* 34014 34795: contig of 782 bp in length
* 34796 34895: gap of 100 bp
```

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* 34896 35664: contig of 769 bp in length
* 35665 35764: gap of 100 bp
* 35765 36518: contig of 754 bp in length
* 36519 36818: gap of 100 bp
* 36819 37380: contig of 762 bp in length
* 37381 37480: gap of 100 bp
* 37481 38255: contig of 775 bp in length
* 38256 38355: gap of 100 bp
* 38356 39130: contig of 775 bp in length
* 39131 39230: gap of 100 bp
* 39231 40008: contig of 778 bp in length
* 40009 40108: gap of 100 bp
* 40109 40880: contig of 772 bp in length
* 40881 40980: gap of 100 bp
* 40981 41764: contig of 784 bp in length
* 41765 41864: gap of 100 bp
* 41865 42636: contig of 772 bp in length
* 42637 42736: gap of 100 bp
* 42737 43501: contig of 765 bp in length
* 43502 43601: gap of 100 bp
* 43602 44371: contig of 770 bp in length
* 44372 44471: gap of 100 bp
* 44472 45253: contig of 782 bp in length
* 45254 45353: gap of 100 bp
* 45354 46125: contig of 772 bp in length
* 46126 46225: gap of 100 bp
* 46226 46999: contig of 774 bp in length
* 47000 47099: gap of 100 bp
* 47100 47864: contig of 765 bp in length
* 47865 47964: gap of 100 bp
* 47965 48747: contig of 783 bp in length
* 48748 48847: gap of 100 bp
* 48848 49618: contig of 771 bp in length
* 49619 49718: gap of 100 bp
* 49719 50525: contig of 807 bp in length
* 50526 50625: gap of 100 bp
* 50626 51401: contig of 776 bp in length
* 51402 51501: gap of 100 bp
* 51502 52267: contig of 766 bp in length
* 52268 52367: gap of 100 bp
* 52368 53155: contig of 788 bp in length
* 53156 53255: gap of 100 bp
* 53256 54024: contig of 769 bp in length
* 54025 54124: gap of 100 bp
* 54125 54904: contig of 780 bp in length
* 54905 55004: gap of 100 bp
* 55005 55795: contig of 791 bp in length
* 55796 55895: gap of 100 bp
* 55896 56652: contig of 757 bp in length
* 56653 56752: gap of 100 bp
* 56753 57525: contig of 773 bp in length
* 57526 57625: gap of 100 bp
* 57626 58402: contig of 777 bp in length
* 58403 58502: gap of 100 bp
* 58503 59282: contig of 780 bp in length
* 59283 59382: gap of 100 bp
* 59383 60160: contig of 778 bp in length
* 60161 60260: gap of 100 bp
```

Query Match 80.9%; Score 17.8; DB 74; Length 74992;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttcacagatga 22

||||||| ||||| |

Db 57162 GACTGTGAACATTCACAGATAA 57142

RESULT 15

AL157945

LOCUS

DEFINITION

AL157945 109120 bp DNA

Homo sapiens chromosome 1 clone RP4-628J24 map p36.31-36.33, ***

SEQUENCING IN PROGRESS ***, 2 unordered pieces.

HTG

08-APR-2001

ACCESSION: AL157945
VERSION: AL157945.15 GI:11610971
KEYWORDS: HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE: human.
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109120)
Frankland, J.
Direct Submission
Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Dec 9, 2000 this sequence version replaced gi:11414491.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: DJ628J24
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 1% of reads
Sequencing vector: plasmid: L08752; 98% of reads
Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 79% of reads
Chemistry: Dye-terminator ET-amersham; 18% of reads
Consensus quality: 108884 bases at least Q30
Consensus quality: 108962 bases at least Q20
Insert size: 109020; sum-of-contigs
Insert size: 109409; 10.4% error; agarose-fp
Quality coverage: 10.62x in Q20 bases; sum-of-contigs Quality
coverage: 10.72x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 25559: contig of 25559 bp in length
* 25360 25659: gap of 100 bp
* 25660 109120: contig of 83461 bp in length.
FEATURES
source
1..109120
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.31-36.33"
/clone="RP4-628J24"
/clone_lib="RPCI-4"
misc_feature
1..25559
/note="assembly_fragment:00655"
misc_feature
25660..109120
/note="assembly_fragment:03347"
clone_end:T7
vector_side:right"
BASE COUNT 23801 a 31255 c 31398 g 22566 t 100 others
ORIGIN

Query Match 80.9% Score 17.8; DB 79; Length 109120;
Best Local Similarity 90.5% Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 tgactgtgacgttccagatg 21
|||||||
Db 69219 TGACTGTGCAGGTTCCAGATG 69239

Search completed: October 9, 2001, 16:19:04
Job time: 2514 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:16 ; Search time 6788.49 seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*
- 12: gb_est12:*
- 13: gb_est13:*
- 14: gb_est14:*
- 15: gb_est15:*
- 16: gb_est16:*
- 17: gb_est17:*
- 18: gb_est18:*
- 19: gb_est19:*
- 20: gb_est20:*
- 21: gb_est21:*
- 22: gb_est22:*
- 23: gb_est23:*
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- 25: gb_est25:*
- 26: gb_est26:*
- 27: gb_est27:*
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- 39: gb_est39:*
- 40: gb_est40:*
- 41: gb_est41:*
- 42: gb_est42:*
- 43: gb_est43:*
- 44: gb_est44:*
- 45: gb_est45:*
- 46: gb_est46:*
- 47: gb_est47:*

44: em_esthum10:*

45: em_esthum11:*

46: em_esthum12:*

47: em_esthum13:*

48: em_esthum14:*

49: em_esthum15:*

50: em_esthum16:*

51: em_esthum17:*

52: em_esthum18:*

53: em_esthum19:*

54: em_esthum20:*

55: em_esthum21:*

56: em_esthum22:*

57: em_esthum23:*

58: em_esthum24:*

59: em_esthum25:*

60: em_esthum26:*

61: em_esthum27:*

62: em_esthum28:*

63: em_estin1:*

64: em_estin2:*

65: em_estin3:*

66: em_estin4:*

67: em_estin5:*

68: em_estom1:*

69: em_estom2:*

70: em_estov1:*

71: em_estov2:*

72: em_estpl1:*

73: em_estpl2:*

74: em_estpl3:*

75: em_estpl4:*

76: em_estpl5:*

77: em_estpl6:*

78: em_estpl7:*

79: em_estpl8:*

80: em_estpl9:*

81: em_estpl10:*

82: em_estro1:*

83: em_estro2:*

84: em_estro3:*

85: em_estro4:*

86: em_estro5:*

87: em_estro6:*

88: em_estro7:*

89: em_estro8:*

90: em_estro9:*

91: em_estro10:*

92: em_estro11:*

93: em_estro12:*

94: em_estro13:*

95: em_estro14:*

96: em_estro15:*

97: em_estro16:*

98: em_estro17:*

99: em_estro18:*

100: em_estro19:*

101: em_estro20:*

102: gb_est25:*

103: gb_est26:*

104: gb_est27:*

105: gb_est28:*

106: gb_est29:*

107: gb_est30:*

108: gb_est31:*

109: gb_est32:*

110: gb_est41:*

111: gb_est42:*

112: gb_est43:*

113: gb_est44:*

114: gb_est45:*

115: gb_est46:*

116: gb_est47:*

```

117: gb_est48:*
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188: gb_est119:*
189: gb_est120:*

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190: gb_est121:*
191: gb_est122:*
192: gb_est123:*
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237: gb_est168:*
238: gb_est169:*
239: gb_est170:*
240: gb_est171:*
241: gb_est172:*
242: gb_est173:*
243: gb_est174:*
244: gb_est175:*
245: gb_est176:*
246: gb_est177:*
247: gb_est178:*
248: gb_est179:*
249: gb_est180:*
250: gb_est181:*
251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1189 row: h column: 11
High quality sequence stop: 555.
Location/Qualifiers
1. .961
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4328890"
/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DHI08 (phage-resistant)"
/note="Organ: uterus; Vector: pORF7; Site: 1; XhoI; Site: 2; ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size of 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 205 a 225 c 240 g 291 t
ORIGIN

Query Match 88.2% Score 19.4; DB 172; Length 961;
Best Local Similarity 95.2%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 gactgtgaacgtccagatga 22
|||||
Db 650 GACTGTGAACGTCGGATGA 670
RESULT 2
LOCUS AA094019 105 bp mRNA EST 25-OCT-1996
DEFINITION cll1619, seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
CDNA 5', mRNA sequence.
ACCESSION AA094019
VERSION AA094019.1 GI:1639612
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Liew, C.C.
CDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: liewccc@utcc.utoronto.ca
PCR Primers
FORWARD: 5' CCAGTGAATGTAATAGCAGTCACTATAGGCG 3'
BACKWARD: 5' GAAATTAACCCCTCACTAAAGG 3'.
Seq primer: 5' GAAATTAACCCCTCACTAAAGG 3'.
Location/Qualifiers
1. .105
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"

FEATURES
source

FEATURES
source

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19.4	88.2	961	172	BF971856	BF971856 602240444
2	18.4	83.6	105	2	AA094019	AA094019 cll1619.se
3	17.8	80.9	401	165	BE275964	BE275964 601120704
4	17.8	80.9	441	22	A1597068	A1597068 vj44e09.x
5	17.8	80.9	457	166	BE367478	BE367478 P11.8.F04
6	17.8	80.9	473	188	R83554	R83554 yq12d03.r1
7	17.8	80.9	514	240	A2265882	A2265882 RPCI-23-1
8	17.8	80.9	537	118	AW610890	AW610890 un13e10.Y
9	17.8	80.9	542	107	AU017198	AU017198 AU017198
10	17.8	80.9	555	165	BE284315	BE284315 601087423
11	17.8	80.9	563	173	BG070885	BG070885 H3091D05-
12	17.8	80.9	572	248	A2699837	A2699837 RPCI-23-2
13	17.8	80.9	615	117	AW564152	AW564152 LG1.285.H
14	17.8	80.9	666	137	BE582546	BE582546 1-10C-MY
15	17.8	80.9	681	175	BG295408	BG295408 602392719
16	17.8	80.9	705	145	BF178492	BF178492 601807652
17	17.8	80.9	792	150	BF582440	BF582440 602094391
18	17.8	80.9	803	235	AQ876162	AQ876162 V152A11.m
19	17.2	78.2	478	236	AQ966996	AQ966996 LERIN76TR
20	17.2	78.2	528	138	BE676474	BE676474 7f30C08.X
21	17.2	78.2	602	104	A1996030	A1996030 701549720
22	17.2	78.2	664	256	B77405	B77405 T31A1TFC.TA
23	17.2	78.2	669	256	B77406	B77406 T31A2TFC.TA
24	17.2	78.2	672	153	BG454943	BG454943 NF110G04L
25	17.2	78.2	688	247	A2644355	A2644355 LM0508G15
26	17.2	78.2	996	220	CNS027GD	AL184630 Tetraodon
27	17.2	78.2	1021	222	CNS055HF	AL322044 Tetraodon
28	17.2	78.2	1061	221	CNS03DC2	AL238907 Tetraodon
29	16.8	76.4	384	103	A1898251	A1898251 EST267694
30	16.8	76.4	472	256	A2930534	A2930534 474.dh255
31	16.8	76.4	526	245	A2501799	A2501799 LM0340J17
32	16.8	76.4	531	256	A2930854	A2930854 474.dh259
33	16.8	76.4	559	21	A1489944	A1489944 EST248283
34	16.8	76.4	801	234	AQ858141	AQ858141 nbe00012G
35	16.8	76.4	1228	144	BF128350	BF128350 601810203
36	16.4	74.5	214	246	A2578289	A2578289 21b05.Sho
37	16.4	74.5	240	2	AA102862	AA102862 mo10f10.r
38	16.4	74.5	373	14	A1006564	A1006564 uc14405.Y
39	16.4	74.5	457	146	BF270840	BF270840 GA_Eb000
40	16.4	74.5	500	155	BG578016	BG578016 df04b10.Y
41	16.4	74.5	534	256	B75188	B75188 RPCI11-13P4
42	16.4	74.5	595	230	AQ583172	AQ583172 RPCI-11-4
43	16.4	74.5	675	106	AL583992	AL583992
44	16.4	74.5	980	218	AF075829	AF075829 AF075829
45	16.2	73.6	150	31	AV626891	AV626891 AV626891

ALIGNMENTS

RESULT 1	BF971856	961 bp	mRNA	EST	22-JAN-2001
LOCUS	602240444F1	NIH_MGC_46	Homo sapiens	cdna clone IMAGE:4328890 5',	
DEFINITION	BF971856	mRNA sequence.			
ACCESSION	BF971856	EST.			
VERSION	BF971856.1	GI:12339071			
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	1 (bases 1 to 961)				
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D.				

/note=vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested Lambda ZAP Express."

BASE COUNT
ORIGIN

Query Match 83.6%; Score 18.4; DB 2; Length 105;
Best Local Similarity 95.0%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgaactgtgaacgttccagat 20
||||| ||||| ||||| |||||
Db 43 TGAAGTGTGAACGTTCCAGAT 62

RESULT 3

BE275964 401 bp mRNA EST 13-JUL-2000
LOCUS 601120704F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967576 5',
DEFINITION mRNA sequence.
ACCESSION BE275964
VERSION BE275964.1 GI:9150926
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 401)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1C72 row: g column: 01
High quality sequence start: 32
High quality sequence stop: 321.
Location/Qualifiers

FEATURES

source

1. 401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_20"

/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

124 a 94 c 77 g 106 t

BASE COUNT
ORIGIN

Query Match 80.9%; Score 17.8; DB 165; Length 401;
Best Local Similarity 90.5%; Pred. No. 1,9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttccagatga 22
||||| ||||| ||||| |||||
Db 264 GACTGGGAACGTTTCAGATGA 284

RESULT 4

AI597068/c
LOCUS
DEFINITION

441 bp mRNA EST 21-APR-1999
VJ44609.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:931912 3', mRNA sequence.

ACCESSION AI597068

VERSION AI597068.1 GI:4606116

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 441)
Marra.M., Hillier.L., Kucaba.T., Martin.J., Beck.C., Wylie.T.,
Underwood.K., Steptoe.M., Theising.B., Allen.M., Bowers.Y., Person
B., Swaller.T., Gibbons.M., Pape.D., Harvey.N., Schurk.R., Ritter
E., Kohn.S., Shin.T., Jackson.Y., Cardenas.M., McCann.R.,
Waterston.R. and Wilson.R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:536832

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

High quality sequence stop: 427.

Location/Qualifiers

FEATURES

source

1. 441

/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone_image="931912"

/clone_lib="Stratagene mouse skin (#937313)"

/sex="females"

/tissue_type="whole skin"

/dev_stage="11 weeks old"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI

; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo

dT. Whole skin from 11 week old C57BL/6 female mice.

Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'

adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

103 a 144 c 111 g 82 t 1 others

BASE COUNT
ORIGIN

Query Match 80.9%; Score 17.8; DB 22; Length 441;

Best Local Similarity 90.5%; Pred. No. 1,9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttccagatga 22

||||| ||||| ||||| |||||

Db 116 GCCTGTGAATGTTCCAGATGA 96

RESULT 5

BE367478

LOCUS

DEFINITION BE367478 457 bp mRNA EST 20-JUL-2000

PII.8.F04.bl.A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,

mRNA sequence.

ACCESSION BE367478

VERSION BE367478.1 GI:9309035

KEYWORDS EST.

SOURCE sorghum.

ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 457)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt L.H.
TITLE An EST database from Sorghum: pathogen-induced plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 456
POLYA=No.

FEATURES

Location/Qualifiers
1..457
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/note="Organ: Anthracnose-infected leaves from two-week-old sorghum plants 48 hr after inoculation; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; Two-week-old sorghum plants (B7X 623 cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: Young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibility to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."
BASE COUNT 89 a 137 c 148 g 83 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 166; Length 457;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 gactgtgaacgttcagatga 22
||||| ||||||| ||
Db 38 GACTGTGACCGTCCAGAAGA 58

RESULT 6
R83554 473 bp mRNA EST 04-AUG-1995
LOCUS yq12d03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196709 5', mRNA sequence.
ACCESSION R83554
VERSION R83554.1 GI:928431
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman M., Hultman,M., Kucababa,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston

R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 958
High quality sequence stops: 332
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 958 Std Error: 0.00
Seq primer: M13Rp1
High quality sequence stop: 332.
Location/Qualifiers
1..473
/organism="Homo sapiens"
/db_xref="GDB:3765759"
/db_xref="taxon:9606"
/clone="IMAGE:196709"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGCAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 144 a 94 c 120 g 110 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 188; Length 473;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttcagatga 22
||||| ||||||| |||
Db 319 GACTCTGAACGTTCAGCTGA 339

RESULT 7
A2265882 514 bp DNA GSS 26-JUL-2000
LOCUS RPCI-23-143A3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-143A3, DNA sequence.
ACCESSION A2265882
VERSION A2265882.1 GI:9478411
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 514)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akintet B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other GSSs: RPCI-23-143A3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Search completed: October 9, 2001, 18:20:19
Job time: 9789 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:49 : Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SIDSB/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SIDSB/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SIDSB/gcgdata/geneseq/geneseq/NA1982.DAT.*
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5: /SIDSB/gcgdata/geneseq/geneseq/NA1984.DAT.*
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7: /SIDSB/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SIDSB/gcgdata/geneseq/geneseq/NA1987.DAT.*
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21: /SIDSB/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV80099	Immunomodulatory o
2	22	100.0	22	AAV80101	Immunomodulatory o
3	22	100.0	22	AAV80254	Sequence of a stab
4	22	100.0	22	AAV80808	Immunostimulatory
5	22	100.0	22	AAV80700	Immunostimulatory
6	22	100.0	22	AAV77043	Immunostimulatory
7	21.2	96.4	22	AAV77045	Immunostimulatory
8	21	95.5	22	AAV25877	Immunomodulatory o
9	20.4	92.7	22	AAV32079	Nucleotide sequenc
10	20.4	92.7	22	AAV36624	ISS-ODN DY1018 nuc
11	20.4	92.7	22	AAV80097	Immunomodulatory o

12	20.4	92.7	22	AAV80102	Immunomodulatory o
13	20.4	92.7	22	AAV80103	Immunomodulatory o
14	20.4	92.7	22	AAV80104	Immunostimulatory
15	20.4	92.7	22	AAV80253	Sequence of a stab
16	20.4	92.7	22	AAV80458	CpG adjuvant oligo
17	20.4	92.7	22	AAV80459	Immunostimulatory
18	20.4	92.7	22	AAV8065	Immunostimulatory
19	20.4	92.7	22	AAV8071	Immunostimulatory
20	20.4	92.7	22	AAV8072	Immunostimulatory
21	20.4	92.7	22	AAV8076	Immunomodulatory o
22	20.4	92.7	22	AAV77040	Immunomodulatory D
23	20.4	92.7	22	AAV29800	Cholera toxin immu
24	20.4	92.7	22	AAV82107	Oligonucleotide OD
25	20.4	92.7	22	AAV82107	CG motif and CFA c
26	19.6	89.1	22	AAV77046	Immunostimulatory
27	19.4	88.2	22	AAV55880	Immunomodulatory o
28	18.8	85.5	22	AAV80105	Oligo used in expe
29	18.8	85.5	22	AAV80096	Immunomodulatory o
30	18.8	85.5	22	AAV80260	Sequence of a stab
31	18.8	85.5	22	AAV8066	Immunostimulatory
32	18.8	85.5	22	AAV77041	Immunostimulatory
33	18.8	85.5	22	AAV77047	Immunostimulatory
34	18.4	83.6	22	AAV55881	Immunomodulatory o
35	17.2	78.2	22	AAV32080	Nucleotide sequenc
36	17.2	78.2	22	AAV36625	ISS-ODN mutant DV1
37	17.2	78.2	22	AAV55790	Immunostimulatory
38	17.2	78.2	22	AAV55797	Immunostimulatory
39	17.2	78.2	22	AAV55788	Immunostimulatory
40	17.2	78.2	22	AAV80106	Oligo used in expe
41	17.2	78.2	22	AAV80104	Oligo used in expe
42	17.2	78.2	22	AAV64052	Non-CpG control ph
43	17.2	78.2	22	AAV80252	Sequence of a stab
44	17.2	78.2	22	AAV80459	CpG adjuvant oligo
45	17.2	78.2	22	AAV82378	CG motif and CFA c

ALIGNMENTS

RESULT 1

AAV80099	AAV80099 standard; DNA; 22 BP.
ID	AAV80099 standard; DNA; 22 BP.
XX	AAV80099;
AC	AAV80099;
XX	12-MAR-1999 (first entry)
DT	12-MAR-1999 (first entry)
XX	Immunomodulatory oligo comprising an ISS sequence.
DE	Immunomodulatory; octanucleotide; immune regulation;
XX	ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW	human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW	B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma.
XX	Synthetic.
OS	Synthetic.
XX	WO9855495-A2.
PN	10-DEC-1998.
XX	10-DEC-1998.
XX	05-JUN-1998; 98WO-US11578.
PF	06-JUN-1997; 97US-0048793.
XX	(DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX	Dina D. Roman M. Schwartz D;
PI	WPI; 1999-059898/05.
XX	Immunostimulatory oligonucleotides regulate the immune system - and
PT	contain an immune-stimulating octanucleotide sequence; for treating
PT	cancer, allergic and infectious diseases

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
 |||||
 Db 1 tgactgtgaacgttcagatga 22

RESULT 4
 AAA38068
 ID AAA38068 standard; DNA; 22 BP.
 AC AAA38068;
 XX
 DT 24-AUG-2000 (first entry)
 XX
 DE Immunostimulatory sequence (ISS) #4.

XX Immunostimulatory sequence; ISS; Immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KW development; ss.
 XX
 OS Synthetic.

XX WO200021556-A1.
 XX
 PN 20-APR-2000.
 XX
 PD 08-OCT-1999; 99WO-US23677.
 XX
 PF 09-OCT-1998; 98US-0103733.
 XX
 PR 07-OCT-1999; 99US-0415186.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;
 XX WPI; 2000-317846/27.
 XX
 DR Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual.
 XX
 PS Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory polynucleotide, or is proximately
 CC conjugated to an immunomodulatory polynucleotide, is used for modulating or
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
 |||||
 Db 1 tgactgtgaacgttcagatga 22

RESULT 5
 AAA38070
 ID AAA38070 standard; DNA; 22 BP.
 XX
 AC AAA38070;
 XX
 DT 24-AUG-2000 (first entry)
 XX
 DE Immunostimulatory sequence (ISS) #6.

XX Immunostimulatory sequence; ISS; Immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KW development; ss.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 11
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "5-Bromocytosine"

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual.

XX Disclosure; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory polynucleotide, or is proximately
 CC conjugated to an immunomodulatory polynucleotide, is used for modulating or
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
 |||||
 Db 1 tgactgtgaacgttcagatga 22

RESULT 6
 AAF77043
 ID AAF77043 standard; DNA; 22 BP.

XX AAF77043;
 AC
 XX
 DT 15-MAY-2001 (first entry)
 DE XX
 DE Immunostimulatory DNA #3.
 XX
 KW Modulate; Immune; antigen; immunostimulatory; ds.
 XX
 OS Synthetic.
 XX
 PN WO200112223-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000WO-US22835.
 XX
 PR 19-AUG-1999; 99US-0149768.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Van Nest-G;
 XX
 DR WPI; 2001-211136/21.
 XX
 XX Modulating immune response to a second antigen in humans involves
 PT administering an immunostimulatory polynucleotide comprising an
 PT immunostimulatory sequence and a first antigen
 XX
 PS Disclosure; Page 15; 63pp; English.
 XX
 CC The present invention relates to modulating an immune response to
 CC a second antigen in an individual, involving
 CC administering to the individual an immunomodulatory polynucleotide
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.
 XX
 SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttccagatga 22
 |||||
 Db 1 tgactgtgaacgttccagatga 22

RESULT 7
 AAF77045
 ID AAF77045 standard; DNA; 22 BP.
 XX
 AC AAF77045;
 XX
 DT 15-MAY-2001 (first entry)
 DE XX
 DE Immunostimulatory DNA #5.
 XX
 KW Modulate; Immune; antigen; immunostimulatory; ds.
 XX
 OS Synthetic.
 XX
 PN WO200112223-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000WO-US22835.
 XX
 PR 19-AUG-1999; 99US-0149768.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Van Nest G;

XX WPI; 2001-211136/21.
 DR
 XX Modulating immune response to a second antigen in humans involves
 PT administering an immunostimulatory polynucleotide comprising an
 PT immunostimulatory sequence and a first antigen
 XX
 XX Disclosure; Page 15; 63pp; English.
 XX
 CC The present invention relates to modulating an immune response to
 CC a second antigen in an individual, involving
 CC administering to the individual an immunomodulatory polynucleotide
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 96.4%; Score 21.2; DB 22; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.095;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttccagatga 22
 |||||
 Db 1 tgactgtgaacgttccagatga 22

RESULT 8
 AAZ55877
 ID AAZ55877 standard; DNA; 22 BP.
 XX
 AC AAZ55877;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Immunomodulatory oligonucleotide SEQ ID NO: 2.
 XX
 KW Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunocontraception; 5-bromocytosine; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..22
 FT /*tag= a
 FT /note= "Phosphorothioate linkages"
 FT misc_feature 9..16
 FT /*tag= b
 FT /note= "Immunostimulatory sequence (ISS)"
 FT modified_base 11
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 XX
 PN WO9962923-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-US12538.
 XX
 PR 05-JUN-1998; 98US-0088310.
 PR 01-JUN-1999; 99US-0324191.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Schwartz D;
 XX
 DR WPI; 2000-105687/09.
 XX
 PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
 XX response, e.g. to tumor antigens
 XX

PS Claim 29; Page 35; 54pp; English.

XX Sequences AA25876-25877 and AA25880-25886 represent immunomodulatory
CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
CC AACGTC, AACGTT, AGCGTC, AGCGTT, AGCGTC, GACGTC, GACGTT, GCGGTT,
CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides
CC comprising one or more ISSs, where the ISS comprises at least
CC one modified cytosine with an electron-withdrawing moiety at
CC position C-5 or C-6 of the base. Sequences AA25877 and AA25880-25886
CC contain ISSs comprising at least one bromocytosine, whereas sequence
CC AA25876 contains an unmodified ISS. The immunomodulatory
CC oligonucleotides have an adjuvant-like effect; when formulated with an
CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
CC and induce a Th1-type immune response (activation of cytotoxic T cells),
CC while simultaneously downregulating the Th2-type response. The Th1
CC response is particularly effective for control of viruses and
CC intracellular parasites. The immunomodulatory oligonucleotides are used,
CC particularly when formulated with an antigen or a facilitator, for
CC modulating immune responses. Such compositions may be used in tumour
CC therapy, in treatment of allergy (including asthma), for inducing a
CC vigorous cellular response (against a virus, bacterium, fungus or
CC protozoan), and also in contraceptive vaccines based on sperm antigens.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacggtccagatga 22
||||||| |||||||
Db 1 tgactgtgaacggtccagatga 22

RESULT 9

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX 09-SEP-1998 (first entry)

XX Nucleotide sequence of DY1018.

DE DY1018; beta-gal; ISS-PN/IMM; antigen; Immune response; antibody;
KW immunisation; anaphylaxis; IgE; retinopathies; ss.
XX synthetic.

OS

XX Key Location/Qualifiers

XX modified_base 1..22

FT /*tag= a

FT /note= "phosphothioate backbone"

XX

PN WO9816247-A1.

XX

PD 23-APR-1998.

XX

XX 09-OCT-1997; 97WO-US19004.

XX

XX 11-OCT-1996; 96US-0028118.

XX

XX (REGC) UNIV CALIFORNIA.

XX

PI Carson DA, Raz E, Roman M;

XX

XX WPI; 1998-261028/23.

XX

XX New immunomodulatory compositions - comprising an antigen conjugated

XX to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

PS

XX

XX This is the nucleotide sequence of DY1018, which is conjugated to
CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
CC (IMM), which comprises an antigen conjugated to a polynucleotide
CC (PN) that contains at least one immunostimulatory nucleotide sequence
CC (ISS). The conjugate synergistically boost the magnitude of the host
CC immune response against an antigen to a level greater than the host
CC immune response to either the IMM, antigen or ISS-PN alone. These
CC responses to ISS-PN/IMM conjugates are particularly acute during
CC the important early phase of the host immune response to an antigen.
CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular
CC (Th1 type) immune responses of the host. Thus, use of the method to
CC boost the immune responsiveness of a host to subsequent challenge by a
CC sensitising antigen without immunisation avoids the risk of
CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE
CC production in response to the antigen challenge. The conjugates can
CC also be used to combat pathogenic infection and to stimulate
CC therapeutic angiogenesis to treat conditions in which localised blood
CC flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 19; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacggtccagatga 22

||||||| |||||||

Db 1 tgactgtgaacggtccagatga 22

RESULT 10

AAX36624

ID AAX36624 standard; DNA; 22 BP.

XX

AC AAX36624;

XX

XX 09-JUL-1999 (first entry)

XX ISS-ODN DY1018 nucleotide sequence.

DE Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
KW granulocyte-mediated tissue inflammation; Th2 type immune response;
KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;
KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

OS

XX WO9911275-A2.

XX

PD 11-MAR-1999.

XX

PF 04-SEP-1998; 98WO-US18382.

XX

PR 05-SEP-1997; 97US-0927120.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Ray E;

XX WPI; 1999-312404/26.

XX

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

XX

XX This is the ISS-ODN DY1018 nucleotide sequence.

XX The invention relates to a method for preventing or reducing

XX antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,

XX by administering an immunostimulatory oligonucleotide (ISS-ODN), where:

XX

CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.24;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22
 |||||
 Db 1 tgactgtgaacgttcagatga 22

RESULT 11
 AAV80097
 ID AAV80097 standard; DNA: 22 BP.
 AC AAV80097;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX
 OS Synthetic.
 XX
 PN WO9855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 XX
 XX WPI: 1999-059898/05.
 XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GAGGTTCC, and GAGGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.24;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22
 |||||
 Db 1 tgactgtgaacgttcagatga 22

RESULT 12
 AAV80102
 ID AAV80102 standard; DNA: 22 BP.
 AC AAV80102;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT modified_base 11
 FT /*tag= a
 FT /*note= "5-bromocytosine"
 XX
 PN WO9855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 XX
 XX WPI: 1999-059898/05.
 XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GAGGTTCC, and GAGGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Query Match 92.7%; Score 20.4; DB 20; Length 22;
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22
|||||
DB 1 tgactgtgaacgttcagatga 22

RESULT 13
AAV80103
ID AAV80103 standard; DNA; 22 BP.

AC AAV80103;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 11
FT /*tag= a
FT /*note= "5-bromocytosine"
XX

PN W09855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcagatga 22
|||||
DB 1 tgactgtgaacgttcagatga 22

RESULT 14
AAC64051
ID AAC64051 standard; DNA; 22 BP.

AC AAC64051;

XX 15-FEB-2001 (first entry)

XX Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
KW enhanced antigen presentation; antigen-presenting cell; APC;
KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
KW vaccine; ss.

XX Synthetic.

XX WO200062787-A1.

XX 26-OCT-2000.

XX 11-APR-2000; 2000WO-US09664.

XX 15-APR-1999; 99US-0292278.

XX (REGC) UNIV CALIFORNIA.

XX Raz E, Martin-Orozco E;

XX WPI; 2000-679548/66.

XX Enhancing antigen presentation capabilities of T-cells for cancer
PT immunotherapy, by contacting cells with an immunostimulatory
PT oligonucleotide
XX Example 1; Page 18; 42pp; English.

XX The invention relates to a method of inducing activation of T-cells
CC to respond to an antigen, comprising contacting antigen-presenting cells
CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC thus treated have enhanced antigen presenting capabilities compared to
CC antigen-activated APCs. APCs with enhanced antigen-presentation
CC capabilities then present the antigen to T-cells. The method is useful
CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC antigen presenting capacity of tumour cells, thereby inducing T-cell
CC activation, and is therefore useful for treating tumours. Additionally,
CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
CC ISS-ODN treated APCs are induced to take up antigen through upregulation
CC of Fc-receptor expression, to present antigen through upregulation of
CC major histocompatibility complex (MHC) Class I and II expression and
CC CD1d expression, to produce co-stimulatory factors (B7 and CD40), to
CC provide cell-to-cell adhesion through upregulation of intercellular
CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
CC cytokine production, all at levels greater than that achieved through
CC contact of APC with antigen alone. The present sequence represents
CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 tgactgtgaacgttcagatga 22
    |||||
Db 1 tgactgtgaacgttcagatga 22

RESULT 15
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX AC
XX AA96253;
XX 08-FEB-2001 (first entry)
XX Sequence of a stabilised oligonucleotide with antitumour activity.
DE
XX
XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.
XX
XX Synthetic.
XX
XX WO200056342-A2.
XX
XX 28-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-FR00676.
XX
XX 19-MAR-1999; 99FR-0003433.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Carpentier A;
PI
XX
XX WPI; 2000-602192/57.
XX
XX Use of stabilised oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic
PT
XX
XX Example 2; Page 16; 57pp; French.
XX
XX The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 5'-purine-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcagatga 22
    |||||
Db 1 tgactgtgaacgttcagatga 22

Search completed: October 9, 2001, 16:26:49
Job time: 2979 sec

```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:37 ; Search time 10334.3 Seconds
(without alignments)
31.457 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgttcagatga 22
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues 28310096
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main.*
1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	16	US-09-296-477-6
2	22	100.0	22	18	US-09-415-186-4
3	22	100.0	22	25	US-09-642-492-4
4	22	100.0	22	28	US-09-713-136-4
5	21.2	96.4	22	18	US-09-415-186-6
6	21	95.5	22	16	US-09-296-477-12
7	21	95.5	22	17	US-09-324-191A-2
8	21	95.5	22	25	US-09-642-492-6
9	21	95.5	22	28	US-09-713-136-6
10	20.4	92.7	22	1	PCT-US00-18229-32
11	20.4	92.7	22	1	PCT-US00-35064-1
12	20.4	92.7	22	1	PCT-US01-03039-1
13	20.4	92.7	22	1	PCT-US01-06034-1
14	20.4	92.7	22	1	PCT-US01-10118-1
15	20.4	92.7	22	1	PCT-US01-10118-3
16	20.4	92.7	22	1	PCT-US01-11290-1
17	20.4	92.7	22	1	PCT-US01-14508-1
18	20.4	92.7	22	1	PCT-US99-21203-19
19	20.4	92.7	22	13	US-09-927-120-19
20	20.4	92.7	22	15	US-09-167-039-19
21	20.4	92.7	22	16	US-09-235-742-19
22	20.4	92.7	22	16	US-09-296-477-2
23	20.4	92.7	22	17	US-09-308-036A-1
24	20.4	92.7	22	17	US-09-324-191A-1
25	20.4	92.7	22	17	US-09-347-343-32
26	20.4	92.7	22	17	US-09-397-198-1
27	20.4	92.7	22	18	US-09-415-186-1
28	20.4	92.7	22	18	US-09-470-382-69
29	20.4	92.7	22	22	US-09-565-908-2
30	20.4	92.7	22	22	US-09-570-325-19
31	20.4	92.7	22	25	US-09-642-492-1
32	20.4	92.7	22	28	US-09-700-354-1
33	20.4	92.7	22	28	US-09-713-136-1
34	20.4	92.7	22	29	US-09-746-130-1
35	20.4	92.7	22	30	US-09-774-403-1
36	20.4	92.7	22	30	US-09-791-500-1
37	20.4	92.7	22	31	US-09-820-484-1
38	20.4	92.7	22	31	US-09-820-484-3
39	20.4	92.7	22	31	US-09-828-505-1
40	19.6	89.1	22	18	US-09-415-186-7
41	19.4	88.2	22	16	US-09-296-477-15
42	19.4	88.2	22	17	US-09-324-191A-5
43	19.4	88.2	22	25	US-09-642-492-7
44	19.4	88.2	22	28	US-09-713-136-7
45	18.8	85.5	22	31	US-09-828-505-2

ALIGNMENTS

RESULT 1
US-09-296-477-6
; Sequence 6, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-6

Query Match 100.0%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22

RESULT 2
US-09-415-186-4
; Sequence 4, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-4

Query Match 100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22

Db 1 tgactgtgaacgttccagatga 22

RESULT 3
US-09-642-492-4
; Sequence 4, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-642-492-4

Query Match 100.0%; Score 22; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22

RESULT 4
US-09-713-136-4
; Sequence 4, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-4

Query Match 100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22

RESULT 5
US-09-415-186-6

; Sequence 6, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-413-186-6

Query Match 96.4%; Score 21.2; DB 18; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.5;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
|||||
DB 1 tgactgtgaabgttccagatga 22

RESULT 6
US-09-296-477-12
; Sequence 12, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINIA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-12

Query Match 95.5%; Score 21; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
|||||
DB 1 tgactgtgaabgttccagatga 22

RESULT 7
US-09-324-191A-2
; Sequence 2, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; TITLE OF INVENTION: MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 377882000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/088,310
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-324-191A-2

Query Match 95.5%; Score 21; DB 17; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
|||||
DB 1 tgactgtgaabgttccagatga 22

RESULT 8
US-09-642-492-6
; Sequence 6, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: N = 5-bromocytosine
; OTHER INFORMATION: Synthetic construct
US-09-642-492-6

Query Match 95.5%; Score 21; DB 25; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttccagatga 22
|||||
DB 1 tgactgtgaabgttccagatga 22

```
RESULT 9
US-09-713-136-6
; Sequence 6, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 37782001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: modified_base
; LOCATION: (11)...(0)
; OTHER INFORMATION: N = 5-bromocytosine
US-09-713-136-6
```

```
Query Match 95.5%; Score 21; DB 28; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 10
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 11
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
```

```
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 12
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides In
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1
```

```
Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22
```

```
RESULT 13
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
```

FILE REFERENCE: 6510-202MO
CURRENT APPLICATION NUMBER: PCT/US01/06034
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic polynucleotide sequence
OTHER INFORMATION: oligonucleotide primer
OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaacggtccagatga 22
|||||
Db 1 tgactgtgaacggtccagatga 22

RESULT 14
PCT-US01-10118-1
Sequence 1, Application PC/TUS0110118
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
APPLICANT: Cho, Hearn Jay
APPLICANT: Richman, Douglas
APPLICANT: Horner, Anthony A.
TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
TITLE OF INVENTION: Lymphocyte Response in vivo.
FILE REFERENCE: 06510-188WO1
CURRENT APPLICATION NUMBER: PCT/US01/10118
CURRENT FILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: US 60/192,537
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: US 60/203,567
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/215,895
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
NAME/KEY: modified_base
LOCATION: (1)...(1)
OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaacggtccagatga 22
|||||
Db 1 tgactgtgaacggtccagatga 22

RESULT 15
PCT-US01-10118-3
Sequence 3, Application PC/TUS0110118
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
APPLICANT: Cho, Hearn Jay

APPLICANT: Richman, Douglas
APPLICANT: Horner, Anthony A.
TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
TITLE OF INVENTION: Lymphocyte Response in vivo.
FILE REFERENCE: 06510-188WO1
CURRENT APPLICATION NUMBER: PCT/US01/10118
CURRENT FILING DATE: 2001-03-17
PRIOR APPLICATION NUMBER: US 60/192,537
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: US 60/203,567
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/215,895
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaacggtccagatga 22
|||||
Db 1 tgactgtgaacggtccagatga 22

Search completed: October 9, 2001, 21:12:37
Job time: 20062 sec

GenCore version 4.5
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OW nucleic - nucleic search, using .sw model

Run on: October 9, 2001, 21:36:13 ; Search time 1391.6 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues
Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Pending_Patents_NA_New.*
- 1: /cgn2_6/ptodata/1/pna/US06_PCT_NEW_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1.*
 - 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
 - 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	7 US-09-802-518-4	Sequence 4, Appli
2	22	100.0	22	7 US-09-802-359-4	Sequence 4, Appli
3	22	100.0	22	7 US-09-802-376-4	Sequence 4, Appli
4	21	95.5	22	7 US-09-802-518-6	Sequence 6, Appli
5	21	95.5	22	7 US-09-802-359-6	Sequence 6, Appli
6	21	95.5	22	7 US-09-802-376-6	Sequence 6, Appli
7	20.4	92.7	22	7 US-09-802-518-1	Sequence 1, Appli
8	20.4	92.7	22	7 US-09-802-359-1	Sequence 1, Appli
9	20.4	92.7	22	7 US-09-802-376-1	Sequence 1, Appli
10	19.4	88.2	22	7 US-09-802-518-7	Sequence 7, Appli
11	19.4	88.2	22	7 US-09-802-359-7	Sequence 7, Appli
12	19.4	88.2	22	7 US-09-802-376-7	Sequence 7, Appli
13	18.8	85.5	22	6 US-09-770-943-2	Sequence 2, Appli
14	18.8	85.5	22	7 US-09-802-518-2	Sequence 2, Appli
15	18.8	85.5	22	7 US-09-802-359-2	Sequence 2, Appli
16	18.8	85.5	22	7 US-09-802-376-2	Sequence 2, Appli
17	18.8	85.5	252	5 US-09-825-790-331	Sequence 331, App
18	18.4	83.6	22	7 US-09-802-518-8	Sequence 8, Appli
19	18.4	83.6	22	7 US-09-802-359-8	Sequence 8, Appli
20	18.4	83.6	22	7 US-09-802-376-8	Sequence 8, Appli
21	17.8	80.9	427	6 US-09-909-629-21114	Sequence 21114, A
22	17.8	80.9	445	6 US-09-906-555-9048	Sequence 9048, Ap
23	17.4	79.1	24853	7 US-09-764-874-10235	Sequence 10235, A
24	17.4	79.1	32212	7 US-09-764-874-10236	Sequence 10236, A
25	17.2	78.2	22	6 US-09-770-943-1	Sequence 1, Appli

Sequence 3, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1362, Ap
Sequence 4959, Ap
Sequence 1286, Ap
Sequence 10462, Ap
Sequence 1982, Ap
Sequence 570, App
Sequence 14227, A
Sequence 10373, A
Sequence 2667, Ap
Sequence 39362, A
Sequence 7434, Ap
Sequence 25567, A

26 17.2 78.2 22 6 US-09-770-943-3
27 17.2 78.2 22 6 US-09-770-943-10
28 17.2 78.2 22 7 US-09-802-518-10
29 17.2 78.2 22 7 US-09-802-518-11
30 17.2 78.2 22 7 US-09-802-359-9
31 17.2 78.2 22 7 US-09-802-359-10
32 17.2 78.2 22 7 US-09-802-376-9
33 17.2 78.2 22 7 US-09-802-376-10
34 17.2 78.2 103785 6 US-09-803-736-1362
35 16.8 76.4 280 5 US-09-534-858-4959
36 16.8 76.4 649 7 US-09-902-540-1286
37 16.4 74.5 303 7 US-09-850-147-10462
38 16.4 74.5 307 5 US-09-534-852-1982
39 16.4 74.5 448 7 US-09-864-761-570
40 16.4 74.5 448 7 US-09-864-761-14227
41 16.2 73.6 132 7 US-09-724-750-10373
42 16.2 73.6 171 7 US-09-764-874-2667
43 16.2 73.6 207 8 US-60-253-457-39362
44 16.2 73.6 268 8 US-60-253-456-7434
45 16.2 73.6 308 8 US-60-253-456-25567

ALIGNMENTS

RESULT 1
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4

Query Match 100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.073; 0; Indels 0; Caps 0;
Matches 22; Conservative 0; Mismatches 0

QY 1 tgactgtgaacgttccagatga 22
Db 1 tgactgtgaacgttccagatga 22
|||||

RESULT 2
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

```
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacagatga 22

RESULT 3
US-09-802-376-4
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacagatga 22

RESULT 4
US-09-802-518-6
; Sequence 6, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802.518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-4

Query Match          100.08; Score 22; DB 7; Length 22;
Best Local Similarity 100.08; Pred. No. 0.073;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacagatga 22

RESULT 5
US-09-802-359-6
; Sequence 6, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802.359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacagatga 22

RESULT 6
US-09-802-376-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-6
```

Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.24; 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttccacgatga 22
||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 37788201100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match 92.7%; Score 20.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacgatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttccacgatga 22
||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:

; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 12
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 13
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory

; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match 85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22

RESULT 14
US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcagatga 22

RESULT 15
US-09-802-359-2
; Sequence 2, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-2

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcagatga 22
||| ||||| |||||
Db 1 tgaccgtgaacgttcagatga 22

Search completed: October 9, 2001, 21:36:14
Job time: 21234 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:02 ; Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

Title: US-09-713-136-4
Perfect score: 22
Sequence: 1 tgactgtgaacgttcacagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	22	4	US-09-092-314-2
2	17.2	78.2	22	4	US-09-092-314-1
3	17.2	78.2	22	4	US-09-092-314-3
4	17.2	78.2	22	4	US-09-092-314-10
5	16.2	73.6	913	2	US-08-975-316-61
6	15.8	71.8	1166	1	US-08-121-063-7
7	15.6	70.9	22	4	US-09-092-314-4
8	15.2	69.1	588	3	US-08-965-904B-1
9	15.2	69.1	773	3	US-08-934-131-2
10	15.2	69.1	5408	1	US-08-471-058-20
11	15.2	69.1	5408	3	US-08-471-057-20
12	14.8	67.3	1743	3	US-09-032-365A-18
13	14.8	67.3	1876	3	US-08-714-918-33
14	14.8	67.3	1876	4	US-09-265-315-33
15	14.8	67.3	1876	4	US-09-265-315-33
16	14.8	67.3	1876	4	US-09-266-417-33
17	14.8	67.3	4975	2	US-08-249-687C-1
18	14.8	67.3	4989	2	US-08-666-392A-3
19	14.8	67.3	4989	2	US-08-625-819-1
20	14.8	67.3	4989	3	US-08-755-558-4
21	14.8	67.3	4989	3	US-08-746-559A-1
22	14.8	67.3	4993	3	US-08-746-559A-3
23	14.8	67.3	10207	1	US-08-920-812-2
24	14.8	67.3	10207	1	US-08-920-827-2
25	14.8	67.3	10207	1	US-08-921-177-2
26	14.8	67.3	10207	1	US-08-362-577C-2
27	14.8	67.3	10207	2	US-08-920-828-2

Sequence 682, Appl
Sequence 1, Appl1
Sequence 22, Appl1
Sequence 22, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 23, Appl1
Sequence 23, Appl1
Sequence 17, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 18, Appl1
Sequence 27, Appl1
Patent No. 5208218

US-09-998-416-682
US-09-118-324-1
US-08-600-982-22
PCT-US94-10261A-22
US-08-975-703-5
US-09-515-884-5
US-08-532-547-4
US-08-379-6568-4
US-08-455-838-4
US-09-019-809-4
US-08-600-982-23
PCT-US94-10261A-23
US-09-128-155-17
US-08-133-038A-1
US-08-161-988A-1
US-08-308-952-18
US-09-124-141-27
US-09-092-314-2
US-09-092-314-2
Sequence 2, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,794
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide

US-09-092-314-2

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 2
US-09-092-314-1
Sequence 1, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,794
PRIOR FILING DATE: 1997-06-06

ALIGNMENTS

RESULT 1

US-09-092-314-2
Sequence 2, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,794
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide

US-09-092-314-2

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttcacagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 2
US-09-092-314-1
Sequence 1, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,794
PRIOR FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match 78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.8;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaactgtgaacgttccagatga 22
||||| ||| ||| ||| |||
DB 1 tgaactgtgaaggtagagatga 22

RESULT 3

US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048.794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match 78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.8;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaactgtgaacgttccagatga 22
||||| ||| ||| ||| |||
DB 1 tgaactgtgaaccttagagatga 22

RESULT 4

US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048.794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10

; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match 78.2%; Score 17.2; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.8;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgaactgtgaacgttccagatga 22
||||| ||| ||| ||| |||
DB 1 tgaactgtgaatgttagagatga 22

RESULT 5

US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; NUMBER OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-975-316-61

Query Match 73.6%; Score 16.2; DB 2; Length 913;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaacgttccagatga 22
||||| ||| ||| ||| |||
DB 513 GACTGTGAATTTTACACATCA 533

RESULT 6

US-08-121-063-7
; Sequence 7, Application US/08121063
; Patent No. 5446143
; GENERAL INFORMATION:
; APPLICANT: Simpson, Evan R.
; APPLICANT: Mahendroo, Mala
; APPLICANT: Mendelson, Carole R.
; TITLE OF INVENTION: Adipose-Specific Promoter Regions of
; TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121.063
; FILING DATE: 14-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSD:351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-121-063-7

Query Match 71.8%; Score 15.8; DB 1; Length 1166;
Best Local Similarity 89.5%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ctgtgtaacgttccagatga 22
||||| ||||||| ||
Db 525 CTGTGTAAGTTCACAGA 543

RESULT 7
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match 70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgttccagatga 22
||||| || |||||
Db 1 tgactgtgaacgttccagatga 22

RESULT 8
US-08-965-904B-1
; Sequence 1, Application US/08965904B
; Patent No. 6030811
; GENERAL INFORMATION:
; APPLICANT: CHABOT-FLETCHER, MARIE
; APPLICANT: ANDERSON, KAREN M.
; TITLE OF INVENTION: A HUMAN MYOTROPHIN CLONE,
; TITLE OF INVENTION: HSABH01
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965.904B
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,677
; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 588 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-965-904B-1

Query Match 59.1%; Score 15.2; DB 3; Length 588;
Best Local Similarity 85.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaacgttccagatg 21
||||| || |||||
Db 341 GACTGTGAAGGCCAGATG 360

RESULT 9
US-08-934-131-2
; Sequence 2, Application US/08934131

Patent No. 6153423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN MYOTROPHIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,131
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0387 US
TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT22
CLONE: 2591910
US-08-934-131-2

Query Match 69.1%; Score 15.2; DB 3; Length 773;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Caps 0;
Oy 2 gactgtgaacgttcagatg 21
||||||| |
Db 544 GACTGTGAAGGCCCATG 563
RESULT 10
US-08-471-058-20/c
Sequence 20, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 5408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1665...1928
OTHER INFORMATION:
US-08-471-058-20
Query Match 69.1%; Score 15.2; DB 1; Length 5408;
Best Local Similarity 85.0%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Caps 0;
Oy 3 actgtgaacgttcagatga 22
||||| |
Db 3226 ACTTAGAACCTTCAGATGA 3207
RESULT 11
US-08-471-057-20/c
Sequence 20, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 5408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1665..1928
US-08-471-057-20

Query Match 69.1%; Score 15.2; DB 3; Length 5408;
Best Local Similarity 85.0%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 actgtgaacgttcacgatga 22
||| |||| ||||| |||||
DB 3226 ACTTAGAACCTTCACGATGA 3207

RESULT 12
US-09-032-365A-18
; Sequence 18, Application US/09032365A
; Patent No. 6114502
; GENERAL INFORMATION:
; APPLICANT: No. 6114502th, Michael
; APPLICANT: Nishina, Patsy
; APPLICANT: Naggart, Juergen
; APPLICANT: No. 6114502en-Trauth, Konrad
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,365A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-2CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650 327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

MOLECULE TYPE: cDNA
US-09-032-365A-18

Query Match 67.3%; Score 14.8; DB 3; Length 1743;
Best Local Similarity 88.9%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaacgttcacg 18
||||||| |||||
DB 1327 TGACTGTGATCCTCCAG 1344

RESULT 13
US-08-714-918-33/c
; Sequence 33, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Waiburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-714-918-33

Query Match 67.3%; Score 14.8; DB 3; Length 1876;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaacgttcaga 19
||||||| |||||

Db 844 GACTGTAATGTTCCAGA 827

RESULT 14

US-09-265-315-33/c
; Sequence 33, Application US/09265315
; Patent No. 6187541

GENERAL INFORMATION:

; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-265-315-33

Query Match 67.3%; Score 14.8; DB 4; Length 1876;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttcaga 19

Db 844 GACTGTAATGTTCCAGA 827

RESULT 15

US-09-265-315-33/c
; Sequence 33, Application US/09265315
; Patent No. 6187541

; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-265-315-33

Query Match 67.3%; Score 14.8; DB 4; Length 1876;
Best Local Similarity 88.9%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaacgttcaga 19

Db 844 GACTGTAATGTTCCAGA 827

Search completed: October 9, 2001, 15:42:03
Job time: 293 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:19:04 ; Search time 2150.93 Seconds
(without alignments)
186.971 Million cell updates/sec

Title: US-09-713-136-5
Perfect score: 26
Sequence: 1 tccataacgttcgcctaacgttcgtc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
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8: gb_ov.*
9: gb_pat1.*
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88: gb_pr4.*
89: gb_pr5.*
90: gb_pr6.*
91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_ro2.*
96: gb_in4.*
97: gb_pr10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match			Length	DB	ID	Description
		Score	Match	Length				
1	26	100.0	26	10	AX083679			AX083679 Sequence
2	18.2	70.0	40400	63	AC012915			AC012915 Drosophila
c	3	18.2	70.0	42141	6	CEY54G9A		AL032648 Caenorhab
	4	18.2	70.0	158322	62	AC011759		AC011759 Drosophila
c	5	18.2	70.0	274388	4	AE003574		AE003574 Drosophila
	6	18.2	70.0	300197	83	CEY54G9		298869 Caenorhabdi
7	18	69.2	1900	89	AK024330			AK024330 Homo sapi
8	18	69.2	80677	13	ATM3E9			AL022223 Arabidops

18 69.2 81975 60 AC005415 Drosophil
18 69.2 92837 60 AC005716 Drosophil
18 69.2 110525 85 AB020878 Homo sapi
18 69.2 175007 4 AC008342 Drosophil
18 69.2 190429 79 ALJ353141 Homo sapi
18 69.2 198320 13 AL353141 Homo sapi
18 69.2 211784 65 AC017903 Drosophil
18 69.2 259445 5 AC003811 Drosophil
17.6 67.7 1016 54 CNS07D50
17.6 67.7 1017 54 CNS07DVI
17.6 67.7 78276 6 CELY38C1AA
17.6 67.7 154091 71 AC044884 Homo sapi
17.6 67.7 163452 84 CNS01RI6
17.6 67.7 172851 70 AC026841 Homo sapi
17.6 67.7 176829 60 AC008741 Caenorhab
17.4 66.9 36749 6 CELM0257
17.4 66.9 250178 60 AC006771 Caenorhab
17.4 66.9 299727 60 AC006738 Caenorhab
17.2 66.2 839 3 PASSESGBD
17.2 66.2 3748 56 AB032347 Cloning v
17.2 66.2 3784 56 AB032348 Cloning v
17.2 66.2 10481 1 AE004840 Pseudomon
17.2 66.2 23889 4 AE002763 Drosophil
17 65.4 1055 6 DMU72893 Drosophila
17 65.4 2203 4 AB026298 Tetrahyme
17 65.4 8371 3 STU51879 Salmonella
17 65.4 12047 1 AE006135 Pasteurel
17 65.4 14713 1 AE004052 Xylella f
17 65.4 24469 6 CEUT16A1 Caenorhab
17 65.4 61204 64 AC017132 Drosophil
17 65.4 146081 13 AP001366 Oryza sat
17 65.4 154378 13 AP001383 Oryza sat
17 65.4 210663 65 AC019525 Drosophil
17 65.4 225655 5 AE003695 Drosophil
17 65.4 310493 4 AE003480 Drosophil
16.8 64.6 974 72 AC046352 Giardia i
16.8 64.6 3774 58 AF133429 Kadipiro

ALIGNMENTS

RESULT 1
AX083679 AX083679 26 bp DNA PAT 28-FEB-2001
LOCUS Sequence 5 from Patent WO0112223.
DEFINITION AX083679
VERSION AX083679.1 GI:13185411
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 26)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
sequences and compositions for use therein
JOURNAL Patent: WO 011223-A 5 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 5 a 9 c 4 g 8 t
ORIGIN
Query Match 100.0%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tccataacgttcgctaacgttcgtc 26
|||||

Db 1 TCATAACGTTCCGCTTACGTCGTC 26
RESULT 2
AC012915 AC012915 40400 bp DNA HTG 03-NOV-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
DEFINITION pieces.
AC012915 AC012915
VERSION AC012915.1 GI:6223407
KEYWORDS HTG: HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 40400)
REFERENCE AC012915
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211446 by the submitter.
For further information on this sequence you may e-mail to
fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES Location/Qualifiers
source 1..40400
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 12236 a 7967 c 7930 g 12267 t
ORIGIN
Query Match 70.0%; Score 18.2; DB 63; Length 40400;
Best Local Similarity 87.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 cataacgttcgctaacgttcgt 25
|||||
Db 36169 CATACCGTTCCGCGAAAGTTCGT 36191
RESULT 3
CEY54G9A/CEY54G9A/CEY54G9A 42141 bp DNA INV 03-APR-2001
LOCUS Caenorhabditis elegans cosmid Y54G9A, complete sequence.
DEFINITION AL032648 298869
AC032648.1 GI:3810715
VERSION AL032648.1
KEYWORDS HTG
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 42141)
REFERENCE none.
AUTHORS Genome sequence of the nematode C. elegans: a platform for
TITLE Investigating biology. The C. elegans Sequencing Consortium
JOURNAL Science 282 (5396), 2012-2018 (1998)
MEDLINE 99069613
REMARK The C. elegans Sequencing Consortium.
REFERENCE 2 (bases 1 to 42141)
AUTHORS Smye, R.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1998) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jesse@sanger.ac.uk or twenematode.wustl.edu
COMMENT Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
 IMPORTANT: This sequence is not the entire insert of clone Y54G9A. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
 The true left end of clone R0689 is at 42042 in this sequence. The true right end of clone Y48E1A is at 100 in this sequence. The start of this sequence (1..100) overlaps with the end of sequence 293392.
 The end of this sequence (42042..42141) overlaps with the start of sequence 283237.
 For a graphical representation of this sequence and its analysis see:- <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y54G9A>.

FEATURES
source

Location/Qualifiers
 1..42141
 /organism="Caenorhabditis elegans"
 /db_xref="taxon:6239"
 /chromosome="II"
 /clone="Y54G9A"
 join(5370..5395,5447..5542,5638..5693,6820..6855,6911..6996)
 /gene="Y54G9A.1"
 join(5370..5395,5447..5542,5638..5693,6820..6855,6911..6996)
 /gene="Y54G9A.1"
 /note="predicted using GeneFinder"
 /codon_start=1
 /protein_id="CAA21697.1"
 /db_xref="GI:3881112"
 /db_xref="SPREMBL:Q9XWH1"
 /translation="MTRKRSIRHSFRNRLKMSFTYFVGSGFVGATYAMNVFSLKFGFTNSVLETFDVFYIEIQTKRKHSKSEASFFLTERNPISFFLSHRK"
 complement(join(11862..12065,13429..13499,13553..13652))
 /gene="Y54G9A.2"
 complement(join(11862..12065,13429..13499,13553..13652))
 /gene="Y54G9A.2"
 /note="predicted using GeneFinder"
 /codon_start=1
 /protein_id="CAA21696.1"
 /db_xref="GI:3881111"
 /db_xref="SPREMBL:Q9XWH2"
 /translation="MPTCLRAYLLQRIISFSLRRVQNTAYLPSADEATEGTELKMHGAAACSFSLKQDQSKLEYQIVDSRPEKCEKSENLLVVENNEMIVSVRREKSAAREGMDTPSTAHLRSNSCSKEH"
 join(14551..14718,15074..15204,15248..15390,15536..16325,17316..17705,17789..17891,18583..18795)
 /gene="Y54G9A.3"
 join(14551..14718,15074..15204,15248..15390,15536..16325,17316..17705,17789..17891,18583..18795)
 /gene="Y54G9A.3"
 /note="contains similarity to Pfam domain: PF00520 (Ion transport protein), Score=-88.8, E-value=0.00034, N=1"
 /codon_start=1
 /protein_id="CAA21699.1"
 /db_xref="GI:3881114"
 /db_xref="SPREMBL:Q9XWG9"
 /translation="MTYRAMIYNCLERPTGWKCFLYHFSVFLVILICLSVLSTVEESHFAEALYILEIVLVVFFSVFVRLWSAGRSKYIGVGRLFKVRKPTILGRFGGRLHQLIDRLRHGSPSCGRDAGDTVSADSDAPRSGAHHWVEIRISKPIEIEKSLKIGIFKNFANWNPQFRKLEFSLKKNLAGRVHYWGSATPSSGDPDLVGCFFPKLHLASFRLLGSVFIHQEILITLIGLGLIIFESSFYVLAEDHIGVDCGROAFTSYADALWGVITMTTIGYDVVPQTLWGLRVASCFISFISFALPAGLIGSGFALKVOQKROKHNRQIPAAATLIQCLARCAAEKVSAWNAHIDPLAHETKETHWNNKKHASSMSNNLTRKOLFVKOSLVNTPFRKGSPTDVMGELAQOERLHRNSDDDEKRIYRGVADIEDIETEEDPTTPROGHTSHVCELTDAHNAIRLRVRYFVARRRQOARPKYDIEDIETEYQSGHLLNMWRIKELQRLDQTLCKPGQYDCKGSKRGKHPVTIGSRLSRLQAKSSLDKRVKSSNRTLNALYRLMADRNLTLTSPSPALLISRPVSPAACLSPRQLSPTSISQSGSGQW"

gene

CDS

complement(join(19069..19173,19824..20201,20541..20805,21176..21306,21813..21893))
 /gene="Y54G9A.4"
 complement(join(19069..19173,19824..20201,20541..20805,21176..21306,21813..21893))
 /gene="Y54G9A.4"
 /note="predicted using GeneFinder"
 /codon_start=1
 /protein_id="CAA21695.1"
 /db_xref="GI:3881110"
 /db_xref="SPREMBL:Q9XWH3"
 /translation="MSLELLKWLMLGVWALMTIIFGLLPKIVISYLTNKTSAIHQHSLLLSLSCFAGVSLVCFLOWLPDCLAEWSVOTDNTVSDYPEVOLIALIGLFFPVYLTLELSSVCNVCVGHSHSDNIMESNVTFFPARLATVGSIFNVGSLVEPCRKRSLENYDDGEGVRQSIITFSAPILFHVFFECFAFQEDAVSVTSIFLGIAHMKATVMSFSLG MKLTRTHPRRSIVVILILFALFNVIIGTAGILSSNNMOTPKDITAVLMSFSLG TFLYTSFPEILAPERANNHNSILOHFIASFGFALLAVNMWAT"
 join(29014..29234,29284..29413,29469..29601,30649..30739,30789..30987)
 /gene="Y54G9A.5"
 join(29014..29234,29284..29413,29469..29601,30649..30739,30789..30987)
 /gene="Y54G9A.5"
 /note="predicted using GeneFinder"
 CDS
 EST YK74C1.3 comes from this gene
 CDS
 EST YK80B1.3 comes from this gene
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 CDS
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 CDS
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 CDS
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 CDS
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 EST YK284D1.5 comes from this gene
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gene

CDS

gene

CDS

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 CDS
 EST YK102H2.3 comes from this gene
 CDS
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 CDS
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 CDS
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gene

CDS

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Drosophila melanogaster BAC library, partial ECORI in
pBACE3.6"
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Best Local Similarity 87.0% Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 cataacgttcgcctaaccgttcgt 25
||||| ||||||| || |||||
Db 105049 CATACCGTTCGCCGAAAGTTCGT 105071
RESULT 5
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LOCUS Drosophila melanogaster genomic scaffold 142000013386033 section 1
DEFINITION of 2, complete sequence.
ACCESSION AE003574 AE002629
VERSION AE003574.3 GI:10803726
KEYWORDS HTG.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 274388)
ADAMS, M.D., CALNIKER, S.E., HOLT, R.A., EVANS, C.A., GOCAYNE, J.D.,
AMANATIDES, P.G., SCHERER, S.E., LI, P.W., HOSKINS, R.A., GALLE, R.F.,
GEORGE, R.A., LEWIS, S.E., RICHARDS, S., ASHBURNER, M., HENDERSON, S.N.,
SUTTON, G.G., WORTMAN, J.R., YANDELL, M.D., ZHANG, Q., CHEN, L.X.,
BRANDON, R.C., ROGERS, Y.H., BLAZEK, R.G., CHAMPER, M., PFELFER, B.D.,
WAN, K.H., DOYLE, C., BAXTER, E.G., HOLT, G., NELSON, C.R., GABOR
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ANDREWS-PIRANKOCH, C., BALDWIN, D., BALLEW, R.M., BASU, A.,
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VENTER, E., WANG, A.H., WANG, X., WANG, Z.Y., WASSERMAN, D.A.,

schuellemips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
 E-mail: michael.bevan@bbsrc.ac.uk
 On Aug 6, 1999 this sequence version replaced gi:4468103.
 Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

COMMENT

FEATURES

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Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 56083 TCAAAAACCTTCTCCTAACGTTCCTC 56108

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LOCUS
DEFINITION
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unordered pieces.
AC005415
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HTG; HTGS_PHASE1.
SOURCE
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 81975)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K.,
Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R.,
Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.,
Richards,S., Sethi,H., Svirskaas,R.R., Wan,K.H., Webster,D.,
Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
Sequencing of Drosophila melanogaster
Unpublished
2 (bases 1 to 81975)
Celniker,S.E., George,R.A., Galle,R., Svirskaas,R.R., Hoskins,R.A.,
Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C.,
Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A.,
Hummasti,S.R., Karra,K., Kearney,L., Lee,B., Lewis,S., Li,P.,
Ling,H., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M.,
Park,S., Pfeiffer,B., Richards,S., Sethi,H., Svirskaas,R.R.,
Wan,K.H., Webster,D., Woolley,P., Yang,S., Yee,M., Yu,C. and
Rubin,G.M.

TITLE
JOURNAL
AUTHORS

Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,
Lomotan,A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R.,
Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E.,
Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R.,
Zieran,L. and Kimmel,B.E.
Direct Submission
Submitted (14-AUG-1998) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Nov 23, 1999 this sequence version replaced gi:6226988.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases. Pl library location:
54-2.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 86 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 69403 69975: contig of 573 bp in length
* 69976 70055: gap of unknown length
* 70056 70631: contig of 576 bp in length
* 70632 70711: gap of unknown length
* 70712 71302: contig of 591 bp in length
* 71303 71382: gap of unknown length
* 71383 71972: contig of 590 bp in length
* 71973 72052: gap of unknown length
* 72053 72668: contig of 616 bp in length
* 72669 72748: gap of unknown length
* 72749 73352: contig of 604 bp in length
* 73353 73432: gap of unknown length
* 73433 74031: contig of 599 bp in length
* 74032 74111: gap of unknown length
* 74112 74689: contig of 578 bp in length
* 74690 74769: gap of unknown length
* 74770 75281: contig of 512 bp in length
* 75282 75361: gap of unknown length

Query Match 69.2%; Score 18; DB 60; Length 81975;

Best Local Similarity 80.8%; Pred. NO. 3.2e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 tccataacgttcgcctaacgttcgtc 26

||||| ||||||| |||||||

Db 56750 TCCAGTACGTCGCTGCTCGAC 56725

RESULT 10

AC005716/c

LOCUS

DEFINITION

AC005716 92837 bp DNA HTG 23-NOV-1999

Drosophila melanogaster chromosome 2 clone DS00150 (D438) map

51E9-51F2 strain Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 13

unordered pieces.

AC005716

AC005716.8 GI:6466502

HTG: HTGS_PHASE1.

SOURCE

fruit fly.

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 92837)

REFERENCE

AUTHORS

Celniker, S.E., Agbayani, A., Arcalena, T.T., Baxter, E., Blazej, R.G.,

Butenkov, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,

Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,

Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Katra, K.,

Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R.,

Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B.,

Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,

Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.

Sequencing of Drosophila melanogaster

Unpublished

2 (bases 1 to 92837)

Celniker, S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A.,

Agbayani, A., Arcalena, T.T., Baxter, E., Blazej, R.G., Chavez, C.,

Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,

Hummasti, S.R., Katra, K., Kearney, L., Kim, S.H., Lee, B.,

Lomtan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,

Moshrefi, M., Nixon, K., Paclet, J.M., Park, S., Pfeiffer, B., Punch, E.,

Shir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R.,

Zier, L.L. and Kimmel, B.E.

Direct Submission

TITLE

JOURNAL

Submitted (26-SEP-1998) Drosophila Genome Center, Lawrence Berkeley

Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

1 (bases 1 to 175007)

REFERENCE
AUTHORS
Celiker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Cocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Hanson, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champagne, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Friese, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Matteli, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleib, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirska, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

TITLE
JOURNAL
REFERENCE
AUTHORS
Sequencing of Drosophila chromosome 2R, region 51F-51F

Unpublished

2 (bases 1 to 175007)

TITLE
JOURNAL
REFERENCE
AUTHORS
Celiker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazef, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleib, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirska, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.

TITLE
JOURNAL
REFERENCE
AUTHORS
Direct Submission

Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Mar 22, 2001 this sequence version replaced gi:7118739.

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdgpf@fruitfly.berkeley.edu.

FEATURES
source
1. .175007
Location/Qualifiers
/organism="Drosophila melanogaster"
/strain="v: cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
/map="51F-51F"
/clone="BACR33K06 (D930)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACE3.6)"
BASE COUNT 51366 a 37558 c 37136 g 48947 t
ORIGIN

Query Match 69.2%; Score 18; DB 4; Length 175007;
Best Local Similarity 80.8%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
|||||
Db 87729 TCCAGTACGTCGCTGCTCGAC 87704

RESULT 13
LOCUS AL353141 190429 bp DNA HTG 19-FEB-2001
DEFINITION Homo sapiens chromosome 9 clone RP11-58C3, *** SEQUENCING IN
PROGRESS ***, 10 unordered pieces.
ACCESSION AL353141
VERSION AL353141.8 GI:13016504
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190429)
Plumb, B.
Direct Submission
Submitted (18-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Feb 20, 2001 this sequence version replaced gi:12964411.

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project information
Center project name: BA58C3
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 184146 bases at least Q40
Consensus quality: 186729 bases at least Q30
Consensus quality: 188260 bases at least Q20
Insert size: 189529; sum-of-contigs
Insert size: 217333; agarose-fp
Quality coverage: 5.94x in Q20 bases; sum-of-contigs Quality
coverage: 5.52x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 72909: contig of 72909 bp in length
* 72910 73009: gap of 100 bp
* 73010 85724: contig of 12715 bp in length
* 85725 85824: gap of 100 bp
* 85825 89598: contig of 3774 bp in length
* 89599 89698: gap of 100 bp
* 89699 94785: contig of 5087 bp in length
* 94786 94885: gap of 100 bp
* 94886 98698: contig of 3813 bp in length
* 98699 98798: gap of 100 bp
* 98799 151407: contig of 52609 bp in length
* 151408 151507: gap of 100 bp
* 151508 155590: contig of 4083 bp in length
* 155591 155690: gap of 100 bp
* 155691 184932: contig of 29242 bp in length
* 184933 185032: gap of 100 bp
* 185033 187234: contig of 2202 bp in length
* 187235 187334: gap of 100 bp
* 187335 190429: contig of 3095 bp in length.
Location/Qualifiers
1. .190429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-58C3"
/clone_lib="RPCI-11.1"
1. .72909
/note="assembly_fragment:02437
fragment_chain:1"
73010 .85724
/note="assembly_fragment:02762
fragment_chain:1"
85825 .89598
/note="assembly_fragment:02835
fragment_chain:1"

misc_feature
misc_feature
misc_feature

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misc_feature      fragment_chain:1"
89699..94785
/note="assembly_fragment:00908
fragment_chain:2"
94886..98698
/note="assembly_fragment:01814
fragment_chain:2"
98799..151407
/note="assembly_fragment:00777.0"
151508..155590
/note="assembly_fragment:02004"
155691..184932
/note="assembly_fragment:02112"
185033..187234
/note="assembly_fragment:02231"
187335..190429
/note="assembly_fragment:02735"
BASE COUNT      56376 a 38536 c 38540 g 56071 t 906 others
ORIGIN

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Query Match      69.2% Score 18; DB 79; Length 190429;
Best Local Similarity 80.8%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 tccataacgttcgcctaagcttcgc 26
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Db 129081 TCCCTAAGGTTCTCCTAACTTCTTC 129056

```

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RESULT 14
ATCHRIV65/c
LOCUS              198320 bp      DNA      PLN      16-MAR-2000
DEFINITION         Arabidopsis thaliana DNA chromosome 4., contig fragment No. 65.
ACCESSION           AL161565
VERSION             AL161565.2 GI:7269481
KEYWORDS            thale cress.
ORGANISM            Arabidopsis thaliana
                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                    Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                    Brassicales; Brassicaceae; Arabidopsids.
REFERENCE           1 (bases 25731 to 106407)
AUTHORS             Vandenbol,M., Jallet,C., Portetelle,D., Mewes,H.W., Lemcke,K. and
                    Mayer,K.F.X.
JOURNAL             Unpublished
REFERENCE           2 (bases 68133 to 160789)
AUTHORS             Zimmermann,M., Grueneisen,A., Wambutt,R., Kalicki,J., Wohldmann,P.,
                    Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
JOURNAL             Unpublished
REFERENCE           3 (bases 92775 to 93172)
AUTHORS             Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W.,
                    Lemcke,K. and Mayer,K.F.X.
JOURNAL             Unpublished
REFERENCE           4 (bases 149164 to 198320)
AUTHORS             Lecharny,A., Cheddor,F., Krivitzky,M., Kreis,M., Mewes,H.W.,
                    Lemcke,K. and Mayer,K.F.X.
JOURNAL             Unpublished
REFERENCE           5 (bases 1 to 42972)
AUTHORS             Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W., Lemcke,K. and
                    Mayer,K.F.X.
JOURNAL             Unpublished
REFERENCE           6 (bases 1 to 198320)
AUTHORS             EU Arabidopsis sequencing,project.
TITLE               Direct Submission
JOURNAL             Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
                    Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                    lemckemips.biochem.mpg.de,mayer@mips.biochem.mpg.de
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbc.ac.uk
COMMENT             Information on performance of analysis and a more detailed
                    annotation of this entry and other sequences of chromosomes 3, 4

```

```

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
this fragment has an overlap with ATCHRIV64 at the 5' end and an
overlap with ATCHRIV66 at the 3' end.
FEATURES             Location/Qualifiers
     1..198320
     /organism="Arabidopsis thaliana"
     /variety="Columbia"
     /db_xref="taxon:3702"
     /chromosome="4"
     complement(5578..5688)
     /gene="AT4g26300"
     /number=1
     complement(join(5578..5688,5802..5900,5995..6063,
6449..6538,6620..6689,6872..6941,7047..7233,7337..7421,
7592..7770,7871..7975,8089..8172,8302..8382,8490..8705,
8795..8896,8975..9050,9148..9287,9374..9448,10198..10287))
     /gene="AT4g26300"
     /note="Contains Aminoacyl-transfer RNA synthetases class-I
signature AA190-201
contains EST gb:AI995766.1, T76307"
     /codon_start=1
     /product="arganyl-tRNA synthetase"
     /protein_id="CAB79485.1"
     /db_xref="GI:7269482"
     /translation="MFIPKDNRRRETLLTKLRFSAHDLTFTVTTEKLRTATAWRFAFS
SRKSVVMAANEETGNLKRQAKLFDVSLKLTVPDEPSVEPLVAASALGKFGDYQC
NNAMGLWSIINGKGTQFGKGPAPVGOALVKSLPTSEMVESCVAGGFTNVLSAKWMA
KSIENMLDGVDTWAPLTVKRAVVDVSPNIAKEMHVGHLRSLTIGTTLARMLEYSH
VEVLRNHHVDMGTQFGMLIYLELFEKFPDTSVTETAGLDQVFKASKHKFDDLEAF
KEKAQAVVRLQGGDPVYKAWAKICDISRTEFAKVKYQRLRLEVEEKGESFYNPRIAK
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DYVRLVDLDEAKTRSKLALIERGKDKETPELDOATAEAVGVGAVYADLKNRRLTN
YTFSPDMLNDKNTAVYLLAHARICSIIRKSKGIDELKKTGKGLADHADERALGL
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     complement(join(5578..5688,5802..5900,5995..6063,
6449..6538,6620..6689,6872..6941,7047..7233,7337..7421,
7592..7770,7871..7975,8089..8172,8302..8382,8490..8705,
8795..8896,8975..9050,9148..9287,9374..9448,10198..10287))
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     /number=3
     complement(6064..6448)
     /number=3
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     /number=4
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     complement(6620..6689)
     /gene="AT4g26300"
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exon         complement(7337..7421)
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intron      complement(7422..7591)
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exon         complement(7592..7770)
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intron      complement(7771..7870)
            /number=9
exon         complement(7871..7975)
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            /number=10
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exon         complement(8302..8382)
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exon         complement(8795..8896)
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exon         complement(9374..9448)
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            /number=17
intron      complement(9449..10197)
            /number=17
exon         complement(10198..10287)
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            /number=18
CDS          complement(join(11284..11361,11487..11526,11704..11827,
12412..12481,12598..12648,12741..12754,12843..12873,
13014..13244))
            /gene="At4g26310"
            /note="similarity to elongation factor P (efp) RP238,
Rickettsia prowazekii, PIR2:B71678
Contains Elongation factor P signature
AA176-195; prokaryotic membrane lipoprotein lipid
attachment site AA42-52
contains EST gb:F20046"
            /codon_start=1
            /product="putative protein"
            /protein_id="C879486.1"
            /db_xref="GI:7269483"
            /translation="MRGLHFKRISIRSLFSFNATSPGAVTTRRSYLSRSLLS
TPYAAGCCRPPLHRSWALQRRGVKNVIAQLRAGNVIRGTRFRVAEHKQOG
RGASIQVLRDVRDGTGNLNLRFSGSESVKEMKVLQQLYDGRALSASIPKHICTVY
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            /number=1
gene       complement(join(11284..11361,11487..11526,11704..11827,
12412..12481,12598..12648,12741..12754,12843..12873,
13014..13244))
            /gene="At4g26310"
            /number=8
            /gene="At4g26310"
            /number=13244
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            /number=1
exon      complement(11487..11526)
            /gene="At4g26310"

Query Match      69.2%; Score 18; DB 13; Length 198320;
Best Local Similarity 80.8%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tcataacgttcgcctaacgttcgtc 26
    ||| ||| ||| ||| ||| ||| |||
Db 50325 TCAAAACCTTCTCCTACGTTCTC 50300

RESULT 15
AC017903/c      AC017903 211784 bp DNA HTG 09-DEC-1999
LOCUS          Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
DEFINITION     pieces.
ACCESSION      AC017903
VERSION        AC017903.1 GI:6553287
KEYWORDS       HTG; HTGS_PHASE2.
SOURCE         fruit fly.
ORGANISM       Drosophila melanogaster
                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 211784)
AUTHORS        Adams,M. and Venter,J.C.
TITLE          Direct Submission
JOURNAL        Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
                Rockville, MD, USA
COMMENT        This sequence was identified as CDM:10212569 by the submitter.
                For more information on this record e-mail to fly@celera.com.
                * NOTE: This is a 'working draft' sequence.
                * This sequence will be replaced
                * by the finished sequence as soon as it is available and
                * the accession number will be preserved.
FEATURES       Location/Qualifiers
                1..211784
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
BASE COUNT     61816 a 45004 c 44716 g 60248 t
ORIGIN

Query Match      69.2%; Score 18; DB 65; Length 211784;
Best Local Similarity 80.8%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tcataacgttcgcctaacgttcgtc 26
    ||| ||| ||| ||| ||| ||| |||
Db 153722 TCCAGTACCTTCGCTGCTTCGAC 153697

Search completed: October 9, 2001, 16:19:55
Job time: 2565 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:19 ; Search time 6788.49 Seconds
(without alignments)
36.205 Million cell updates/sec

Title: US-09-713-136-5
Perfect score: 26

Sequence: 1 tccataacgttcgcctaacttcgtc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1:	gb_est1:	*
2:	gb_est2:	*
3:	gb_est3:	*
4:	gb_est4:	*
5:	gb_est5:	*
6:	gb_est6:	*
7:	gb_est7:	*
8:	gb_est8:	*
9:	gb_est9:	*
10:	gb_est10:	*
11:	gb_est11:	*
12:	gb_est12:	*
13:	gb_est13:	*
14:	gb_est14:	*
15:	gb_est15:	*
16:	gb_est16:	*
17:	gb_est17:	*
18:	gb_est18:	*
19:	gb_est19:	*
20:	gb_est20:	*
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24:	gb_est24:	*
25:	gb_est33:	*
26:	gb_est34:	*
27:	gb_est35:	*
28:	gb_est36:	*
29:	gb_est37:	*
30:	gb_est38:	*
31:	gb_est39:	*
32:	gb_est40:	*
33:	em_estba:	*
34:	em_estfun:	*
35:	em_esthum1:	*
36:	em_esthum2:	*
37:	em_esthum3:	*
38:	em_esthum4:	*
39:	em_esthum5:	*
40:	em_esthum6:	*
41:	em_esthum7:	*
42:	em_esthum8:	*
43:	em_esthum9:	*

44:	em_esthum10:	*
45:	em_esthum11:	*
46:	em_esthum12:	*
47:	em_esthum13:	*
48:	em_esthum14:	*
49:	em_esthum15:	*
50:	em_esthum16:	*
51:	em_esthum17:	*
52:	em_esthum18:	*
53:	em_esthum19:	*
54:	em_esthum20:	*
55:	em_esthum21:	*
56:	em_esthum22:	*
57:	em_esthum23:	*
58:	em_esthum24:	*
59:	em_esthum25:	*
60:	em_esthum26:	*
61:	em_esthum27:	*
62:	em_esthum28:	*
63:	em_estin1:	*
64:	em_estin2:	*
65:	em_estin3:	*
66:	em_estin4:	*
67:	em_estin5:	*
68:	em_estom1:	*
69:	em_estom2:	*
70:	em_estov1:	*
71:	em_estov2:	*
72:	em_estpl1:	*
73:	em_estpl2:	*
74:	em_estpl3:	*
75:	em_estpl4:	*
76:	em_estpl5:	*
77:	em_estpl6:	*
78:	em_estpl7:	*
79:	em_estpl8:	*
80:	em_estpl9:	*
81:	em_estpl10:	*
82:	em_estro1:	*
83:	em_estro2:	*
84:	em_estro3:	*
85:	em_estro4:	*
86:	em_estro5:	*
87:	em_estro6:	*
88:	em_estro7:	*
89:	em_estro8:	*
90:	em_estro9:	*
91:	em_estro10:	*
92:	em_estro11:	*
93:	em_estro12:	*
94:	em_estro13:	*
95:	em_estro14:	*
96:	em_estro15:	*
97:	em_estro16:	*
98:	em_estro17:	*
99:	em_estro18:	*
100:	em_estro19:	*
101:	em_estro20:	*
102:	gb_est25:	*
103:	gb_est26:	*
104:	gb_est27:	*
105:	gb_est28:	*
106:	gb_est29:	*
107:	gb_est30:	*
108:	gb_est31:	*
109:	gb_est32:	*
110:	gb_est41:	*
111:	gb_est42:	*
112:	gb_est43:	*
113:	gb_est44:	*
114:	gb_est45:	*
115:	gb_est46:	*
116:	gb_est47:	*

117: gb_est48:*
 118: gb_est49:*
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 252: gb_est183:*
 253: gb_est184:*
 254: gb_est185:*
 255: gb_est186:*
 256: gb_est187:*
 257: gb_est188:*
 258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	18.6	71.5	788	137	BE547778	601073614
C 2	18.6	71.5	820	168	BF679824	602154407
C 3	18.2	70.0	241	104	AJ285626	4A3B-RAV-
C 4	17.6	67.7	694	23	A1657535	AEHBD55
C 5	17.4	66.9	639	32	AV679043	AV679043
C 6	17.2	66.2	511	238	A2139831	SP_0002_B
C 7	17.2	66.2	666	11	AA736360	SWOVL3CAN
C 8	17.2	66.2	970	219	CNS0184T	AL108887 Drosophil
C 9	17	65.4	318	121	AW883193	AW883193 OV2-OT006
C 10	17	65.4	392	225	AQ182480	AQ182480 HS_3077_A
C 11	17	65.4	461	12	AA787178	AA787178 mC02al.f
C 12	17	65.4	544	154	BG486179	BG486179 dad23h02
C 13	17	65.4	635	142	BE976680	bs54el12.y
C 14	17	65.4	673	142	BE975036	BS975036 bs37h07.y
C 15	17	65.4	894	136	BE542042	BE542042 601066950
C 16	16.8	64.6	242	161	BB576549	BB576549
C 17	16.8	64.6	360	156	C13137	C13137 C13137 YuJ1
C 18	16.8	64.6	376	156	C68546	C68546 C68546 YuJ1
C 19	16.8	64.6	388	1	AA002481	mq42cl2.r
C 20	16.8	64.6	439	151	BF648336	BF648336 NF044H02E
C 21	16.8	64.6	535	151	BF643349	NF003E11E
C 22	16.8	64.6	576	175	BG269530	LO-3615T3
C 23	16.8	64.6	581	137	BE576991	LO-1602T3
C 24	16.8	64.6	656	151	BF646041	BF646041 NF065A11E
C 25	16.8	64.6	735	162	BE034900	ML05H05 M
C 26	16.8	64.6	862	162	BE035137	MM03G09 M
C 27	16.6	63.8	329	157	D64542	CELK054B9R
C 28	16.6	63.8	460	31	AV639729	AV639729
C 29	16.6	63.8	470	20	AI466838	mz48e08.y
C 30	16.6	63.8	504	164	BE195754	HVSMEH009
C 31	16.6	63.8	574	16	AI113909	GH10417.5
C 32	16.6	63.8	598	231	AQ657044	AQ657044 Sheared D
C 33	16.6	63.8	608	232	AQ676154	HS_2133_B
C 34	16.6	63.8	750	239	AZ183794	SP_1002_A
C 35	16.6	63.8	843	172	BF975514	602245859
C 36	16.6	63.8	902	136	BE541188	601064049
C 37	16.6	63.8	1098	220	CNS037VI	Tetraodon
C 38	16.4	63.1	179	120	AW799829	PML-UM005
C 39	16.4	63.1	211	121	AW838879	CMO-LT005
C 40	16.4	63.1	216	170	BF820251	CMO-RT001
C 41	16.4	63.1	290	120	AW728832	GA-Ea002
C 42	16.4	63.1	345	19	AI359428	gy31g02.x
C 43	16.4	63.1	352	110	AW023566	df56h03.y
C 44	16.4	63.1	360	26	AV190522	AV190522
C 45	16.4	63.1	360	156	C40605	C40605 C40605 YuJ1

ALIGNMENTS

RESULT BE547778/c 1
 LOCUS 601073614F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459602 5',
 DEFINITION mRNA sequence. EST 09-AUG-2000

ACCESSION BE547778
 VERSION BE547778.1 GI:9776423
 KEYWORDS EST

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 788)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM8452 row: 1 column: 03
 High quality sequence stop: 372.
 Location/Qualifiers

FEATURES

source
 1..788
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3459602"
 /clone_lib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life Technologies."
 BASE COUNT 168 a 247 c 197 g 176 t
 ORIGIN

Query Match 71.5%; Score 18.6; DB 137; Length 788;
 Best Local Similarity 84.0%; Pred. No. 30;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ccataacgttcgcctaacgttcgc 26

||||| ||||||| ||||||| ||

Db 412 CCAGAAAGTTCGCTCAGTTCCTC 388

RESULT 2

BF679824/c

LOCUS

DEFINITION

BF679824

ACCESSION

BF679824

VERSION

BF679824.1 GI:11953633

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 820)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1CM1146 row: m column: 02

High quality sequence stop: 599.

Location/Qualifiers

1..820

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4295593"

/clone_lib="NIH_MGC_83"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site:1: SfiI (ggcgctcgcc); Site:2: SfiI (ggcattatggcc

); 5' and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCCATTTATGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGGAGCGCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT
ORIGIN

264 a 180 c 201 g 175 t

Query Match 71.5%; Score 18.6; DB 168; Length 820;
Best Local Similarity 84.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactcgt 25

Db 593 TCCATCAGTCGCGCTAACTTTGT 569

RESULT 3

LOCUS AJ285626 241 bp mRNA EST 30-JUN-2000
DEFINITION 4A3B-AAV-D-11-R Anopheles gambiae immune competent 4A3B Anopheles
gambiae cDNA clone 4A3B-AAV-D-11, mRNA sequence.

ACCESSION AJ285626

VERSION AJ285626.1 GI:6933507

KEYWORDS EST.

SOURCE African malaria mosquito.

ORGANISM

REFERENCE 1 (bases 1 to 241)
AUTHORS Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.

TITLE Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

MEDLINE 20300950

COMMENT Contact: Dimopoulos G
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.

FEATURES

source

1..241

/organism="Anopheles gambiae"

/strain="4A r/r"

/db_xref="taxon:7165"

/clone="4A3B-AAV-D-11"

/clone_lib="Anopheles gambiae immune competent 4A3B"

/cell_line="immune competent 4A3B"

/lab_host="E. coli DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
the forward priming site that reads from the 3' end of
cDNA. The 4A3B is a directionally cloned and normalized
cDNA library that was constructed from the 4A3B cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996): Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."

BASE COUNT

ORIGIN

40 a 43 c 40 g 118 t

Query Match 70.0%; Score 18.2; DB 104; Length 241;
Best Local Similarity 87.0%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ccataacgttcgcctaactcgt 24

Db 189 CCATAACGTTCCCTAACGCTCG 211

RESULT 4

LOCUS AI657535/c

DEFINITION AEMTBD55 Aedes aegypti MT pSPORT Library Aedes aegypti cDNA clone

BD55 5', mRNA sequence.

ACCESSION AI657535

VERSION AI657535.1 GI:4753625

KEYWORDS EST.

SOURCE yellow fever mosquito.

ORGANISM Aedes aegypti

REFERENCE 1 (bases 1 to 694)

AUTHORS Gill, S.S., Ross, L.S. and Wadiak, H.

TITLE Expressed sequence tags of cDNA clones from an enriched Malpighian
tubule and gut library from Aedes aegypti

JOURNAL Unpublished (1999)

COMMENT Contact: Gill SS
Environmental Toxicology
University of California, Riverside
5419 Boyce Hall, Riverside, CA 92521, USA
Tel: 909 787 3547
Fax: 909 787 3087
Email: sarjeet.gill@ucr.edu
Seq primer: CCAAGCTTAATACGACTCACTAT
High quality sequence stop: 694.
Location/Qualifiers
1..694
/organism="Aedes aegypti"
/db_xref="taxon:7159"
/clone="BD55"
/clone_lib="Aedes aegypti MT pSPORT Library"
/sex="female"
/tissue_type="malpighian tubules and gut"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; The
cDNA was cloned into the SalI/NotI sites of pSPORT1."

BASE COUNT

ORIGIN

195 a 150 c 154 g 195 t

Query Match 67.7%; Score 17.6; DB 23; Length 694;

Best Local Similarity 83.3%; Pred. No. 98;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3 cataacgttcgcctaactcgt 26

Db 422 CACATCGTTCCTCAACGCTTGT 399

RESULT 5

LOCUS AV679043

DEFINITION AV679043 Nori Satoh unpublished cDNA library Ciona intestinalis

CDNA clone rcitb14j20 3', mRNA sequence.

ACCESSION AV679043

VERSION AV679043.1 GI:10117042

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

REFERENCE 1 (bases 1 to 639)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL Unpublished (2000)

COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University

BASE COUNT

ORIGIN

639 bp mRNA EST 05-OCT-2000

LOCUS AV679043

DEFINITION AV679043 Nori Satoh unpublished cDNA library Ciona intestinalis

CDNA clone rcitb14j20 3', mRNA sequence.

ACCESSION AV679043

VERSION AV679043.1 GI:10117042

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

REFERENCE 1 (bases 1 to 639)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

TITLE Expressed genes in Ciona intestinalis

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ACCESSION AV679043

VERSION AV679043.1 GI:10117042

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

REFERENCE 1 (bases 1 to 639)

AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.

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Kyoto University

BASE COUNT

ORIGIN

639 bp mRNA EST 05-OCT-2000

LOCUS AV679043

DEFINITION AV679043 Nori Satoh unpublished cDNA library Ciona intestinalis

CDNA clone rcitb14j20 3', mRNA sequence.

ACCESSION AV679043

VERSION AV679043.1 GI:10117042

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

<http://seqa.tokyo.nih.go.jp/ntnuc/people/peoples/peoples.htm>
 Tissue Isolation and Library construction performed at the National
 Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
<http://www.niddk.nih.gov/ntnuc/people/peoples/peoples.htm>). DNA sequencing
 and analyses performed by National Institutes of Health Intramural
 Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
 Plate: 54 row: e column: 12
 Seq primer: M13RP1 reverse primer (ABI).

round of Poly(A)⁺ selection using Oligotex (Qiagen). cDNA library constructed using Stratagene ZAP-cDNA synthesis kit. Oligo dT-primed, size fractionated -1.6 kb, and directionally cloned at EcoRI and XhoI in Uni-ZAP XR. Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."

RESULT 15
BE542042/c
LOCUS
DEFINITION
BE542042 894 bp mRNA EST 09-AUG-2000
601086950F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453252 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
human

Email: oliver@helix.nih.gov,
<http://www.niddk.nih.gov/intram/people/boliver.htm>
 Tissue isolation and library construction performed at the National
 Institute of Diabetes and Digestive and Kidney Diseases, NIH (see

```

1. .894
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3453252"

```

```
/clone_lib="NIH_MGC_10"
/lab_line="MGC36"
/lab_host="DH10B"
/Note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT      250 a      143 c      233 g      267 t      1 others
ORIGIN

Query Match      65.4%; Score 17; DB 136; Length 894;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgt 25
   ||||| ||||| ||||| |||||
Db 426 TCCATATCGTTCATCTACATTCCT 402

Search completed: October 9, 2001, 18:20:22
Job time: 9792 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:49 ; Search time 515.84 Seconds
(without alignments)
31.648 Million cell updates/sec

Title: US-09-713-136-5

Perfect score: 26
Sequence: 1 tccataacgttcgcctaacttcgtc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	26	100.0	26	AAV80100	Immunomodulatory o
2	26	100.0	26	AA338069	Immunostimulatory
3	26	100.0	26	AAF77044	Immunostimulatory
4	24	92.3	24	AAV80115	Oligo used in expe
5	24	92.3	24	AAV80116	Oligo used in expe
6	23	88.5	24	AAZ55885	Immunomodulatory o
7	22	84.6	24	AAZ55886	Immunomodulatory o
8	16.4	63.1	1034	AACT4251	Human secreted pro
9	16.4	63.1	1317	AAZ13867	Enterococcus faeca
10	16.4	63.1	1413	AAZ42901	Arabidopsis thalia
11	16.4	63.1	1830	AAAC84343	Wheat Nph2-2 prote

12	16.4	63.1	2120	22	AAAC84345	Wheat Nph2-2 cDNA
13	16.4	63.1	3096	22	AAF75864	Histidine protein k
14	16.4	63.1	3708	22	AAF75866	Histidine protein k
15	16.4	63.1	4679	22	AAF75865	Histidine protein k
16	16.4	63.1	5245	21	AACT75103	Human ORFX ORF658
17	16.4	63.1	6184	22	AAAC86935	Nucleotide sequenc
18	16.4	63.1	7669	21	AAZ52956	Xenorhabdus lumine
19	16	61.5	646	21	AACT38576	Arabidopsis thalia
20	16	61.5	44453	20	AAZ33519	Human kidney amino
21	15.6	60.0	801	20	AAZ32664	Cassava Cuzn super
22	15.6	60.0	1005	21	AAZ49769	Human ARF-Related
23	15.6	60.0	119950	20	AAZ90201	Human yes1 gene.
24	15.4	59.2	46	21	AAAC99364	Human serum albumi
25	15.4	59.2	46	21	AAAC99511	Human serum albumi
26	15.4	59.2	51	21	AAAC99371	Human serum albumi
27	15.4	59.2	51	21	AAAC99518	Human serum albumi
28	15.4	59.2	542	18	AAZ84047	DNA encoding a Sta
29	15.4	59.2	555	20	AAV89091	EST clone CD107.
30	15.4	59.2	563	21	AAA30907	Breast cancer DDPC
31	15.4	59.2	624	21	AAZ10147	Fusarium venenatum
32	15.4	59.2	648	21	AAAC00981	Human secreted pro
33	15.4	59.2	1029	17	AAZ30113	1-aminocyclopropan
34	15.4	59.2	1029	19	AAV09720	P. chloroaphis iso
35	15.4	59.2	1064	21	AACT6897	Human ORFX ORF2452
36	15.4	59.2	1411	22	AAZ32659	Human DNA encodin
37	15.4	59.2	1440	18	AAV74847	Staphylococcus aur
38	15.4	59.2	1758	13	AAO27462	Human serum albumi
39	15.4	59.2	1761	10	AAAC9097	Artificial gene co
40	15.4	59.2	1778	21	AAAC99458	Human serum albumi
41	15.4	59.2	1778	21	AAAC99310	Human serum albumi
42	15.4	59.2	1801	21	AAAC99310	Human serum albumi
43	15.4	59.2	1801	21	AAAC99457	Recombinant human
44	15.4	59.2	1849	21	AAAC99308	Recombinant human
45	15.4	59.2	1849	21	AAAC99455	Recombinant human

ALIGNMENTS

RESULT 1
AAV80100
ID AAV80100 standard; DNA; 26 BP.
XX AAV80100;
AC AAV80100;
DT 12-MAR-1999 (first entry)
DE Immunomodulatory oligo comprising an ISS sequence.
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; trypanosoma; Schistosoma.
XX Synthetic.
XX WO9855495-A2.
XX 10-DEC-1998.
XX 05-JUN-1998; 98WO-US11578.
XX 06-JUN-1997; 97US-0048793.
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX Dina D, Roman M, Schwartz D;
XX WPI; 1999-059898/05.
XX Immunostimulatory oligonucleotides regulate the immune system - and
XX contain an immune-stimulating octanucleotide sequence; for treating
XX cancer, allergic and infectious diseases

XX Claim 9; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise

XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent

XX specific claimed examples of such immunomodulatory oligonucleotides.

SQ Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgcttcgc 26

DB 1 tccataacgttcgcctaacgcttcgc 26

RESULT 2

AAA38069

ID AAA38069 standard; DNA; 26 BP.

XX

AC AAA38069;

XX

DT 24-AUG-2000 (first entry)

XX

DE Immunostimulatory sequence (ISS) #5:

XX

KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

KW gp120; human immunodeficiency virus; HIV; immune response; infection;

KW development; ss.

XX

OS Synthetic.

XX

PN WO200021556-A1.

XX

PD 20-APR-2000.

XX

PF 08-OCT-1999; 99WO-US23677.

XX

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX

XX WPI; 2000-317846/27.

XX

PT Anti-HIV composition comprises immunostimulatory polynucleotides and

PT HIV glycoprotein gp120 useful for modulating, stimulating an immune

PT response against HIV in an HIV infected individual.

XX

PS Disclosure; Page 16; 65pp; English.

XX

CC The present invention relates to an immunostimulatory composition

CC comprising a human immunodeficiency virus (HIV) antigen, and an

CC immunomodulatory polynucleotide comprising an immunostimulatory sequence

CC (ISS). This sequence represents an ISS that can be used in the

CC composition. An immunostimulatory composition which comprises a gp120

CC conjugated to an immunomodulatory polynucleotide, or is proximately

CC associated to it and not conjugated, is used for modulating or

CC stimulating a specific immune response against gp120 in an individual

CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

CC is also used for suppressing or delaying development of HIV infection in

CC an individual infected with HIV or an individual at risk of infection

CC with HIV, respectively. It is also used for treating an individual

CC infected with HIV in need of immune modulation.

XX

SQ Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgcttcgc 26

DB 1 tccataacgttcgcctaacgcttcgc 26

RESULT 3

AAAF77044

ID AA77044 standard; DNA; 26 BP.

XX

AC AA77044;

XX

DT 15-MAY-2001 (first entry)

XX

DE Immunostimulatory DNA #4.

XX

KW Modulate; immune; antigen; immunostimulatory; ds.

XX

OS Synthetic.

XX

PN WO200112223-A2.

XX

PD 22-FEB-2001.

XX

PF 18-AUG-2000; 2000WO-US22835.

XX

PR 19-AUG-1999; 99US-0149768.

XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX

PI Van Nest G;

XX

DR WPI; 2001-211136/21.

XX

PT Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen.

XX

PS Disclosure; Page 15; 63pp; English.

XX

CC The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX

SQ Sequence 26 BP; 5 A; 9 C; 4 G; 8 T; 0 other;

Query Match 100.0%; Score 26; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacgcttcgc 26

DB 1 tccataacgttcgcctaacgcttcgc 26

RESULT 4

AAV80115


```

ID  AAV80115 standard; DNA; 24 BP.
XX  AAV80115;
XX  12-MAR-1999 (first entry)
XX  Oligo used in experiments for stimulation of cytokine production.
XX  Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX  ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX  human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
XX  B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX  Synthetic.
XX  Key modified_base 8 Location/Qualifiers
XX  modified_base 8 /*tag= a
XX  modified_base 19 /*tag= "5-bromocytosine"
XX  modified_base 19 /*tag= b
XX  modified_base 19 /*tag= "5-bromocytosine"
XX  W09855495-A2.
XX  10-DEC-1998.
XX  05-JUN-1998; 98WO-US11578.
XX  06-JUN-1997; 97US-0048793.
XX  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX  Dina D, Roman M, Schwartz D;
XX  WPI; 1999-059898/05.
XX  Immunostimulatory oligonucleotides regulate the immune system - and
XX  contain an immune-stimulating octanucleotide sequence; for treating
XX  cancer, allergic and infectious diseases
XX  Example 2; Page 30; 63pp; English.
XX  The invention relates to immunomodulatory oligonucleotides that comprise
XX  at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX  sequences are selected from the group consisting of AACGTTC, AACGTTCG,
XX  GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
XX  patients needing immune regulation, such as those suffering from cancer,
XX  an allergic disease and asthma. They are also used to prevent infectious
XX  diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX  and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX  Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and
XX  schistosoma. The immunomodulatory sequences are used to screen for human
XX  immunostimulatory activity by incubating macrophage cells and the
XX  oligonucleotide; and determining the relative amount of Th1-biased
XX  cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
XX  oligonucleotides that were tested for immunostimulatory activity. These
XX  were used in experiments for the stimulation of cytokine production and
XX  were found to lack immunostimulatory activity. The invention provides
XX  specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX  Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 other;
XX  Query Match 92.3%; Score 24; DB 20; Length 24;
XX  Best Local Similarity 100.0%; Pred. No. 0.0056;
XX  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1 tccataacgttcgcctaacttcg 24
XX  Db 1 tccataacgttcgcctaacttcg 24
XX  RESULT 5
XX  AAV80116
XX  ID AAV80116 standard; DNA; 24 BP.
XX  AAV80115;
XX  12-MAR-1999 (first entry)
XX  Oligo used in experiments for stimulation of cytokine production.
XX  Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX  ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX  human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
XX  B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX  Synthetic.
XX  Key modified_base 8 Location/Qualifiers
XX  modified_base 8 /*tag= a
XX  modified_base 19 /*tag= "5-bromocytosine"
XX  modified_base 19 /*tag= b
XX  modified_base 19 /*tag= "5-bromocytosine"
XX  W09855495-A2.
XX  10-DEC-1998.
XX  05-JUN-1998; 98WO-US11578.
XX  06-JUN-1997; 97US-0048793.
XX  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX  Dina D, Roman M, Schwartz D;
XX  WPI; 1999-059898/05.
XX  Immunostimulatory oligonucleotides regulate the immune system - and
XX  contain an immune-stimulating octanucleotide sequence; for treating
XX  cancer, allergic and infectious diseases
XX  Example 2; Page 30; 63pp; English.
XX  The invention relates to immunomodulatory oligonucleotides that comprise
XX  at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX  sequences are selected from the group consisting of AACGTTC, AACGTTCG,
XX  GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
XX  patients needing immune regulation, such as those suffering from cancer,
XX  an allergic disease and asthma. They are also used to prevent infectious
XX  diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX  and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX  Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and
XX  schistosoma. The immunomodulatory sequences are used to screen for human
XX  immunostimulatory activity by incubating macrophage cells and the
XX  oligonucleotide; and determining the relative amount of Th1-biased
XX  cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
XX  oligonucleotides that were tested for immunostimulatory activity. These
XX  were used in experiments for the stimulation of cytokine production and
XX  were found to lack immunostimulatory activity. The invention provides
XX  specific claimed examples (AAV80096-103) of immunomodulatory sequences.
XX  Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 other;
XX  Query Match 92.3%; Score 24; DB 20; Length 24;
XX  Best Local Similarity 100.0%; Pred. No. 0.0056;
XX  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1 tccataacgttcgcctaacttcg 24
XX  Db 1 tccataacgttcgcctaacttcg 24
XX  RESULT 5
XX  AAV80116
XX  ID AAV80116 standard; DNA; 24 BP.

```

AAZ55885
 ID AAZ55885 standard; DNA; 24 BP.
 AC AAZ55885;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Immunomodulatory oligonucleotide SEQ ID NO: 10.
 XX
 KW Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunocontraception; 5-bromocytosine; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..24
 FT /*tag= a
 FT /*note= "Phosphorothioate linkages"
 FT 6..13
 FT /*tag= b
 FT /*note= "Immunostimulatory sequence (ISS) 1"
 FT modified_base 8
 FT /*tag= c
 FT /*mod_base= OTHER
 FT /*note= "5-bromocytosine"
 FT 17..24
 FT /*tag= d
 FT /*note= "Immunostimulatory sequence (ISS) 2"
 FT
 XX
 PN WO9962923-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-US12538.
 XX
 PR 05-JUN-1998; 98US-0088310.
 PR 01-JUN-1999; 99US-0324191.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA
 PI Schwartz D;
 XX
 DR WPI; 2000-105687/09.
 XX
 PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
 PT response, e.g. to tumor antigens
 XX
 PS Example 1; Page 35; 54pp; English.
 CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
 CC AACGTC, AACGTT, AGCGTC, AGCGT, AGCGT, GACGTC, GACGTT, GCGGTT,
 CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides
 CC comprising one or more ISSs, where the ISS comprises at least
 CC one modified cytosine with an electron-withdrawing moiety at
 CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
 CC contain ISSs comprising at least one bromocytosine, whereas sequence
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory
 CC oligonucleotides have an adjuvant-like effect; when formulated with an
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),
 CC while simultaneously downregulating the Th2-type response. The Th1
 CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX Sequence 24 BP; 5 A; 7 C; 4 G; 7 T; 1 other;

Query Match 88.5%; Score 23; DB 21; Length 24;
 Best Local Similarity 95.8%; Pred. No. 0.018;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tccataacgttcgctgaacgttcg 24
 ||||| ||||| ||||| |||||
 Db 1 tccataangttcgctgaacgttcg 24
 RESULT 7
 AAZ55886
 ID AAZ55886 standard; DNA; 24 BP.
 XX
 AC AAZ55886;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Immunomodulatory oligonucleotide SEQ ID NO: 11.
 XX
 KW Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunocontraception; 5-bromocytosine; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..24
 FT /*tag= a
 FT /*note= "Phosphorothioate linkages"
 FT 6..13
 FT /*tag= b
 FT /*note= "Immunostimulatory sequence (ISS) 1"
 FT modified_base 8
 FT /*tag= c
 FT /*mod_base= OTHER
 FT /*note= "5-bromocytosine"
 FT 17..24
 FT /*tag= d
 FT /*note= "Immunostimulatory sequence (ISS) 2"
 FT modified_base 19
 FT /*tag= e
 FT /*mod_base= OTHER
 FT /*note= "5-bromocytosine"
 FT
 XX
 PN WO9962923-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-US12538.
 XX
 PR 05-JUN-1998; 98US-0088310.
 PR 01-JUN-1999; 99US-0324191.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA
 PI Schwartz D;
 XX
 DR WPI; 2000-105687/09.
 XX
 PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
 PT response, e.g. to tumor antigens
 XX
 PS Example 1; Page 35; 54pp; English.
 CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
 CC AACGTC, AACGTT, AGCGTC, AGCGT, AGCGT, GACGTC, GACGTT, GCGGTT,
 CC AACGTTCC and GACGTTCC). The invention relates to oligonucleotides
 CC comprising one or more ISSs, where the ISS comprises at least
 CC one modified cytosine with an electron-withdrawing moiety at
 CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
 CC contain ISSs comprising at least one bromocytosine, whereas sequence
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory
 CC oligonucleotides have an adjuvant-like effect; when formulated with an
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),
 CC while simultaneously downregulating the Th2-type response. The Th1
 CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX Sequence 24 BP; 5 A; 7 C; 4 G; 7 T; 1 other;

CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
 CC contain ISSs comprising at least one bromocytosine, whereas sequence
 CC AAZ55876 contains an unmodified ISS. The immunomodulatory
 CC oligonucleotides have an adjuvant-like effect: when formulated with an
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),
 CC while simultaneously downregulating the Th2-type response. The Th1
 CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX Sequence 24 BP; 5 A; 6 C; 4 G; 7 T; 2 other;
 SQ

Query Match 84.6%; Score 22; DB 21; Length 24;
 Best Local Similarity 91.7%; Pred. No. 0.055;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcg 24
 ||||| ||||| ||||| ||||| |||||
 Db 1 tccataangttcgcctaaagtctg 24

RESULT 8
 AAC74251
 ID AAC74251 standard; cDNA; 1034 BP.
 XX AAC74251;
 AC
 XX
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human secreted protein gene 29 SEQ ID NO:39.
 XX
 XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW neuroprotective; antibacterial; virucide; fungicide; neoplasm;
 KW ophthalmological; autoimmune disease; rheumatoid arthritis; angiogenesis;
 KW hyperproliferative disorder; cardiovascular disorder; infection;
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;
 KW wound healing; chemotaxis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200056754-A1.
 PN
 XX
 PD 28-SEP-2000.
 XX
 XX 16-MAR-2000; 2000WO-US06792.
 PF
 XX
 PR 19-MAR-1999; 99US-0125362.
 XX
 PR 10-DEC-1999; 99US-0169980.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen GA, Ruben SM, Komatsoulis G;
 XX
 XX WPI; 2000-579483/54.
 DR
 DR P-PSDB; AAB39207.
 XX
 XX Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 PT
 XX
 XX Claim 1; Page 356-357; 434pp; English.
 PS
 XX The polynucleotide sequences given in AAC74223-C74279 encode the human
 CC secreted proteins represented in AAB39179-B39226. Sequences
 CC AAB39227-B39308 are alternative proteins encoded by the genes, and also
 CC protein sequences with which they share homology. The proteins have
 CC activities based on the tissues and cells in which they are expressed.

CC Examples of activities include: immunosuppressive; antiarthritic;
 CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 CC cerebroprotective; neuroprotective; antibacterial; virucide;
 CC fungicide; and ophthalmological. The human secreted proteins,
 CC polynucleotides, antagonists and agonists of the invention may be useful
 CC in the treatment, prevention, and/or diagnosis of various disease,
 CC disorders and conditions such as autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC regenerate tissues, maintain organs before transplantation, in
 CC chemotaxis and as a food additive or preservative e.g. to increase
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used
 CC during the isolation and characterisation of the genes of the invention.
 XX
 SQ Sequence 1034 BP; 325 A; 146 C; 171 G; 391 T; 1 other;

Query Match 63.1%; Score 16.4; DB 21; Length 1034;
 Best Local Similarity 76.9%; Pred. No. 45;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgctc 26
 ||||| ||||| ||||| ||||| |||||
 Db 636 tccattaagttgcgaacattgtgc 661

RESULT 9
 AAX13867/C
 ID AAX13867 standard; DNA; 1317 BP.
 XX AAX13867;
 AC
 XX
 XX 19-MAR-1999 (first entry)
 DT
 XX Enterococcus faecalis genome contig SEQ ID NO:930.
 DE
 XX Enterococcus faecalis; contig; detection; Enterococcal infection;
 KW vaccine; attenuation; computer readable medium; ds.
 KW
 XX Enterococcus faecalis.
 OS
 XX WO9850555-A2.
 PN
 XX
 PD 12-NOV-1998.
 XX
 XX 04-MAY-1998; 98WO-US08985.
 PF
 XX
 PR 14-NOV-1997; 97US-0066009.
 XX
 PR 06-MAY-1997; 97US-0044031.
 XX
 PR 16-MAY-1997; 97US-0046655.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Barash SC, Dillon PJ, Kunsch CA;
 XX
 XX WPI; 1999-045171/04.
 DR
 XX New isolated Enterococcus faecalis polynucleotides and polypeptides
 PT - used to develop products for the detection of Enterococcus and for
 PT use in vaccines for prevention or attenuation of Enterococcus
 PT infection.
 XX
 XX Claim 1; Page 2052-2053; 2084pp; English.
 PS
 XX A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
 CC AAX12938 to AAX13919 represent these nucleotide sequences which are
 CC primary nucleotide sequences, also known as contigs. The computer-based
 CC system can identify fragments of the Enterococcus faecalis genome with

CC commercial importance. The products can be used to detect the presence
 CC of Enterococcus faecalis in samples. They can also be used for
 CC diagnosing Enterococcal infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to
 CC modulate the growth or pathogenicity of Enterococcus faecalis, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an Enterococcal
 CC infection.

XX Sequence 1317 BP; 357 A; 314 C; 223 G; 422 T; 1 other;

Query Match 63.1%; Score 16.4; DB 20; Length 1317;

Best Local Similarity 76.9%; Pred. No. 46;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaactcgtcgc 26

||||| ||||| ||||| |||||

DB 623 TGCAGAACGTTGCTTAACCTACCTC 598

RESULT 10

AAC42901/c

ID AAC42901 standard; DNA; 1413 BP.

XX

AC AAC42901;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37283.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; terminator; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR

PR 05-MAR-1999; 99US-0123180.

PR

PR 09-MAR-1999; 99US-0123548.

PR

PR 23-MAR-1999; 99US-0125788.

PR

PR 25-MAR-1999; 99US-0126264.

PR

PR 29-MAR-1999; 99US-0126785.

PR

PR 01-APR-1999; 99US-0127462.

PR

PR 06-APR-1999; 99US-0128234.

PR

PR 08-APR-1999; 99US-0128714.

PR

PR 16-APR-1999; 99US-0129845.

PR

PR 19-APR-1999; 99US-0130077.

PR

PR 21-APR-1999; 99US-0130449.

PR

PR 23-APR-1999; 99US-0130510.

PR

PR 28-APR-1999; 99US-0130891.

PR

PR 28-APR-1999; 99US-0131449.

PR

PR 30-APR-1999; 99US-0132048.

PR

PR 30-APR-1999; 99US-0132407.

PR

PR 04-MAY-1999; 99US-0132484.

PR

PR 05-MAY-1999; 99US-0132485.

PR

PR 06-MAY-1999; 99US-0132486.

PR

PR 06-MAY-1999; 99US-0132487.

PR

PR 07-MAY-1999; 99US-0132863.

PR

PR 11-MAY-1999; 99US-0134256.

PR

PR 14-MAY-1999; 99US-0134218.

PR

PR 14-MAY-1999; 99US-0134219.

PR

PR 14-MAY-1999; 99US-0134221.

PR

PR 14-MAY-1999; 99US-0134370.

PR

PR 18-MAY-1999; 99US-0134768.

PR

PR 19-MAY-1999; 99US-0134941.

PR

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 63.1%; Score 16.4; DB 21; Length 1413;
Best Local Similarity 76.9%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaacttcgtc 26
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DB 536 TCCATAGCTTTCTCCTCAAGTTTGC 511

RESULT 11
AAC84343
ID AAC84343 standard; cDNA; 1830 BP.
XX
AC AAC84343;
XX
DT 19-MAR-2001 (first entry)
XX
DE Wheat Nph2-2 protein coding sequence.
XX
KW Acquired resistance gene; Nph1; Nph2; rice; Nph2-1; Nph2-2; wheat;
KW plant pathogen; transgenic; disease resistance; ss.
XX
OS Triticum aestivum.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1830
FT /*tag= a
XX
XX WO200070069-A1.
XX
PN 23-NOV-2000.
XX
PD
XX
PF 12-MAY-2000; 2000WO-US13307.
XX
XX
PR 13-MAY-1999; 99US-0133965.
XX
XX (MONS) MONSANTO CO.
XX
XX Bougri OV, Rommens CMT, Srivastava N, Swords KM;
PI
XX
XX WPI: 2001-01G244/P2.
DR P-PSDB: AAB48088.
XX
XX
PT New acquired resistance genes Nph1 from rice, Oryza sativa, and Nph2-1
PT and Nph2-2 from wheat, Triticum aestivum, useful for producing
PT transgenic plants with increased disease resistance
XX
XX Claim 4; Page 81-82; 101pp; English.
XX
XX The invention relates to acquired resistance genes Nph1 from rice, and
CC Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be
CC expressed by standard recombinant methodology. The Nph1 and Nph2
CC polynucleotides or polypeptides can be used to enhance acquired
CC resistance in plants (e.g. wheat or rice) to control plant pathogens e.g.
CC the genes can be introduced to make transgenic plants with increased
CC disease resistance. The polynucleotides are also useful to produce probes
CC and primers useful to detect the polynucleotides (to identify transgenic
CC plants containing an acquired resistance gene) and to isolate similar
CC sequences e.g. from other species. The polypeptides can be used to make
CC antibodies useful to monitor protein production e.g. in transgenic
CC plants. The present sequence represents the coding sequence of the wheat
CC Nph2-2 gene.
XX
XX Sequence 1830 BP; 433 A; 481 C; 519 G; 397 T; 0 other;

Query Match 63.1%; Score 16.4; DB 22; Length 1830;

Best Local Similarity 76.9%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgtc 26
||||| ||||| ||||| |||||
DB 16 tccataacgttcgcctcctcgtcgtc 41

RESULT 12

AAC84345
ID AAC84345 standard; cDNA; 2120 BP.

XX AC
XX AAC84345;

DT 19-MAR-2001 (first entry)

XX Wheat Nph2-2 cDNA sequence.

DE Acquired resistance gene; Nph1; Nph2; rice; Nph2-2; wheat;
KW plant pathogen; transgenic; disease resistance; ss.

XX OS Triticum aestivum.

XX FH Key Location/Qualifiers
FT CDS 157..1986
FT /*tag= a
FT /*note= "the coding sequence (AAC84343) is specifically
FT. claimed for in claim 4"

XX WO200070069-A1.

XX 23-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US13307.

XX PR 13-MAY-1999; 99US-0133965.

XX PA (MONS) MONSANTO CO.

XX PI Bougri OV, Rommens CMT, Srivastava N, Swords KM;

XX WPI; 2001-016244/02.

XX P-PSDB; AAB48088.

XX PT New acquired resistance genes Nph1 from rice, Oryza sativa, and Nph2-1
PT and Nph2-2 from wheat, Triticum aestivum, useful for producing
PT transgenic plants with increased disease resistance

XX PS Claim 17; Page 83; 101pp; English.

XX CC The invention relates to acquired resistance genes Nph1 from rice, and
CC Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be
CC expressed by standard recombinant methodology. The Nph1 and Nph2
CC polynucleotides or polypeptides can be used to enhance acquired
CC resistance in plants (e.g. wheat or rice) to control plant pathogens e.g.
CC the genes can be introduced to make transgenic plants with increased
CC disease resistance. The polynucleotides are also useful to produce probes
CC and primers useful to detect the polynucleotides (to identify transgenic
CC plants containing an acquired resistance gene) and to isolate similar
CC sequences e.g. from other species. The polypeptides can be used to make
CC antibodies useful to monitor protein production e.g. in transgenic
CC plants. The present sequence represents the cDNA sequence of the wheat
CC Nph2-2 gene.

XX SQ Sequence 2120 BP; 497 A; 559 C; 606 G; 458 T; 0 other;

Query Match

Best Local Similarity 63.1%; Score 16.4; DB 22; Length 2120;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgtc 26
||||| ||||| ||||| |||||

DB 172 tccataacgttcgcctcctcgtcgtc 197

RESULT 13

AAF75864/c

ID AAF75864 standard; cDNA; 3096 BP.

XX AC
XX AAF75864;

DT 18-MAY-2001 (first entry)

XX Histidine protein kinase coding sequence #1.

XX KW Histidine protein kinase; signal transduction; cytokinin; plant breeding;
KW plant flowering; plant aging prevention; side root elongation; ss.

XX OS Arabidopsis thaliana.

XX PN WO200116332-A1.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-JP05772.

XX PR 26-AUG-1999; 99JP-0240433.

XX PA (SUNR) SUNTORY LTD.

XX PA (SAOK) NIPPON PAPER IND CO LTD.

XX PI Kakimoto T;

XX WPI; 2001-235110/24.

XX P-PSDB; AAB73274.

XX PT New Arabidopsis thaliana gene encoding a protein participating in
PT signal transduction of cytokinin, for use in plant breeding with
PT regulation of regeneration, differentiation and growth

XX PS Claim 3; Page 34-41; 78pp; Japanese.

XX CC The present sequence is a coding sequence for histidine protein kinase
CC from Arabidopsis thaliana. Histidine protein kinase participates in the
CC signal transduction of cytokinin. Histidine protein kinase is useful in
CC plant breeding, in regulating growth of a plant or plant cell and
CC regulating the flowering period of a plant or plant cell. Using histidine
CC protein kinase, it is possible to provide the regulation of regeneration,
CC differentiation and growth, thereby controlling physiological functions
CC like elongation of side roots, prevention of aging, flowering period,
CC promoting increase of fruit size and prevention of fruit dropping.

XX SQ Sequence 3096 BP; 1001 A; 522 C; 760 G; 813 T; 0 other;

Query Match 63.1%; Score 16.4; DB 22; Length 3096;
Best Local Similarity 76.9%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 tccataacgttcgcctaaacgttcgtc 26
||||| ||||| ||||| |||||

DB 2888 TCACATACATTTGCATACATTCCTC 2863

RESULT 14

AAF75866/c

ID AAF75866 standard; DNA; 3708 BP.

XX AC
XX AAF75866;

DT 18-MAY-2001 (first entry)

XX DE Histidine protein kinase coding sequence #3.

XX KW Histidine protein kinase; signal transduction; cytokinin; plant breeding;

```
KW plant flowering; plant aging prevention; side root elongation; ds.
XX Arabidopsis thaliana.
XX WO200116332-A1.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-JP05772.
XX 26-AUG-1999; 99JP-0240433.
XX (SUNR ) SUNTORY LTD.
XX (SAOK ) NIPPON PAPER IND CO LTD.
XX Kakimoto T;
XX WPI: 2001-235110/24.
XX P-PSDB; AAB73275.
XX New Arabidopsis thaliana gene encoding a protein participating in
PT signal transduction of cytokinin, for use in plant breeding with
PT regulation of regeneration, differentiation and growth
XX Example 2; Page 60-68; 78pp; Japanese.
XX The present sequence is a coding sequence for histidine protein kinase
CC from Arabidopsis thaliana. Histidine protein kinase participates in the
CC signal transduction of cytokinin. Histidine protein kinase is useful in
CC plant breeding, in regulating growth of a plant or plant cell and
CC regulating the flowering period of a plant or plant cell. Using histidine
CC protein kinase, it is possible to provide the regulation of regeneration,
CC differentiation and growth, thereby controlling physiological functions
CC like elongation of side roots, prevention of aging, flowering period,
CC promoting increase of fruit size and prevention of fruit dropping.
XX Sequence 3708 BP; 1170 A; 612 C; 854 G; 1072 T; 0 other;
SQ
Query Match 63.1%; Score 16.4; DB 22; Length 3708;
Best Local Similarity 76.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 tccataacgttcgcctaacgcttcgc 26
Db 3641 TCCATACCATTGTCATAACATTCTTC 3616
RESULT 15
AAF75865/c
ID AAF75865 standard; DNA; 4679 BP.
XX
AC AAF75865;
XX
DT 18-MAY-2001 (first entry)
XX
DE Histidine protein kinase coding sequence #2.
XX
KW Histidine protein kinase; signal transduction; cytokinin; plant breeding;
KW plant flowering; plant aging prevention; side root elongation; ds.
XX
OS Arabidopsis thaliana.
XX WO200116332-A1.
XX
PN 08-MAR-2001.
PD
XX 25-AUG-2000; 2000WO-JP05772.
XX
XX 26-AUG-1999; 99JP-0240433.
XX
XX (SUNR ) SUNTORY LTD.
XX (SAOK ) NIPPON PAPER IND CO LTD.
PA
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```
XX Kakimoto T;
XX WPI: 2001-235110/24.
XX P-PSDB; AAB73275.
XX New Arabidopsis thaliana gene encoding a protein participating in
PT signal transduction of cytokinin, for use in plant breeding with
PT regulation of regeneration, differentiation and growth
XX Example 2; Page 46-54; 78pp; Japanese.
XX The present sequence is a coding sequence for histidine protein kinase
CC from Arabidopsis thaliana. Histidine protein kinase participates in the
CC signal transduction of cytokinin. Histidine protein kinase is useful in
CC plant breeding, in regulating growth of a plant or plant cell and
CC regulating the flowering period of a plant or plant cell. Using histidine
CC protein kinase, it is possible to provide the regulation of regeneration,
CC differentiation and growth, thereby controlling physiological functions
CC like elongation of side roots, prevention of aging, flowering period,
CC promoting increase of fruit size and prevention of fruit dropping.
XX Sequence 4679 BP; 1416 A; 811 C; 999 G; 1453 T; 0 other;
SQ
Query Match 63.1%; Score 16.4; DB 22; Length 4679;
Best Local Similarity 76.9%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 tccataacgttcgcctaacgcttcgc 26
Db 4612 TCCATACCATTGTCATAACATTCTTC 4587
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model
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(without alignments)
37.177 Million cell updates/sec

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Perfect score: 26
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 7388405095 residues
Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0
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59:	/cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
60:	/cgn2_6/ptodata/1/pna/US6028_COMB.seq.*

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	100.0	26	16	US-09-296-477-7 Sequence 7, Appl
2	26	100.0	26	18	US-09-415-186-5 Sequence 5, Appl
3	26	100.0	26	25	US-09-642-492-5 Sequence 5, Appl
4	26	100.0	26	28	US-09-713-136-5 Sequence 20, Appl
5	23	88.5	24	16	US-09-296-477-20 Sequence 21, Appl
6	23	88.5	24	16	US-09-296-477-21 Sequence 10, Appl
7	23	88.5	24	17	US-09-324-191A-10 Sequence 11, Appl
8	22	84.6	24	17	US-09-324-191A-11 Sequence 21974, A
9	18.8	72.3	324	18	US-09-417-507-21974 Sequence 69495, A
10	18.6	71.5	25	55	US-60-234-049-69495 Sequence 126, App
11	18.2	70.0	40400	48	US-60-161-932-126 Sequence 188, App
12	18.2	70.0	267904	19	US-09-528-237A-818 Sequence 168972, Sequence 168972,
13	18	69.2	366	25	US-09-654-617-168972 Sequence 168112, Sequence 168112,
14	18	69.2	366	27	US-09-684-016-168112 Sequence 168112, Sequence 168112,
15	18	69.2	383	25	US-09-654-617-168112 Sequence 130014, Sequence 130014,
16	18	69.2	383	27	US-09-684-016-168112 Sequence 130014, Sequence 130014,
17	18	69.2	385	25	US-09-654-617-130014 Sequence 3800, Ap
18	18	69.2	385	27	US-09-684-016-130014 Sequence 15844, A
19	18	69.2	624	18	US-09-489-039A-3800 Sequence 20511, A
20	18	69.2	7803	48	US-60-167-217-15844 Sequence 19701, A
21	18	69.2	29553	49	US-60-173-464-20558 Sequence 631, App
22	18	69.2	29555	51	US-60-191-637-25011 Sequence 1269, Ap
23	18	69.2	29555	51	US-60-191-681-19701 Sequence 36319, A
24	18	69.2	80677	20	US-09-534-859-631 Sequence 99316, A
25	18	69.2	219666	19	US-09-528-237A-1269 Sequence 226531, Sequence 226531,
26	17.2	66.2	298	19	US-09-521-640-36319 Sequence 139795, Sequence 139795,
27	17.2	66.2	318	19	US-09-521-640-99316 Sequence 172477, Sequence 172477,
28	17.2	66.2	333	19	US-09-521-640-226531 Sequence 159397, Sequence 159397,
29	17.2	66.2	344	19	US-09-521-640-139795 Sequence 3782, Ap
30	17.2	66.2	379	19	US-09-521-640-172477 Sequence 125779, Sequence 125779,
31	17.2	66.2	382	19	US-09-521-640-159397 Sequence 99173, A
32	17.2	66.2	382	46	US-60-140-769-3782 Sequence 218971, A
33	17.2	66.2	401	19	US-09-521-640-99173 Sequence 154536, Sequence 154536,
34	17.2	66.2	405	19	US-09-521-640-218971 Sequence 864041, A
35	17.2	66.2	434	19	US-09-521-640-154536 Sequence 49827, A
36	17.2	66.2	441	19	US-09-521-640-65052 Sequence 171560, Sequence 171560,
37	17.2	66.2	452	19	US-09-521-640-264041 Sequence 7866, Ap
38	17.2	66.2	453	19	US-09-521-640-49827 Sequence 5539, Ap
39	17.2	66.2	453	46	US-60-140-769-49827 Sequence 152076, Ap
40	17.2	66.2	469	19	US-09-521-640-171560 Sequence 24842, A
41	17.2	66.2	469	46	US-60-140-769-7866 Sequence 4812, Ap
42	17.2	66.2	472	19	US-09-521-640-5539 Sequence 152076, Ap
43	17.2	66.2	474	16	US-09-270-849B-152076 Sequence 24842, A
44	17.2	66.2	583	19	US-09-521-640-24842 Sequence 4812, Ap
45	17.2	66.2	1473	16	US-09-252-991A-4812

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Qy 1 tccataacggttcgcctaacggttcgtc 26

; Sequence 20, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)...(8)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-20

Query Match 88.5%; Score 23; DB 16; Length 24;
Best Local Similarity 95.8%; Pred. No. 0.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24
||||| ||||||| |||||||
DB 1 tcataaangttgcctaacgttcg 24

RESULT 6
US-09-296-477-21
; Sequence 21, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; COMPOSITIONS THEREOF AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)...(8)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-21

Query Match 88.5%; Score 23; DB 16; Length 24;
Best Local Similarity 95.8%; Pred. No. 0.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24
||||| ||||||| |||||||
DB 1 tcataaangttgcctaacgttcg 24

RESULT 7
US-09-324-191A-10
; Sequence 10, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 377882000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/088,310
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct
; NAME/KEY: modified_base
; LOCATION: (8)...(8)
; OTHER INFORMATION: 5-bromocytosine
US-09-324-191A-10

Query Match 88.5%; Score 23; DB 17; Length 24;
Best Local Similarity 95.8%; Pred. No. 0.2;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcataacgttcgcctaacgttcg 24
||||| ||||||| |||||||
DB 1 tcataaangttgcctaacgttcg 24

RESULT 8
US-09-324-191A-11
; Sequence 11, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 377882000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/088,310
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct
; NAME/KEY: modified_base
; LOCATION: (8)...(8)
; OTHER INFORMATION: 5-bromocytosine
; NAME/KEY: modified_base
; LOCATION: (19)...(19)
; OTHER INFORMATION: 5-bromocytosine
US-09-324-191A-11

```
Query Match      84.6%; Score 22; DB 17; Length 24;
Best Local Similarity 91.7%; Pred. No. 0.65;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcg 24
    ||||| ||||| ||||| |||||
Db 1 tccataaangttcgctaangttcg 24

RESULT 9
US-09-417-507-21974/c
; Sequence 21974, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417.507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 21974
; LENGTH: 324
; TYPE: DNA
; ORGANISM: A.fumigatus
US-09-417-507-21974

Query Match      72.3%; Score 18.8; DB 18; Length 324;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ataacgttcgcctaacgttcg 25
    ||||| ||||| ||||| |||||
Db 116 ATAACGTTCCGCTGACGTTCT 95

RESULT 10
US-60-234-049-69495
; Sequence 69495, Application US/60234049
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; FILE REFERENCE: 3117
; CURRENT APPLICATION NUMBER: US/60/234.049
; CURRENT FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Eschericia coli
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-69495

Query Match      71.5%; Score 18.6; DB 55; Length 25;
Best Local Similarity 84.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcg 25
    ||||| ||||| ||||| |||||
Db 1 tccataacgttcgcctaacgttcg 25

RESULT 11
US-60-161-932-126
; Sequence 126, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
```

```
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161.932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 40400
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-126

Query Match      70.0%; Score 18.2; DB 48; Length 40400;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 cataacgttcgcctaacgttcg 25
    ||||| ||||| ||||| |||||
Db 36169 catacgttcgcgaaagtctg 36191

RESULT 12
US-09-528-237A-818/c
; Sequence 818, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528.237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 818
; LENGTH: 267904
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-818

Query Match      70.0%; Score 18.2; DB 19; Length 267904;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 cataacgttcgcctaacgttcg 25
    ||||| ||||| ||||| |||||
Db 231735 CATACGTTCCGCGAAAGTTCGT 231713

RESULT 13
US-09-654-617-168972/c
; Sequence 168972, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654.617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 168972
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana nossen
US-09-654-617-168972

Query Match      69.2%; Score 18; DB 25; Length 366;
Best Local Similarity 80.8%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

Wed Oct 10 05:59:12 2001

QY 1 tccataacgcttcgcctaacgcttcgctc 26
||| ||| ||| ||| ||| ||| ||| |||
Db 172 TCAAAACTTTCTCCTAACGTTCTC 147

RESULT 14
US-09-684-016-168972/c
; Sequence 168972, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 168972
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana nossen
US-09-684-016-168972

Query Match 69.2%; Score 18; DB 27; Length 366;
Best Local Similarity 80.8%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgcttcgcctaacgcttcgctc 26
||| ||| ||| ||| ||| ||| ||| |||
Db 172 TCAAAACTTTCTCCTAACGTTCTC 147

RESULT 15
US-09-654-617-168112/c
; Sequence 168112, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 168112
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana nossen
US-09-654-617-168112

Query Match 69.2%; Score 18; DB 25; Length 383;
Best Local Similarity 80.8%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 tccataacgcttcgcctaacgcttcgctc 26
||| ||| ||| ||| ||| ||| ||| |||
Db 171 TCAAAACTTTCTCCTAACGTTCTC 146

Search completed: October 9, 2001, 21:12:47
Job time: 20072 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:14 ; Search time 1391.6 seconds
(without alignments)
42.642 Million cell updates/sec

Title: US-09-713-136-5

Perfect score: 26

Sequence: 1 tccataacgttcgcctaacgttcgtc 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 204985 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2.6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2.6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2.6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 7: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 8: /cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	7 US-09-802-518-5	Sequence 5, Appli
2	26	100.0	26	7 US-09-802-359-5	Sequence 5, Appli
3	26	100.0	26	7 US-09-802-376-5	Sequence 5, Appli
4	18	69.2	80677	6 US-09-803-736-631	Sequence 631, App
5	16.6	63.8	424	7 US-09-692-257A-3964	Sequence 3964, Ap
6	16.6	63.8	42459	6 US-09-803-736-361	Sequence 361, App
7	16.6	63.8	96066	6 US-09-803-736-360	Sequence 360, App
8	16.4	63.1	194	1 PCT-US01-08631-4195	Sequence 4195, Ap
9	16.4	63.1	424	6 US-09-904-703-5632	Sequence 5632, Ap
10	16.4	63.1	424	7 US-09-840-145-6383	Sequence 6383, Ap
11	16.4	63.1	462	6 US-09-804-730-13181	Sequence 13181, A
12	16.4	63.1	541	7 US-09-823-327-2465	Sequence 2465, Ap
13	16.4	63.1	669	7 US-09-764-905-6468	Sequence 6468, Ap
14	16.4	63.1	1290	1 PCT-US01-08631-5184	Sequence 5184, Ap
15	16.4	63.1	1290	1 PCT-US01-08631-5184	Sequence 5184, Ap
16	16.4	63.1	1953	1 PCT-US01-08631-28832	Sequence 28832, A
17	16.4	63.1	2659	1 PCT-US01-08631-28643	Sequence 28643, A
18	16.4	63.1	3421	6 US-09-836-472-1284	Sequence 1284, Ap
19	16.4	63.1	5274	8 US-60-278-232-7126	Sequence 7126, Ap
20	16.4	63.1	14212	7 US-09-764-905-34504	Sequence 34504, A
21	16.4	63.1	14212	7 US-09-764-905-34836	Sequence 34836, A
22	16.4	63.1	14212	7 US-09-764-905-40733	Sequence 40733, A
23	16.4	63.1	42694	6 US-09-803-736-1418	Sequence 1418, Ap
24	16.4	63.1	86424	6 US-09-803-736-1	Sequence 1, Appli
25	16.4	63.1	99123	6 US-09-803-736-740	Sequence 740, App

C 26	16.4	63.1	104386	6	US-09-803-736-1385	Sequence 1385, Ap
C 27	16.4	63.1	118718	6	US-09-803-736-579	Sequence 579, App
C 28	16.2	62.3	1206	6	US-09-738-626-1966	Sequence 1966, Ap
C 29	16.2	62.3	91825	6	US-09-803-736-1142	Sequence 1142, Ap
C 30	16	61.5	244	7	US-09-440-305A-7	Sequence 7, Appli
C 31	16	61.5	368	7	US-09-783-590-740	Sequence 740, App
C 32	16	61.5	1899	7	US-09-902-540-4427	Sequence 4427, Ap
C 33	16	61.5	2865	1	PCT-US01-08631-15928	Sequence 15928, A
C 34	16	61.5	2865	1	PCT-US01-08631-15941	Sequence 15941, A
C 35	16	61.5	2865	1	PCT-US01-08631-28923	Sequence 28923, A
C 36	16	61.5	2865	1	PCT-US01-08631-30323	Sequence 30323, A
C 37	16	61.5	3672	1	PCT-US01-08631-25889	Sequence 25889, A
C 38	16	61.5	22761	7	US-09-902-540-1219	Sequence 1219, Ap
C 39	16	61.5	93695	6	US-09-803-736-640	Sequence 640, App
C 40	16	61.5	205065	6	US-09-803-736-584	Sequence 584, App
C 41	16	61.5	206420	6	US-09-803-736-678	Sequence 678, App
C 42	15.8	60.8	75475	6	US-09-803-736-692	Sequence 692, App
C 43	15.8	60.8	96936	6	US-09-803-736-1402	Sequence 1402, Ap
C 44	15.6	60.0	126	6	US-09-504-576A-1871	Sequence 1871, Ap
C 45	15.6	60.0	445	7	US-09-813-155-10330	Sequence 10330, A

ALIGNMENTS

RESULT 1
US-09-802-518-5
; Sequence 5, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-5

Query Match 100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgtc 26
|||||
Db 1 tccataacgttcgcctaacgttcgtc 26

RESULT 2
US-09-802-359-5
; Sequence 5, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5

; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-5

Query Match 100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tccataacgttcgcctaacgttcgc 26
|||||
Db 1 tccataacgttcgcctaacgttcgc 26

RESULT 3
US-09-802-376-5
; Sequence 5, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802.376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-5

Query Match 100.0%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
|||||
Db 1 tccataacgttcgcctaacgttcgc 26

RESULT 4
US-09-803-736-631
; Sequence 631, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803.736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 631
; LENGTH: 80677
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-631

Query Match 69.2%; Score 18; DB 6; Length 80677;
Best Local Similarity 80.8%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
|||||
Db 56083 tcaaaactttctcctaacgttcgc 56108

RESULT 5
US-09-692-257A-3964/c
; Sequence 3964, Application US/09692257A
; GENERAL INFORMATION:
; APPLICANT: Miller, Philip W.
; APPLICANT: Peng, Ming
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15771)B
; CURRENT APPLICATION NUMBER: US/09/692.257A
; CURRENT FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/162,747
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 14882
; SEQ ID NO 3964
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-001-Pl-K1-A4
US-09-692-257A-3964

Query Match 63.8%; Score 16.6; DB 7; Length 424;
Best Local Similarity 82.6%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ccataacgttcgcctaacgttcgc 24
|||||
Db 51 CCATCTCGATCGCCTACGATCG 29

RESULT 6
US-09-803-736-361
; Sequence 361, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803.736
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 361
; LENGTH: 42499
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-361

Query Match 63.8%; Score 16.6; DB 6; Length 42499;
Best Local Similarity 82.6%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 tccataacgttcgcctaacgttc 23
|||||

Db 67 TCGTTAAAGCGCGCCCAACGTTTCGTC 42

Db 67 TCGTTAAAGCGCGCCCCAACGTTCTC 42

```

; NAME/KEY: MISC_record
; LOCATION: (417)
; OTHER INFORMATION: n equals a.t.g.

```

```

; NAME/REL: misc_feature
; LOCATION: (417)
; OTHER INFORMATION: n equals a t g. or c

```

Query Match 63.1%; Score 16.4; DB 7; Length 424;
Best Local Similarity 76.9%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctgc 26
||||| ||| ||| ||| ||| ||| |||
Db 74 tccattaagtgttgcacaaacattgtc 99

RESULT 11
US-09-804-730-13181/c
; Sequence 13181, Application US/09804730
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Hammond-Kosack, Kim
; APPLICANT: Masucci, James D.
; APPLICANT: Urban, Martin
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51838)B
; CURRENT APPLICATION NUMBER: US/09/804,730
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,657
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 22828
; SEQ ID NO 13181
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(462)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3399-002-PI-K1-C8
US-09-804-730-13181

Query Match 63.1%; Score 16.4; DB 6; Length 462;
Best Local Similarity 76.9%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctgc 26
||||| ||| ||| ||| ||| ||| |||
Db 172 TTCATAACCTTCTCCAACTGTCGTC 147

RESULT 12
US-09-823-327-2465
; Sequence 2465, Application US/09823327
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: MacBeth, Kyle J.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2083-001
; CURRENT APPLICATION NUMBER: US/09/823,327
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,433
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9746
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2465
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(541)
; OTHER INFORMATION: n = A,T,C or G
US-09-823-327-2465

Query Match 63.1%; Score 16.4; DB 7; Length 541;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 tccataacgttcgcctaactgctgc 26
||||| ||| ||| ||| ||| ||| |||
Db 330 tccattaagtgttgcacaaacattgtc 355

RESULT 13
US-09-764-905-6468
; Sequence 6468, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004
; CURRENT APPLICATION NUMBER: US/09/764,905
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29

;; PRIOR APPLICATION NUMBER: 60/241,785
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/244,617
;; PRIOR FILING DATE: 2000-11-01
;; PRIOR APPLICATION NUMBER: 60/225,268
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/236,368
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/251,856
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/251,868
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/229,344
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/234,997
;; PRIOR FILING DATE: 2000-09-25
;; PRIOR APPLICATION NUMBER: 60/229,343
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/229,345
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/229,287
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/229,513
;; PRIOR FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/231,413
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/229,509
;; PRIOR FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/236,367
;; PRIOR FILING DATE: 2000-09-29
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;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/237,038
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/236,370
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/236,802
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/237,037
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/237,040
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/240,960
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/239,935
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/239,937
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/241,787
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,474
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/246,532
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/249,216
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,210
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/226,681
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 60/225,759
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/225,213
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/227,182
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 60/225,214
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/235,836
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: 60/230,438
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/215,135

;; PRIOR FILING DATE: 2000-06-30
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;; PRIOR APPLICATION NUMBER: 60/249,218
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,208
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,213
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,244
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;; PRIOR APPLICATION NUMBER: 60/249,217
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,264
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,214
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/232,400
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,081
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,080
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,414
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,244
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,064
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 63.1%; Score 16.4; DB 7; Length 669;
Best Local Similarity 76.9%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Caps 0;
QY 1 tccataacgttcgcctaacttcgtc 26
||||||| | ||||| ||| ||

Search completed: October 9, 2001, 21:36:22
Job time: 21242 sec

Db 206 tccataacataactcctaatttcctc 231

RESULT 14
PCT-US01-08631-5184/C
; Sequence 5184, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 5184
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (817)..(1287)
; OTHER INFORMATION: 96% homologous to Escherichia coli No definition line
; OTHER INFORMATION: found,accession number U00039,Smith-Waterman Score=805.
PCT-US01-08631-5184

Query Match 63.1%; Score 16.4; DB 1; Length 1290;
Best Local Similarity 76.9%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 tccataacgttcgcctaactcgtc 26
|| ||| | ||| ||||| |||||
Db 740 TCGTTAAAGCGCGCCCAACGTTGTC 715

RESULT 15
PCT-US01-08631-25681
; Sequence 25681, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 25681
; LENGTH: 1290
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (474)..(4)
; OTHER INFORMATION: 96% homologous to Escherichia coli No definition line
; OTHER INFORMATION: found,accession number U00039,Smith-Waterman Score=805.
PCT-US01-08631-25681

Query Match 63.1%; Score 16.4; DB 1; Length 1290;
Best Local Similarity 76.9%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 tccataacgttcgcctaactcgtc 26
|| ||| | ||| ||||| |||||
Db 551 tcgtfaaagcgcgcccaacgctc 576

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:03 ; Search time 217.64 seconds
(without alignments)
22.616 Million cell updates/sec

Title: US-09-713-136-5
Perfect score: 26
Sequence: 1 tcataacgttcgctaaccgttcgctc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.6	60.0	801	3	US-09-291-562-1
C 2	15.6	60.0	1005	3	US-09-103-359-4
C 3	15.4	59.2	1029	1	US-07-809-457A-15
C 4	15.4	59.2	1029	1	US-08-553-943-15
C 5	15.4	59.2	1029	5	PCT-US91-09437-15
C 6	15.4	59.2	1758	5	PCT-US92-01015-1
C 7	15	57.7	3027	2	US-09-132-619-9
C 8	15	57.7	3027	3	US-09-282-803B-9
C 9	15	57.7	26700	1	US-08-472-217-1
C 10	15	57.7	26700	2	US-08-488-199-5
C 11	15	57.7	26700	3	US-08-760-534A-1
C 12	14.8	56.9	1587	3	US-08-680-506-6
C 13	14.8	56.9	2210	1	US-07-710-361-2
C 14	14.8	56.9	2400	1	US-08-967-513-1
C 15	14.8	56.9	2400	2	US-08-687-645B-1
C 16	14.8	56.9	4781	2	US-09-001-273-1
C 17	14.8	56.9	4781	4	US-08-843-459A-1
C 18	14.8	56.9	4847	3	US-09-061-400-1
C 19	14.6	56.2	538	4	US-08-998-416-649
C 20	14.6	56.2	1040	3	US-08-682-643-2
C 21	14.6	56.2	1934	1	US-07-941-651-1
C 22	14.6	56.2	1934	1	US-08-279-996-1
C 23	14.6	56.2	3635	1	US-08-252-626A-1
C 24	14.4	55.4	1020	3	US-09-146-675-1
C 25	14.4	55.4	1149	2	US-08-844-305-1
C 26	14.4	55.4	1650	2	US-09-001-826-24
C 27	14.4	55.4	2468	1	US-07-779-049-2

C 28	14.4	55.4	2468	1	US-08-080-240-2	Sequence 2, Appli
C 29	14.4	55.4	2809	3	US-08-448-194-5	Sequence 5, Appli
C 30	14.4	55.4	3536	3	US-09-418-640-3	Sequence 3, Appli
C 31	14.4	55.4	3720	1	US-08-074-967-1	Sequence 1, Appli
C 32	14.4	55.4	3720	2	US-08-553-541B-1	Sequence 1, Appli
C 33	14.4	55.4	3720	4	US-09-268-202-1	Sequence 1, Appli
C 34	14.4	55.4	3720	5	PCT-US94-06669-1	Sequence 1, Appli
C 35	14.4	55.4	21126	1	US-08-008-216-19	Sequence 19, Appli
C 36	14.4	55.4	21126	1	US-08-459-569-19	Sequence 19, Appli
C 37	14.4	55.4	21126	1	US-08-458-831-19	Sequence 19, Appli
C 38	14.2	54.6	648	4	US-08-998-416-1064	Sequence 1064, Ap
C 39	14.2	54.6	807	1	US-07-706-691G-53	Sequence 53, Appl
C 40	14.2	54.6	807	1	US-07-706-691G-54	Sequence 54, Appl
C 41	14.2	54.6	807	1	US-07-706-691G-55	Sequence 55, Appl
C 42	14.2	54.6	807	1	US-07-706-691G-56	Sequence 56, Appl
C 43	14.2	54.6	807	1	US-07-706-691G-57	Sequence 57, Appl
C 44	14.2	54.6	807	1	US-07-706-691G-58	Sequence 58, Appl
C 45	14.2	54.6	807	1	US-07-706-691G-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-291-562-1/c
; Sequence 1, Application US/09291562
; Patent No. 6084152
; GENERAL INFORMATION:
; APPLICANT: Sang Soo Kwak
; APPLICANT: Jae-Whune Kim
; APPLICANT: Haeng-Soon Lee
; APPLICANT: Suk Yoon Kwon
; TITLE OF INVENTION: METHOD FOR PRODUCING TRANSGENIC CUCUMBER
; FILE REFERENCE: 118.1-US-01
; CURRENT APPLICATION NUMBER: US/09/291.562
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: KS 98 13205
; EARLIER FILING DATE: 1998-04-14
; EARLIER APPLICATION NUMBER: KS 98 33947
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: KS 99 11848
; EARLIER FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Manihot esculenta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)...(510)
; NAME/KEY: polyA_site
; LOCATION: (781)...(801)
; NAME/KEY: polyA_signal
; LOCATION: (611)...(616)
US-09-291-562-1

Query Match 60.0%; Score 15.6; DB 3; Length 801;
Best Local Similarity 81.8%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 taacgttcgcttaaccgttcgctc 26
|||||
Db 601 TAATGGTCTCTTACAGTTCTTC 580

RESULT 2
US-09-103-359-4/c
; Sequence 4, Application US/09103359
; Patent No. 6057108
; GENERAL INFORMATION:

US-09-132-619-9
; Sequence 9, Application US/09132619B

Patent No. 5958697
GENERAL INFORMATION:
APPLICANT: Shan, Bei
TITLE OF INVENTION: CYP7 Promoter-Binding Factors
FILE REFERENCE: T97-013
CURRENT APPLICATION NUMBER: US/09/132.619B
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 60/067.708
EARLIER FILING DATE: 1997-12-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 3027
TYPE: DNA
ORGANISM: human
FEATURE:
NAME/KEY: CDS
LOCATION: (159)..(1838)
US-09-132-619-9

Query Match 57.7%; Score 15; DB 2; Length 3027;
Best Local Similarity 78.3%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 ccataacggttcgcctaacggttcg 24
||||| ||| ||| ||| ||| ||| |||
Db 509 ccattacggttcctcctcaagtcgcg 531

RESULT 8
US-09-282-803B-9
Sequence 9, Application US/09282803B
Patent No. 6027901
GENERAL INFORMATION:
APPLICANT: Shan, Bei
APPLICANT: Nitta, Masahiro
TITLE OF INVENTION: CYP7 Promoter-Binding Factors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282.803B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3027 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 159..1838

US-09-282-803B-9

Query Match 57.7%; Score 15; DB 3; Length 3027;
Best Local Similarity 78.3%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 ccataacggttcgcctaacggttcg 24
||||| ||| ||| ||| ||| ||| |||
Db 509 CCATTACGGTCTCTCTCAGTCGC 531

RESULT 9
US-08-472-217-1/c
Sequence 1, Application US/08472217
Patent No. 5726058
GENERAL INFORMATION:
APPLICANT: Alanen-Kurki, Leena
APPLICANT: Auvinen, Petri
APPLICANT: Jaakkola, Panu
APPLICANT: Jalkanen, Markku
APPLICANT: Lepp, Sirpa
APPLICANT: Maki, Markku
APPLICANT: Vihinen, Tapani
APPLICANT: W rri, Anni
TITLE OF INVENTION: Syndecan Stimulation Of Cellular
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472.217
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,427
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1102.0050003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26700 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 101n(4378..4443, 22026..22106, 23001..23483,
LOCATION: 23905..24039, 24251..24418)
US-08-472-217-1

Query Match 57.7%; Score 15; DB 1; Length 26700;
Best Local Similarity 78.3%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23
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Db 9461 TCCAAATGTTCCCTAGCATTC 9439

RESULT 10
US-08-488-199-5/c
; Sequence 5, Application US/08488199
; Patent No. 5851993
; GENERAL INFORMATION:
; APPLICANT: Jalkanen, Markku
; APPLICANT: Mali, Markku
; TITLE OF INVENTION: Suppression of Tumor Cell Growth By
; TITLE OF INVENTION: Syndecan-1 Ectodomain
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,862
; FILING DATE: 13-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0130001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4378..4443
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22026..22107
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23002..23483
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23905..24040
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 24252..24418
US-08-488-199-5

Query Match 57.7%; Score 15; DB 2; Length 26700;
Best Local Similarity 78.3%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23
||||| || ||||| ||||| |||||
Db 9461 TCCAAATGTTCCCTAGCATTC 9439

RESULT 11
US-08-760-534A-1/c
; Sequence 1, Application US/08760534A
; Patent No. 6017727
; GENERAL INFORMATION:
; APPLICANT: JALKANEN, MARKKU
; APPLICANT: JAANKOLA, PANU
; APPLICANT: VIHINEN, TAPANI
; TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN
; TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,534A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,186
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI93/00514
; FILING DATE: 01-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1708.0050004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(4378..4443, 22026..22106, 23001..23483,
; LOCATION: 23905..24039, 24251..24418)
US-08-760-534A-1

Query Match 57.7%; Score 15; DB 3; Length 26700;
Best Local Similarity 78.3%; Pred. No. 93;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttc 23
||||| || ||||| ||||| |||||
Db 9461 TCCAAATGTTCCCTAGCATTC 9439

RESULT 12
US-08-680-506-6/c
; Sequence 6, Application US/08680506C
; Patent No. 6008013
; GENERAL INFORMATION:

APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 1587
TYPE: DNA
ORGANISM: Gallus gallus
US-08-680-506-6

Query Match 56.9%; Score 14.8; DB 3; Length 1587;
Best Local Similarity 73.1%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaacgttcgc 26
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Db 1444 TCCATTTCATCCCTCAAGTTCGTC 1419

RESULT 13

US-07-710-361-2
Sequence 2, Application US/07710361
Patent No. 5242820
GENERAL INFORMATION:
APPLICANT: LO, Shyh-Ching
TITLE OF INVENTION: NOVEL PATHOGENIC MYOPLASMA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue NW, Suite 1000
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/710,361
FILING DATE: 19910606
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 265,920
FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 875,535
FILING DATE: 18-JUN-1986
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18596-90428
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2210 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Mycoplasma fermentans

STRAIN: incognitus
IMMEDIATE SOURCE:
CLONE: psb 2.2
US-07-710-361-2

Query Match 56.9%; Score 14.8; DB 1; Length 2210;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18
||||| ||||| ||||| |||||
Db 2020 TCCATAACTTTCTCCTAA 2037

RESULT 14

US-08-967-513-1/c
Sequence 1, Application US/08967513
Patent No. 5783436
GENERAL INFORMATION:
APPLICANT: Robert P. Hausinger
TITLE OF INVENTION: Mutant Urease and Method
TITLE OF INVENTION: of Use For Determination
TITLE OF INVENTION: of Urea
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,513
FILING DATE: 11-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,645
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5783436e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2400
TYPE: nucleotides
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella aerogenes
STRAIN: CG253
INDIVIDUAL ISOLATE:
CELL TYPE: N/A
FEATURE:
NAME/KEY: CDNA encoding mutant urease
NAME/KEY: 'H219Q
LOCATION: Modification at position 1312 to
LOCATION: glutamine

IDENTIFICATION METHOD: Sequencing
OTHER INFORMATION:
US-08-967-513-1

Query Match 56.9%; Score 14.8; DB 1; Length 2400;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18
|||||
Db 35 TCCATAACGTTCTCTTAA 18

RESULT 15

US-08-687-645B-1/c
Sequence 1, Application US/08687645B

Patent No. 5846752

GENERAL INFORMATION:

APPLICANT: Robert P. Hausinger

TITLE OF INVENTION: Mutant Urease and Method

TITLE OF INVENTION: Of Use For Determination

TITLE OF INVENTION: Of Urea

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,645B

FILING DATE: July 26, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-309

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100

TELEFAX: (517) 347-4103

TELEX: NO. 5846752e

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2400

TYPE: nucleotides

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE:

DESCRIPTION: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Klebsiella aerogenes

STRAIN: CG253

INDIVIDUAL ISOLATE:

CELL TYPE: N/A

FEATURE:

NAME/KEY: cDNA encoding mutant urease

NAME/KEY: 'H2190

LOCATION: Modification at position 1312 to

LOCATION: glutamine

IDENTIFICATION METHOD: Sequencing

OTHER INFORMATION:

US-08-687-645B-1

Query Match 56.9%; Score 14.8; DB 2; Length 2400;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tccataacgttcgcctaa 18
|||||
Db 35 TCCATAACGTTCTCTTAA 18

Search completed: October 9, 2001, 15:42:06
Job time: 296 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: October 9, 2001, 16:19:55 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-6
Perfect score: 22
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : GenEmbl:*
- 1: gb_ba1:*
 - 2: gb_ba2:*
 - 3: gb_ba3:*
 - 4: gb_in1:*
 - 5: gb_in2:*
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 - 7: gb_om:*
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 - 9: gb_pat1:*
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 - 13: gb_pil2:*
 - 14: gb_pil3:*
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 - 20: em_htgo_inv:*
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 - 29: em_htg_hum8:*
 - 30: em_htg_inv1:*
 - 31: em_htg_inv2:*
 - 32: em_htg_other:*
 - 33: em_htg_rod:*
 - 34: em_hum1:*
 - 35: em_hum2:*
 - 36: em_hum3:*
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 - 38: em_hum5:*
 - 39: em_hum6:*
 - 40: em_hum7:*
 - 41: em_in:*
 - 42: em_om:*
 - 43: em_or:*

- 44: em_ov:*
- 45: em_pat:*
- 46: em_ph:*
- 47: em_pl:*
- 48: em_ro:*
- 49: em_sts:*
- 50: em_sy:*
- 51: em_un:*
- 52: em_vl:*
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- 56: gb_sy:*
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- 59: gb_vl2:*
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- 86: gb_pr2:*
- 87: gb_pr3:*
- 88: gb_pr4:*
- 89: gb_pr5:*
- 90: gb_pr6:*
- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_ro1:*
- 95: gb_ro2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	95.5	22	9 AX036946	AX036946 Sequence
2	21	95.5	22	10 AX083678	AX083678 Sequence
3	21	95.5	22	10 AX083680	AX083680 Sequence
4	20	90.9	145939	79 AL158143	AL158143 Homo sapi
5	19.4	88.2	22	9 AX036945	AX036945 Sequence
6	19.4	88.2	22	9 AX046993	AX046993 Sequence
7	19.4	88.2	22	10 AX083675	AX083675 Sequence
8	19.4	88.2	22	10 AX083681	AX083681 Sequence

```

c 9 18.4 83.6 22 10 AX083682 Sequence
c 10 18.4 83.6 4334 85 AB033099 Homo sapi
c 11 18.4 83.6 109120 79 AL157945 Homo sapi
c 12 18.4 83.6 110762 81 AL391244 Homo sapi
c 13 18.4 83.6 197748 70 AC026283 Homo sapi
c 14 18.4 83.6 197748 70 AC026283 Homo sapi
c 15 18.4 81.8 108055 61 AC009521 Homo sapi
c 16 18.4 81.8 168601 86 AC008123 Homo sapi
c 17 18.4 81.8 169423 74 AC069309 Mus muscu
c 18 18.4 81.8 169532 62 AC012513 Homo sapi
c 19 17.8 80.9 22 9 AX036944 Sequence
c 20 17.8 80.9 22 9 AX036952 Sequence
c 21 17.8 80.9 22 10 AX083676 Sequence
c 22 17.8 80.9 152318 66 AC021766 Homo sapi
c 23 17.8 80.9 190866 64 AC015954 Homo sapi
c 24 17.4 79.1 1754 4 AB029058 Anthocida
c 25 17.4 79.1 102798 78 AL138730 Homo sapi
c 26 17.4 79.1 135714 90 AL160037 Human DNA
c 27 17.4 79.1 142172 69 AC025957 Homo sapi
c 28 17.4 79.1 178593 83 AP003376 Oryza sat
c 29 17.4 77.3 98411 87 AC010289 Homo sapi
c 30 17.4 77.3 151620 65 AC018589 Homo sapi
c 31 17.4 77.3 188697 61 AC010542 Homo sapi
c 32 16.8 76.4 488 9 A64089 Sequence 15
c 33 16.8 76.4 521 93 HSPAL9B5 278909 H.sapiens f
c 34 16.8 76.4 642 71 AC032512 Giardial
c 35 16.8 76.4 781 71 AC035787 Giardial
c 36 16.8 76.4 858 72 AC064490 Giardial
c 37 16.8 76.4 895 93 HSA279145 A1279145 Homo sapi
c 38 16.8 76.4 913 9 AR074152 Sequence
c 39 16.8 76.4 1014 72 AC048567 Giardial
c 40 16.8 76.4 1076 72 AC048568 Giardial
c 41 16.8 76.4 5068 85 AB051476 Homo sapi
c 42 16.8 76.4 7207 93 HSA238520 A1238520 Homo sapi
c 43 16.8 76.4 8077 94 HML5A3B X84014 M.musculus
c 44 16.8 76.4 10818 1 AE000829 Methanoba
c 45 16.8 76.4 74992 74 AC069574 Homo sapi

```

ALIGNMENTS

```

RESULT 1
AX036946
LOCUS AX036946 22 bp DNA
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX036946
VERSION AX036946.1 GI:11226374
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 a 4 c 6 g
BASE COUNT 6 a
ORIGIN
Query Match 95.5%; Score 21; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 2
AX083678
LOCUS AX083678 22 bp DNA
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION AX083678
VERSION AX083678.1 GI:13185410
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 4 22-FEB-2001;
DYNavax Technologies Corporation (US)
FEATURES
Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g
BASE COUNT 6 a
ORIGIN
Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 TGACTGTGAANGTTCCAGATGA 22

RESULT 3
AX083680
LOCUS AX083680 22 bp DNA
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION AX083680
VERSION AX083680.1 GI:13185412
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;
DYNavax Technologies Corporation (US)
FEATURES
Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5-bromocytosine"
modified_base 11
6 a 3 c 6 g
BASE COUNT 6 a
ORIGIN
Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 4
AL158143
LOCUS AL158143 22 bp DNA
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION AL158143
VERSION AL158143.1 GI:13185412
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Patent: WO 0112223-A 6 22-FEB-2001;
DYNavax Technologies Corporation (US)
FEATURES
Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 a 4 c 6 g
BASE COUNT 6 a
ORIGIN
Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

```

LOCUS AL158143 145939 bp DNA HTG 08-APR-2001
DEFINITION Homo sapiens chromosome X clone RP5-107418, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.
ACCESSION AL158143
VERSION AL158143.12 GI:13567909
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 145939)
AUTHORS McLeay, K.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT requests: clonerequest@sanger.ac.uk
 On Apr 9, 2001 this sequence version replaced gi:9931672.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: dj107418
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 7% of reads
 Dye-terminator Big Dye; 92% of reads
 Consensus quality: 137464 bases at least Q40
 Consensus quality: 141229 bases at least Q30
 Consensus quality: 143037 bases at least Q20
 Insert size: 144339; sum-of-contigs
 Insert size: 111741; 30.4% error; agarose-fp
 Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality coverage: 9.27x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence. * as soon as it is available and the accession number will be preserved. *
 * 1 3024: contig of 3024 bp in length
 * 3025 3124: gap of 100 bp
 * 3125 10834: contig of 7710 bp in length
 * 10835 10934: gap of 100 bp
 * 10935 13595: contig of 2661 bp in length
 * 13596 13695: gap of 100 bp
 * 13696 16092: contig of 2397 bp in length
 * 16093 16192: gap of 100 bp
 * 16193 22530: contig of 8338 bp in length
 * 22531 22630: gap of 100 bp
 * 22631 27253: contig of 4623 bp in length
 * 27254 27353: gap of 100 bp
 * 27354 30261: contig of 2908 bp in length
 * 30262 30361: gap of 100 bp
 * 30362 33611: contig of 3250 bp in length
 * 33612 33711: gap of 100 bp
 * 33712 38262: contig of 4551 bp in length
 * 38263 38362: gap of 100 bp
 * 38363 40615: contig of 2253 bp in length
 * 40616 40715: gap of 100 bp
 * 40716 44299: contig of 3584 bp in length
 * 44300 44399: gap of 100 bp
 * 44400 47229: contig of 2830 bp in length
 * 47230 47329: gap of 100 bp
 * 47330 52776: contig of 5447 bp in length
 * 52777 52876: gap of 100 bp
 * 52877 60226: contig of 7350 bp in length
 * 60227 60326: gap of 100 bp

* 60327 62930: contig of 2604 bp in length
 * 62931 63030: gap of 100 bp
 * 63031 67419: contig of 4389 bp in length
 * 67420 67519: gap of 100 bp
 * 67520 145939: contig of 78420 bp in length.

FEATURES

Location/Qualifiers

1..145939

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="X"

/clone="RP5-107418"

/clone_lib="RPC1-5"

1..3024

/note="assembly_fragment:00567"

clone_end:SP6

vector_side:left

3125..10834

/note="assembly_fragment:00921"

fragment_chain:1

10935..13595

/note="assembly_fragment:01789"

fragment_chain:1

13696..16092

/note="assembly_fragment:01424"

fragment_chain:2

16193..22530

/note="assembly_fragment:01022"

fragment_chain:2

22631..27253

/note="assembly_fragment:00011"

27354..30261

/note="assembly_fragment:00127"

30362..33611

/note="assembly_fragment:00247"

33712..38262

/note="assembly_fragment:00335"

38363..40615

/note="assembly_fragment:00495"

40716..44299

/note="assembly_fragment:00561"

44400..47229

/note="assembly_fragment:00700"

47330..52776

/note="assembly_fragment:00832"

52877..60226

/note="assembly_fragment:00912"

60327..62930

/note="assembly_fragment:01119"

63031..67419

/note="assembly_fragment:01935"

67520..145939

/note="assembly_fragment:02239"

BASE COUNT 45121 a 27951 c 28095 g 43161 t 1611 others

ORIGIN

Query Match 90.9%; Score 20; DB 79; Length 145939;
 Best Local Similarity 95.2%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccagatga 22
 |||||
 Db 37628 GACTGTGAATGTTCCAGATGA 37648

RESULT 5

AX036945 AX036945 22 bp DNA PAT 16-NOV-2000
 LOCUS
 DEFINITION Sequence 2 from Patent FR2790955.
 ACCESSION AX036945
 VERSION AX036945.1 GI:11226373
 KEYWORDS synthetic construct.
 SOURCE

```

ORGANISM      synthetic construct
REFERENCE      1 (bases 1 to 22)
AUTHORS       Carpentier,A.
JOURNAL       Patent: FR 2790955-A 2 22-SEP-2000;
              ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES      Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="oligodesoxynucleotide"
BASE COUNT    6 a 3 c 7 g 6 t
ORIGIN

Query Match      88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 6
AX046993      AX046993      22 bp      DNA      PAT      15-DEC-2000
LOCUS          Sequence 2 from Patent WO0067787.
DEFINITION     AX046993
ACCESSION      AX046993
VERSION        AX046993.1 GI:11876420
KEYWORDS       synthetic construct.
SOURCE         synthetic construct.
ORGANISM       artificial construct.
REFERENCE      1 (bases 1 to 22)
AUTHORS       Moss,R.B.
TITLE         Hiv immunogenic compositions and methods
JOURNAL       Patent: WO 0067787-A 2 16-NOV-2000;
              THE IMMUNE RESPONSE CORPORATION (US)
FEATURES      Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="phosphorothioate-modified synthetic
              oligodeoxynucleotide"
BASE COUNT    6 a 3 c 7 g 6 t
ORIGIN

Query Match      88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 7
AX083675      AX083675      22 bp      DNA      PAT      28-FEB-2001
LOCUS          Sequence 1 from Patent WO0112223.
DEFINITION     AX083675
ACCESSION      AX083675
VERSION        AX083675.1 GI:13185407
KEYWORDS       synthetic construct.
SOURCE         synthetic construct.
ORGANISM       artificial construct.
REFERENCE      1 (bases 1 to 22)
AUTHORS       van Nest,G.
TITLE         Methods of modulating an immune response using immunostimulatory s
              equences and compositions for use therein
JOURNAL       Patent: WO 0112223-A 1 22-FEB-2001;
              Dynavax Technologies Corporation (US)
FEATURES      Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="5-bromocytosine"
              /mod_base=OTHER
BASE COUNT    6 a 2 c 7 g 6 t 1 others
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAANGTTTCGAGATGA 22

RESULT 9
AX083682      AX083682      22 bp      DNA      PAT      28-FEB-2001
LOCUS          Sequence 8 from Patent WO0112223.
DEFINITION     AX083682
ACCESSION      AX083682
VERSION        AX083682.1 GI:13185414
KEYWORDS       synthetic construct.
SOURCE         synthetic construct.
ORGANISM       artificial construct.
REFERENCE      1 (bases 1 to 22)
AUTHORS       van Nest,G.
TITLE         Methods of modulating an immune response using immunostimulatory s
              equences and compositions for use therein
JOURNAL       Patent: WO 0112223-A 8 22-FEB-2001;
              Dynavax Technologies Corporation (US)
FEATURES      Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="5-bromocytosine"
              /mod_base=OTHER
BASE COUNT    6 a 2 c 7 g 6 t 1 others
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
    ||||| ||||| ||||| |||||
Db 1 TGACTGTGAANGTTTCGAGATGA 22

RESULT 9
AX083682      AX083682      22 bp      DNA      PAT      28-FEB-2001
LOCUS          Sequence 8 from Patent WO0112223.
DEFINITION     AX083682
ACCESSION      AX083682
VERSION        AX083682.1 GI:13185414
KEYWORDS       synthetic construct.
SOURCE         synthetic construct.
ORGANISM       artificial construct.
REFERENCE      1 (bases 1 to 22)
AUTHORS       van Nest,G.
TITLE         Methods of modulating an immune response using immunostimulatory s
              equences and compositions for use therein
JOURNAL       Patent: WO 0112223-A 8 22-FEB-2001;
              Dynavax Technologies Corporation (US)
FEATURES      Location/Qualifiers
              1..22
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="5-bromocytosine"
              /mod_base=OTHER
BASE COUNT    6 a 2 c 7 g 6 t 1 others
ORIGIN

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/organism="synthetic construct"
/db_xref="taxon:32630"
11
modified_base
/mod_base=OTHER
/mod_base=OTHER
15
/mod_base="5-bromocytosine"
/mod_base="5-bromocytosine"
6 a 1 c 7 g 6 t 2 others
BASE COUNT
ORIGIN

Query Match      83.6%; Score 18.4; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 TGACTGTGAANGTTNGAGATGA 22

RESULT 10
AB033099/c 4334 bp mRNA PRI 11-NOV-1999
LOCUS
DEFINITION Homo sapiens mRNA for KIAA1273 protein, partial cds.
ACCESSION AB033099
VERSION AB033099.1 GI:6382027
KEYWORDS
SOURCE Homo sapiens brain cDNA to mRNA, clone_lib:pb1uescriptII SK plus
clone:hk09394.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nagase,T., Ishikawa,K., Kikuno,R., Hirotsawa,M., Nomura,N. and
Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
JOURNAL DNA Res. 6 (5), 337-345 (1999)
MEDLINE 20039619
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu
Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology;
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdna.info@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/,
Tel:+81-438-52-3913, Fax:+81-438-52-3914)
FEATURES
source
1 . 4334
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hk09394"
/clone_lib="pb1uescriptII SK plus"
/tissue_type="brain"
463 . .2283
/gene="KIAA1273"
<463 . .2283
/gene="KIAA1273"
/note="Start codon is not identified."
/codon_start=1
/product="KIAA1273 protein"
/protein_id="BAA86587.1"
/db_xref="GI:6382028"
/translation="SWQMQLEALNLLHTLVWASLRCAGAVQVQERLSCSAPROVP
AGECALQYEAQVEQLKSEQIRQAQERRKTLSETRHQHQAQYQDKLARQTEQD
LKQOALLNEERLQKQEQEAMRRATVERELRHKNEMLRVETEARAKAREE
NADIIREQDIRLKASPHROTLESIRTAGTLFCEGFPAFVTDKVTATVAGTLLVAG
VYSANNAATVGRFIEARLGLKPSLVRETSRTLVLEALRHPIQVSRRLSRPODVLEGV
VLSPPKATVARDIAIATRNTRKNRGLYRHILLYGPPTGKTLFAKKLALHSGMDYAIM
TGCDVAPMGREGVTAMHKLFDWANTSRRLGLLFMDQADAFLLKRRATEISKDLRATLN
APLYHMGQHSNKMFLVLASNLNLPQEQDCAINSRIDYVNVHFDLPQQERERLVRHFDNC
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```

/map="p36.31-36.33"
/clone="RP4-628J24"
/clone_lib="RPCI-4"
1. 25559
/misc_feature
/notice="assembly_fragment:00655"
25660. 109120
/misc_feature
/notice="assembly_fragment:03347"
clone_end:T7
vector_side:right"
23801 a 31255 c 31398 g 22566 t 100 others
ORIGIN

Query Match 83.6%; Score 18.4; DB 79; Length 109120;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||| | ||||| |
DB 69219 TGACTGTGCAGGTTCCAGATG 69239

RESULT 12
AL391244 110762 bp DNA HTG 22-MAR-2001
LOCUS Homo sapiens chromosome 1 clone RP4-758J18 map p36.31-36.33, ***
DEFINITION SEQUENCING IN PROGRESS ***, 2 unordered pieces.
ACCESSION AL391244
VERSION AL391244.10 GI:13445424
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEPIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110762)
REFERENCE
AUTHORS Hall, R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Mar 24, 2001 this sequence version replaced gi:13274814.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ758J18
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-terminator ET-amersham; 8% of reads
Quality: 110363 bases at least Q40
Consensus quality: 110564 bases at least Q30
Consensus quality: 110615 bases at least Q20
Insert size: 110662; sum-of-contigs
Insert size: 116314; 4.8% error; agarose-fp
Quality coverage: 9.10x in Q20 bases; sum-of-contigs Quality
coverage: 10.07x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 102958: contig of 102958 bp in length
* 102959 103058: gap of 100 bp

```

```

FEATURES
Location/Qualifiers
1. 110762
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chr="p36.31-36.33"
/clone="RP4-758J18"
/clone_lib="RPCI-4"
1. 102958
/notice="assembly_fragment:00018"
clone_end:SP6
vector_side:left
clone_end:T7
vector_side:right"
103059-110762
/misc_feature
/notice="assembly_fragment:00253"
BASE COUNT 24820 a 31446 c 31405 g 22991 t 100 others
ORIGIN

Query Match 83.6%; Score 18.4; DB 81; Length 110762;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||| | ||||| |
DB 47152 TGACTGTGCAGGTTCCAGATG 47172

RESULT 13
AC026283 197748 bp DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 1 clone RP11-421C4, WORKING DRAFT SEQUENCE,
DEFINITION 17 unordered pieces.
ACCESSION AC026283
VERSION AC026283.2 GI:7523967
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197748)
REFERENCE
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 197748)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Apr 7, 2000 this sequence version replaced gi:7272307.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0421C04
----- Summary Statistics -----
Sequencing vector: M13; 98%
Sequencing vector: plasmid; 2%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 2% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 186690 bases at least Q40
Consensus quality: 190557 bases at least Q30
Consensus quality: 192407 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 196148; sum-of-contigs
Quality coverage: 5.63 in Q20 bases; agarose-fp
Quality coverage: 5.60 in Q20 bases; sum-of-contigs

```

----- NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1057: contig of 1057 bp in length
1058 1157: gap of unknown length
1158 3482: contig of 2325 bp in length
3482 3582: gap of unknown length
3582 5498: contig of 1916 bp in length
5498 5599: gap of unknown length
5599 9301: contig of 3703 bp in length
9301 9401: gap of unknown length
9401 12779: contig of 3378 bp in length
12779 12879: gap of unknown length
12879 15999: contig of 3019 bp in length
15999 21627: gap of unknown length
21627 21728: gap of unknown length
21728 28379: contig of 6652 bp in length
28379 28479: gap of unknown length
28479 36334: contig of 7855 bp in length
36334 36434: gap of unknown length
36434 50951: contig of 14417 bp in length
50951 50952: gap of unknown length
50952 60928: gap of unknown length
60928 71240: contig of 10312 bp in length
71240 71341: gap of unknown length
71341 88918: contig of 17578 bp in length
88918 89018: gap of unknown length
89018 108716: contig of 19698 bp in length
108716 108817: gap of unknown length
108817 128174: contig of 19358 bp in length
128174 128275: gap of unknown length
128275 164211: contig of 35936 bp in length
164211 164311: gap of unknown length
164311 197748: contig of 33438 bp in length.

FEATURES

source
1. 197748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-421C4"
misc_feature
1. 1057
/note="assembly_name:Contig4"
misc_feature
1158. 3482
/note="assembly_name:Contig5"
misc_feature
3583. 5498
/note="assembly_name:Contig6"
clone_end:SP6
vector_side:left
5599. 9301
/note="assembly_name:Contig7"
misc_feature
9402. 12779
/note="assembly_name:Contig8"
misc_feature
12880. 15898
/note="assembly_name:Contig9"
clone_end:T7
vector_side:right
15999. 21627
/note="assembly_name:Contig10"
misc_feature
21728. 28379
/note="assembly_name:Contig11"
misc_feature
28480. 36334
/note="assembly_name:Contig12"
misc_feature
36435. 50851
/note="assembly_name:Contig13"
50952. 60828

/note="assembly_name:Contig14"
60929. 71240
/note="assembly_name:Contig15"
71341. 88918
/note="assembly_name:Contig16"
89019. 108716
/note="assembly_name:Contig17"
108817. 128174
/note="assembly_name:Contig18"
128275. 164210
/note="assembly_name:Contig19"
164311. 197748
/note="assembly_name:Contig20"
BASE COUNT 42194 a 54729 c 55209 g 44011 t 1605 others
ORIGIN

Query Match 83.6%; Score 18.4; DB 70; Length 197748;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatg 21
||||||| | |||||
Db 91850 TGACTGTGCGAGGTCCAGATG 91870

RESULT 14
AC026283/1 197748 bp DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 1 clone RP11-421C4, WORKING DRAFT SEQUENCE,
DEFINITION 17 unordered clones.
AC026283
VERSION AC026283.2 GI:7523967
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 197748)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Apr 7, 2000 this sequence version replaced gi:7272307.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Center project name: H_NH0421C04
----- Summary Statistics -----
Sequencing vector: M13, 98%
Chemistry: Dye-terminator ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 2% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 186690 bases at least Q40
Consensus quality: 190557 bases at least Q30
Consensus quality: 192407 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 196148; sum-of-contigs
Quality coverage: 5.63 in Q20 bases; agarose-fp
Quality coverage: 5.60 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1 1057: contig of 1057 bp in length
* 1058 1157: gap of unknown length
* 1158 3482: contig of 2325 bp in length
* 3483 3482: gap of unknown length
* 3483 5498: contig of 1916 bp in length
* 3583 5498: gap of unknown length
* 5499 9301: contig of 3703 bp in length
* 5599 9301: gap of unknown length
* 9302 12779: contig of 3378 bp in length
* 9402 12779: gap of unknown length
* 12780 15998: contig of 3019 bp in length
* 12880 15998: gap of unknown length
* 15999 21627: contig of 5629 bp in length
* 21628 21727: gap of unknown length
* 21728 28379: contig of 6652 bp in length
* 28380 28479: gap of unknown length
* 28480 36334: contig of 7855 bp in length
* 36335 36434: gap of unknown length
* 36435 50851: contig of 14417 bp in length
* 50852 50951: gap of unknown length
* 50952 60828: contig of 9877 bp in length
* 60829 60929: gap of unknown length
* 60929 71240: contig of 10312 bp in length
* 71241 88918: contig of 17578 bp in length
* 88919 89018: gap of unknown length
* 89019 108716: contig of 19698 bp in length
* 108717 108817: gap of unknown length
* 108817 128474: contig of 19358 bp in length
* 128475 128474: gap of unknown length
* 128475 164210: contig of 35936 bp in length
* 164211 164311: gap of unknown length
* 164311 197748: contig of 33438 bp in length.
  
```

FEATURES

```

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-421C4"
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misc_feature
/feature="assembly_name:Contig5"
3583..5498
misc_feature
/feature="assembly_name:Contig6"
clone_end:SP6
vector_side:left"
5599..9301
misc_feature
/feature="assembly_name:Contig7"
9402..12779
misc_feature
/feature="assembly_name:Contig8"
12880..15998
misc_feature
/feature="assembly_name:Contig9"
clone_end:17
vector_side:right"
15999..21627
misc_feature
/feature="assembly_name:Contig10"
21728..28379
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50952..60828
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/feature="assembly_name:Contig14"
60929..71240
misc_feature
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71341..88918
  
```

```

/feature="assembly_name:Contig16"
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128275..164210
/feature="assembly_name:Contig19"
164311..197748
/feature="assembly_name:Contig20"
42194 a 54729 c 55209 g 44011 t 1605 others
ORIGIN

Query Match      83.6%; Score 18.4; DB 70; Length 197748;
Best Local Similarity 90.5%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatg 21
||||||| |||||||||
Db 160181 TGACTGTGCAGGTTCCAGATG 160161

RESULT 15
AC009521 108055 bp DNA HTG 14-APR-2001
LOCUS Homo sapiens clone Rp5-944N2, WORKING DRAFT SEQUENCE, 4 unordered
DEFINITION pieces.
ACCESSION AC009521
VERSION AC009521.17 GI:9966733
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 108055)
REFERENCE
AUTHORS
  
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Al-Sayid, S. L., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C.,
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 Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S.,
 Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.

and Gibbs, R.
Direct Submission
Unpublished
REFERENCE 2 (bases 1 to 108055)
AUTHORS Worley, K.C.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Sep 5, 2000 this sequence version replaced g1:9966185.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMHX
Center clone name: RP5-944N2
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator; M13; L08821
Chemistry: Dye-terminator; Big Dye; 87% of reads
Assembly: Dye-terminator; Phrap; version 0.990329
Consensus quality: 105193 bases at least Q40
Consensus quality: 105945 bases at least Q30
Consensus quality: 106299 bases at least Q20
Estimated insert size: 105170; sum-of-contigs estimation
Quality coverage: 7.7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 99571: contig of 99571 bp in length
* 99572 99671: gap of unknown length
* 99672 105349: contig of 5678 bp in length
* 105350 105449: gap of unknown length
* 105450 106581: contig of 1132 bp in length
* 106582 106681: gap of unknown length
* 106682 108055: contig of 1374 bp in length.
FEATURES
source
1..108055
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP5-944N2"
BASE COUNT 30896 a 20974 c 22948 g 32930 t 307 others
ORIGIN

Query Match 81.8%; Score 18; DB 61; Length 108055;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccaga 19
|||||||
Db 64387 TCACGTGTAATGTTCCAGA 64405

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:22 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-6
Perfect score: 22
Sequence: 1 tgaagtgaangttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*
12: gb_est12.*
13: gb_est13.*
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258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Qy 2 gacigtgaangttccagatga 22

TITLE
JOURNAL
COMMENT

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-235F18-TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center-Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.tigr.org/bacpac/orderingframe.html>). BAC end page: http://www.tigr.org/ldb/bac_ends/mouse/bac_end_intro.html
Plate: 235 row: f column: 18
Seq primer: SP6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
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/clone="RPCI-23-235F18"
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/sex="Female"
/lab_host="DH108"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcORI; Site_2: EcORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcORI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcORI sites. The ligation products were transformed into DH108 electrocompetent cells (BRL Life Technologies)."

BASE COUNT 111 a 121 c 176 g 164 t
ORIGIN

Query Match 83.6%; Score 18.4; DB 248; Length 572;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatga 22
1 ||||| ||||| ||||| |||||
Db 63 GCGTGTGAATGTTCCAGATGA 83

RESULT 8
BG295408
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

602392719F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4504324 5',
mRNA sequence.
BG295408
BG295408
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Prepared by: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10376 row: f column: 05

High quality sequence stop: 681.
Location/Qualifiers
1..681
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4504324"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 128 a 167 c 222 g 164 t
ORIGIN

Query Match 83.6%; Score 18.4; DB 175; Length 681;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatga 22
1 ||||| ||||| ||||| |||||
Db 519 GCGTGTGAATGTTCCAGATGA 539

RESULT 9
BF178492
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

601807652F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4038564 5',
mRNA sequence.
BF178492
BF178492.1 GI:11056634
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Prepared by: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM9317 row: g column: 13
High quality sequence stop: 652.

FEATURES
source

Location/Qualifiers
1..705
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:4038564"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH108"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 134 a 172 c 234 g 165 t
ORIGIN


```

VERSION  AI489944.1  GI:4385315
KEYWORDS  EST.
SOURCE    tomato...
ORGANISM  Lycopersicon esculentum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
           Lycopersicon.
REFERENCE 1 (bases 1 to 559)
AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
           , Liang,P., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
           ,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
           ,S.D. and Giovannoni,J.
TITLE     Generation of ESTs from tomato carpel tissue
JOURNAL   Unpublished (1999)
COMMENT   Contact: David Frisch
           Clemson University Genomics Institute
           Clemson University
           100 Jordan Hall, Clemson, SC 29634, USA
           Tel: 864 656 4366
           Fax: 864 656 4293
           Email: dfrisch@CLEMSON.EDU.

FEATURES  source
           1..559
            /organism="Lycopersicon esculentum"
            /cultivar="TA496"
            /db_xref="taxon:4081"
            /clone="cLED14114"
            /clone_lib="tomato ovary, TAMU"
            /tissue_type="carpel"
            /dev_stage="5 days pre-anthesis to 5 days post-anthesis"
            /lab_host="XLI-Blue MRF"
            /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and
            directionally cloned cDNA in vector Lambda ZAP II with 5',
            and 3' ends located at the EcoRI and XhoI sites,
            respectively."
BASE COUNT 157 a 98 c 128 g 176 t
ORIGIN

Query Match      79.18; Score 17.4; DB 21; Length 559;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy  1  tgactgtggaangttccagat 20
    ||||| ||||| ||||| |||||
Db  141 TCAGTTTCAGAGGTTCCAGAT 160

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Search completed: October '9, 2001, 18:20:24
 Job time: 9794 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-6
Perfect score: 22
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
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2: /SID88/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseqn/NA1983.DAT.*
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22: /SID88/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	21	95.5	22	AAV80099	Immunomodulatory o
2	21	95.5	22	AAV80101	Immunomodulatory o
3	21	95.5	22	AAA96254	Sequence of a stab
4	21	95.5	22	AAA38068	Immunostimulatory
5	21	95.5	22	AAA38070	Immunostimulatory
6	21	95.5	22	AAZ55877	Immunomodulatory o
7	21	95.5	22	AAF77043	Immunostimulatory
8	21	95.5	22	AAF77045	Immunostimulatory
9	19.4	88.2	22	AAV32079	Nucleotide sequenc
10	19.4	88.2	22	AAV36624	ISS-ODN DY1018 nuc
11	19.4	88.2	22	AAV80097	Immunomodulatory o

12	19.4	88.2	22	20	AAV80102	Immunomodulatory o
13	19.4	88.2	22	20	AAV80103	Immunomodulatory o
14	19.4	88.2	22	21	AAC64051	Immunostimulatory
15	19.4	88.2	22	21	AAA96253	Sequence of a stab
16	19.4	88.2	22	21	AAA90458	CpG adjuvant oligo
17	19.4	88.2	22	21	AAA14467	Immunostimulatory
18	19.4	88.2	22	21	AAA38065	Immunostimulatory
19	19.4	88.2	22	21	AAA38071	Immunostimulatory
20	19.4	88.2	22	21	AAA38072	Immunostimulatory
21	19.4	88.2	22	21	AAS55876	Immunomodulatory o
22	19.4	88.2	22	21	AAS55880	Immunomodulatory o
23	19.4	88.2	22	22	AAF77040	Immunomodulatory D
24	19.4	88.2	22	22	AAF77046	Immunostimulatory
25	19.4	88.2	22	22	AAE29800	Cholera toxin immu
26	19.4	88.2	22	22	AAC82107	Oligonucleotide OD
27	19.4	88.2	22	22	AAE92377	CG motif and CFA C
28	18.6	84.5	22	22	AAF77047	Immunostimulatory
29	18.4	83.6	22	21	AAZ55881	Immunomodulatory o
30	17.8	80.9	22	19	AAV32080	Nucleotide sequenc
31	17.8	80.9	22	20	AAV36625	ISS-ODN mutant DY1
32	17.8	80.9	22	20	AAV55797	Immunostimulatory
33	17.8	80.9	22	20	AAV55788	Immunostimulatory
34	17.8	80.9	22	20	AAV80105	Oligo used in expe
35	17.8	80.9	22	20	AAV80096	Immunomodulatory o
36	17.8	80.9	22	20	AAV80104	Oligo used in expe
37	17.8	80.9	22	21	AAC64052	Non-CpG control ph
38	17.8	80.9	22	21	AAE96252	Sequence of a stab
39	17.8	80.9	22	21	AAE96250	Sequence of a stab
40	17.8	80.9	22	21	AAA14468	Inactive immunost
41	17.8	80.9	22	21	AAV38066	Immunostimulatory
42	17.8	80.9	22	22	AAF77041	Immunostimulatory
43	16.8	76.4	488	18	AAE91140	Strawberry fruit r
44	16.8	76.4	913	19	AAV23881	Plant CCR enzyme D
45	16.8	76.4	913	20	AAZ06885	Pine cinnamoyl-CoA

ALIGNMENTS

RESULT 1
AAV80099
ID AAV80099 standard; DNA; 22 BP.
XX AAV80099;
AC AAV80099;
XX
XX 12-MAR-1999 (first entry)
DT
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
XX WO9855495-A2.
XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-US11578.
XX
XX 06-JUN-1997; 97US-0048793.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Dina D, Roman M, Schwartz D;
XX
XX WPI; 1999-059898/05.
XX
XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX Claim 8; Page 29; 63pp; English.

PS The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.17;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 2

AAV80101
ID AAV80101 standard; DNA; 22 BP.

XX AAV80101;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulating; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 11
FT /*tag= a
FT /*note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX Claim 22; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.17;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 3

AAA96254

ID AAA96254 standard; DNA; 22 BP.

XX AAA96254;

DT 08-FEB-2001 (first entry)

DE Sequence of a stabilised oligonucleotide with antitumour activity.

XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.

XX Synthetic.

XX WO200056342-A2.

XX 28-SEP-2000.

XX 17-MAR-2000; 2000WO-FR00676.

XX 19-MAR-1999; 99FR-0003433.

XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX Carpentier A;

XX WPI; 2000-602192/57.

XX Use of stabilized oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic

XX Example 13; Page 46; 57pp; French.

XX The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.

XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.17;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttccagatga 22

RESULT 4
 AAA38068
 ID AAA38068 standard; DNA: 22 BP.
 XX AC AAA38068;
 XX DT 24-AUG-2000 (first entry)
 XX DE Immunostimulatory sequence (ISS) #4.
 XX KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KW development; ss.
 XX OS Synthetic.
 XX PN WO200021556-A1.
 XX PD 20-APR-2000.
 XX PF 08-OCT-1999; 99WO-US23677.
 XX PR 09-OCT-1998; 98US-0103733.
 XX PR 07-OCT-1999; 99US-0415186.
 XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX PI Tighe H, Raz E, Schwartz D, Takabayashi K;
 XX WPI; 2000-317846/27.
 XX PT Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual -
 XX PS Disclosure; Page 16; 65pp; English.
 XX CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.
 XX SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.17;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttccagatga 22

RESULT 5
 AAA38070
 ID AAA38070 standard; DNA: 22 BP.
 XX AC AAA38070;
 XX DT 24-AUG-2000 (first entry)
 XX DE Immunostimulatory sequence (ISS) #6.
 XX KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KW development; ss.
 XX OS Synthetic.
 XX PN WO200021556-A1.
 XX PD 20-APR-2000.
 XX PF 08-OCT-1999; 99WO-US23677.
 XX PR 09-OCT-1998; 98US-0103733.
 XX PR 07-OCT-1999; 99US-0415186.
 XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX PI Tighe H, Raz E, Schwartz D, Takabayashi K;
 XX WPI; 2000-317846/27.
 XX PT Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual -
 XX PS Disclosure; Page 16; 65pp; English.
 XX CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.
 XX SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.17;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttccagatga 22

RESULT 6
 AA255877
 ID AA255877 standard; DNA: 22 BP.

XX AAF77043;
 XX 10-APR-2000 (first entry)
 XX Immunomodulatory oligonucleotide SEQ ID NO: 2.
 DE Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunosuppression; 5-bromocytosine; ss.
 XX Mus musculus.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
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 FT /note= "Phosphorothioate linkages"
 FT misc_feature 9..16
 FT /*tag= b
 FT /note= "Immunostimulatory sequence (ISS)"
 FT modified_base 11
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 XX
 XX WO9962923-A2.
 XX
 XX 09-DEC-1999.
 XX
 XX 04-JUN-1999; 99WO-US12538.
 XX
 XX 05-JUN-1998; 98US-0088310.
 XX 01-JUN-1999; 99US-0324191.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 XX Schwartz D;
 XX
 XX WPI: 2000-105687/09.
 XX
 XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens
 XX
 XX Claim 29; Page 35; 54pp; English.
 XX
 XX Sequences AA55876-255877 and AA55880-255886 represent immunomodulatory oligonucleotides comprising an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT, AGCGTC, AGCGTC, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTCC and GACGTTCC). The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886 contain ISSs comprising at least one bromocytosine, whereas sequence AA255876 contains an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect; when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells), while simultaneously downregulating the Th2-type response. The Th1 response is particularly effective for control of viruses and intracellular parasites. The immunomodulatory oligonucleotides are used, particularly when formulated with an antigen or a facilitator, for modulating immune responses. Such compositions may be used in tumor therapy, in treatment of allergy (including asthma), for inducing a vigorous cellular response (against a virus, bacterium, fungus or protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;
 XX

Query Match 95.5%; Score 21; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
 Db 1 tgactgtgaangttccagatga 22
 RESULT 7
 AAF77043
 ID AAF77043 standard; DNA; 22 BP.
 XX
 AC AAF77043;
 XX 15-MAY-2001 (first entry)
 DT
 DE Immunostimulatory DNA #3.
 XX
 KW Modulate; immune; antigen; immunostimulatory; ds.
 XX
 OS Synthetic.
 XX
 PN WO200112223-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000WO-US22835.
 XX
 PR 19-AUG-1999; 99US-0149768.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 XX Van Nest G;
 XX
 XX WPI: 2001-211136/21.
 XX
 XX Modulating immune response to a second antigen in humans involves administering an immunostimulatory polynucleotide comprising an immunostimulatory sequence and a first antigen
 XX
 XX Disclosure; Page 15; 63pp; English.
 XX
 XX The present invention relates to modulating an immune response to a second antigen in an individual, involving administering to the individual an immunomodulatory polynucleotide comprising an immunostimulatory sequence (ISS) and a first antigen.
 XX
 XX Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 other;
 XX

Query Match 95.5%; Score 21; DB 22; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.17;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
 Db 1 tgactgtgaangttccagatga 22
 RESULT 8
 AAF77045
 ID AAF77045 standard; DNA; 22 BP.
 XX
 AC AAF77045;
 XX 15-MAY-2001 (first entry)
 DT
 DE Immunostimulatory DNA #5.
 XX
 KW Modulate; immune; antigen; immunostimulatory; ds.
 XX
 OS Synthetic.
 XX
 PN WO200112223-A2.
 XX

PD 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US22835.

XX 19-AUG-1999; 99US-0149768.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2001-211136/21.

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

PT immunostimulatory sequence and a first antigen

XX Disclosure; Page 15; 63pp; English.

XX The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 6 T; 1 other;

Query Match 95.5%; Score 21; DB 22; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.17;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22

Db 1 tgactgtgaabgtccagatga 22

RESULT 9

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX

DT 09-SEP-1998 (first entry)

XX

DE Nucleotide sequence of DY1018.

XX

XX DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;

KW immunisation; anaphylaxis; IgE; retinopathies; ss.

KW synthetic.

OS

XX Key Location/Qualifiers

FH modified_base 1..22

FT /*tag= a

FT /note= "phosphothioate backbone"

XX

XX WO9816247-A1.

XX

XX 23-APR-1998.

XX

XX 09-OCT-1997; 97WO-US19004.

XX

XX 11-OCT-1996; 96US-0028118.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Carson DA, Raz E, Roman M;

XX

XX WPI; 1998-261028/23.

XX

XX New immunomodulatory compositions - comprising an antigen conjugated

PT to a polynucleotide that contains an immunostimulatory sequence

XX

XX Example 1; Page 36; 69pp; English.

XX This is the nucleotide sequence of DY1018, which is conjugated to

CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule

CC (IMM), which comprises an antigen conjugated to a polynucleotide

CC (PN) that contains at least one immunostimulatory nucleotide sequence

CC (ISS). The conjugate synergistically boost the magnitude of the host

CC immune response against an antigen to a level greater than the host

CC immune response to either the IMM, antigen or ISS-PN alone. These

CC responses to ISS-PN/IMM conjugates are particularly acute during

CC the important early phase of the host immune response to an antigen.

CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular

CC (Th1 type) immune responses of the host. Thus, use of the method to

CC boost the immune responsiveness of a host to subsequent challenge by a

CC sensitising antigen without immunisation avoids the risk of

CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE

CC production in response to the antigen challenge. The conjugates can

CC also be used to combat pathogenic infection and to stimulate

CC therapeutic angiogenesis to treat conditions in which localised blood

CC flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 19; Length 22;

Best Local Similarity 90.9%; Pred. No. 1;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 10

AAAX36624

ID AAX36624 standard; DNA; 22 BP.

XX

AC AAX36624;

XX

DT 09-JUL-1999 (first entry)

XX

DE ISS-ODN DY1018 nucleotide sequence.

XX

KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;

KW granulocyte-mediated tissue inflammation; Th2 type immune response;

KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;

KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;

KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;

KW eosinophilic fasciitis; therapy; ss.

XX

OS Synthetic.

XX

XX WO9911275-A2.

XX

PD 11-MAR-1999.

XX

XX 04-SEP-1998; 98WO-US18382.

XX

XX 05-SEP-1997; 97US-0927120.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Ray E;

XX

XX WPI; 1999-312404/26.

XX

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX

XX Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DY1018 nucleotide sequence.

CC The invention relates to a method for preventing or reducing

CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,

CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:

CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 11
 AAV80097
 ID AAV80097 standard; DNA; 22 BP.
 XX
 AC AAV80097;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX
 OS Synthetic.
 XX
 PN WO9855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Dina D. Roman M. Schwartz D;
 XX
 DR WPI; 1999-059898/05.
 XX

PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 5; Page 29; 63pp; English.
 XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
 AAV80102
 ID AAV80102 standard; DNA; 22 BP.
 XX
 AC AAV80102;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; Immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 11
 FT /*tag= a
 FT /note= "5-bromocytosine"
 XX
 PN WO9855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Dina D. Roman M. Schwartz D;
 XX
 DR WPI; 1999-059898/05.
 XX

PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 23; Page 30; 63pp; English.
 XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

Query Match 88.2%; Score 19.4; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13

AAV80103
ID AAV80103 standard; DNA; 22 BP.

XX
AC AAV80103;

DT 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
XX
OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 11

FT /*tag= a

FT /note= "5-bromocytosine"

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

PS Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 14

AAV80103

ID AAC64051 standard; DNA; 22 BP.

XX
AC AAC64051;

XX 15-FEB-2001 (first entry)

XX Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.

XX CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
KW enhanced antigen presentation; antigen-presenting cell; APC;
KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
KW vaccine; ss.

XX OS Synthetic.

XX WO2000062787-Al.

XX 26-OCT-2000.

XX 11-APR-2000; 2000WO-US09664.

XX 15-APR-1999; 99US-0292278.

XX (REGC) UNIV CALIFORNIA.

XX Raz E, Martin-Orozco E;

XX WPI; 2000-679548/66.

XX Enhancing antigen-presentation capabilities of T-cells for cancer
PT immunotherapy, by contacting cells with an immunostimulatory
PT oligonucleotide

XX Example I; Page 18; 42pp; English.

XX The invention relates to a method of inducing activation of T-cells
CC to respond to an antigen, comprising contacting antigen-presenting cells
CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
CC thus treated have enhanced antigen presenting capabilities compared to
CC antigen-activated APCs. APCs with enhanced antigen-presentation
CC capabilities then present the antigen to T-cells. The method is useful
CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
CC antigen presenting capacity of tumour cells, thereby inducing T-cell
CC activation, and is therefore useful for treating tumours. Additionally,
CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
CC ISS-ODN treated APCs are induced to take up antigen through upregulation
CC of Fc-receptor expression, to present antigen through upregulation of
CC major histocompatibility complex (MHC) Class I and II expression and
CC Cd1d expression, to produce co-stimulatory factors (B7 and CD40), to
CC provide cell-to-cell adhesion through upregulation of intercellular
CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
CC cytokine production, all at levels greater than that achieved through
CC contact of APC with antigen alone. The present sequence represents
CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19.4; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 tgactgtgaangttccagatga 22
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Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
AAA96253
ID AAA96253 standard; DNA; 22 BP.
XX
AC AAA96253;
XX
DT 08-FEB-2001 (first entry)
DE
DE Sequence of a stabilised oligonucleotide with antitumour activity.
XX
KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS Synthetic.
XX
PN WO200056342-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-FR00676.
XX
PR 19-MAR-1999; 99FR-0003433.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI Carpentier A;
XX
DR WPI; 2000-602192/57.
XX
PT Use of stabilised oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic
PT .
XX
PS Example 2; Page 16; 57pp; French.
XX
CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octamer motif
CC of the type 3'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
CC immunostimulatory, and are not toxic. They may be adapted for use in
CC animals or humans. The stabilised oligonucleotides are used for
CC treating tumours, of any type and any degree of anaplasia, particularly
CC human tumours in the peripheral or central nervous systems, specifically
CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 88.2%; Score 19,4; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22
    ||||| |||| |||| |||||
Db 1 tgactgtgaacgttcgagatga 22

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GenCore version 4.5
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5	21	95.5	22	18	US-09-415-186-6
6	21	95.5	22	25	US-09-642-492-4
7	21	95.5	22	25	US-09-642-492-6
8	21	95.5	22	28	US-09-713-136-4
9	21	95.5	22	28	US-09-713-136-6
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12	19.4	88.2	22	1	PCT-US01-03029-2
13	19.4	88.2	22	1	PCT-US01-03029-2
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26	19.4	88.2	22	17	US-09-308-036A-1
27	19.4	88.2	22	17	US-09-324-191A-1
28	19.4	88.2	22	17	US-09-324-191A-5
29	19.4	88.2	22	17	US-09-347-343-32
30	19.4	88.2	22	17	US-09-397-198-1
31	19.4	88.2	22	18	US-09-415-186-1
32	19.4	88.2	22	18	US-09-415-186-7
33	19.4	88.2	22	18	US-09-470-382-69
34	19.4	88.2	22	22	US-09-565-906-2
35	19.4	88.2	22	22	US-09-570-325-19
36	19.4	88.2	22	22	US-09-642-492-1
37	19.4	88.2	22	25	US-09-642-492-7
38	19.4	88.2	22	25	US-09-700-354-1
39	19.4	88.2	22	28	US-09-713-136-1
40	19.4	88.2	22	28	US-09-713-136-7
41	19.4	88.2	22	29	US-09-746-130-1
42	19.4	88.2	22	29	US-09-746-130-2
43	19.4	88.2	22	31	US-09-828-505-2
44	19.4	88.2	22	31	US-09-828-505-2
45	19.4	88.2	22	31	US-09-828-505-2

ALIGNMENTS

RESULT 1
US-09-296-477-6
; Sequence 6, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-296-477-6

Query Match 95.5%; Score 21; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 2
US-09-296-477-12
; Sequence 12, Application US/09296477A
; GENERAL INFORMATION:
; APPLICANT: RAZ, E.
; APPLICANT: SCHWARTZ, D.
; APPLICANT: ROMAN, M.
; APPLICANT: DINA, D.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
; TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
; FILE REFERENCE: 377882000420
; CURRENT APPLICATION NUMBER: US/09/296,477A
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: 09/092,329
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/048,793
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-296-477-12

Query Match 95.5%; Score 21; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 3
US-09-324-191A-2
; Sequence 2, Application US/09324191A
; GENERAL INFORMATION:
; APPLICANT: Schwartz, David
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES WITH
; TITLE OF INVENTION: MODIFIED BASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 377882000200
; CURRENT APPLICATION NUMBER: US/09/324,191A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/088,310
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: 5-bromocytosine
US-09-324-191A-2

Query Match 95.5%; Score 21; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 4
US-09-415-186-4
; Sequence 4, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-4

Query Match 95.5%; Score 21; DB 18; Length 22;

Best Local Similarity 95.5%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaacgttccagatga 22

RESULT 5

US-09-415-186-6
; Sequence 6, Application US/09415186
; GENERAL INFORMATION:
; APPLICANT: Tighe, Helen
; APPLICANT: Raz, Eyal
; APPLICANT: Schwartz, David
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Anti-Viral Compositions and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 377882000700
; CURRENT APPLICATION NUMBER: US/09/415,186
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,733
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-415-186-6

Query Match 95.5%; Score 21; DB 18; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaabgttccagatga 22

RESULT 6

US-09-642-492-4
; Sequence 4, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-642-492-4

Query Match 95.5%; Score 21; DB 25; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||

Db 1 tgactgtgaacgttccagatga 22

RESULT 7

US-09-642-492-6
; Sequence 6, Application US/09642492
; GENERAL INFORMATION:
; APPLICANT: Van Nest, G.
; TITLE OF INVENTION: METHODS OF MODULATING AN IMMUNE RESPONSE
; TITLE OF INVENTION: USING IMMUNOSTIMULATORY SEQUENCES AND COMPOSITIONS FOR USE
; FILE REFERENCE: 377882000800
; CURRENT APPLICATION NUMBER: US/09/642,492
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,768
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (11)...(11)
; OTHER INFORMATION: N = 5-bromocytosine
; OTHER INFORMATION: Synthetic construct
US-09-642-492-6

Query Match 95.5%; Score 21; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 8

US-09-713-136-4
; Sequence 4, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Method:
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-4

Query Match 95.5%; Score 21; DB 28; Length 22;
Best Local Similarity 95.5%; Pred. No. 4.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaacgttccagatga 22

RESULT 9
US-09-713-136-6
; Sequence 6, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: modified base
; LOCATION: (11)...(0)
; OTHER INFORMATION: N = 5-bromocytosine
US-09-713-136-6

Query Match 95.5%; Score 21; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 10
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 11
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 12
PCT-US00-35064-2
; Sequence 2, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant
PCT-US00-35064-2

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
Db 1 tgactgtgaangttccagatga 22

RESULT 13
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides In
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen

; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 14
PCT-US01-03029-2
; Sequence 2, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eval Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

RESULT 15
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match 88.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttcgagatga 22

Search completed: October 9, 2001, 21:12:47
Job time: 20072 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 ; Search time 1391.6 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-713-136-6
Perfect score: 22
Sequence: 1 tgactgtgaangttccagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1.*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	7	US-09-802-518-4
2	21	95.5	22	7	US-09-802-518-6
3	21	95.5	22	7	US-09-802-359-4
4	21	95.5	22	7	US-09-802-359-6
5	21	95.5	22	7	US-09-802-376-4
6	21	95.5	22	7	US-09-802-376-6
7	19.4	88.2	22	7	US-09-802-518-1
8	19.4	88.2	22	7	US-09-802-518-7
9	19.4	88.2	22	7	US-09-802-359-1
10	19.4	88.2	22	7	US-09-802-359-7
11	19.4	88.2	22	7	US-09-802-376-1
12	19.4	88.2	22	7	US-09-802-376-7
13	18.4	83.6	22	7	US-09-802-518-8
14	18.4	83.6	22	7	US-09-802-359-8
15	18.4	83.6	22	7	US-09-802-376-8
16	18	81.8	24853	7	US-09-764-874-10235
17	18	81.8	32212	7	US-09-764-874-10236
18	17.8	80.9	22	6	US-09-770-943-1
19	17.8	80.9	22	6	US-09-770-943-2
20	17.8	80.9	22	6	US-09-770-943-10
21	17.8	80.9	22	7	US-09-802-518-2
22	17.8	80.9	22	7	US-09-802-518-10
23	17.8	80.9	22	7	US-09-802-359-2
24	17.8	80.9	22	7	US-09-802-359-9
25	17.8	80.9	22	7	US-09-802-376-2

Sequence 9, Appli
Sequence 331, App
Sequence 10462, A
Sequence 10373, A
Sequence 2667, Ap
Sequence 39362, A
Sequence 7434, Ap
Sequence 25567, A
Sequence 20696, A
Sequence 33706, A
Sequence 25491, A
Sequence 25115, A
Sequence 40617, A
Sequence 17824, A
Sequence 40571, A
Sequence 40550, A
Sequence 36285, A
Sequence 36273, A
Sequence 40494, A
Sequence 7398, Ap

26 17.8 80.9 22 7 US-09-802-376-9
27 17.8 80.9 252 5 US-09-825-790-331
28 17.3 77.3 303 7 US-09-850-147-10462
29 16.8 76.4 132 7 US-09-724-750-10373
30 16.8 76.4 171 7 US-09-764-874-2667
31 16.8 76.4 207 8 US-09-253-457-39362
32 16.8 76.4 268 8 US-09-253-456-7434
33 16.8 76.4 308 8 US-09-253-456-25567
34 16.8 76.4 310 8 US-09-253-457-20696
35 16.8 76.4 312 7 US-09-540-213-33706
36 16.8 76.4 318 8 US-09-253-456-25491
37 16.8 76.4 321 8 US-09-253-456-25115
38 16.8 76.4 338 8 US-09-253-457-40617
39 16.8 76.4 345 6 US-09-909-629-17824
40 16.8 76.4 347 8 US-09-253-457-40571
41 16.8 76.4 350 8 US-09-253-457-40550
42 16.8 76.4 352 8 US-09-253-378-36285
43 16.8 76.4 357 8 US-09-253-378-36273
44 16.8 76.4 361 8 US-09-253-457-40494
45 16.8 76.4 368 8 US-09-253-456-7398

ALIGNMENTS

RESULT 1
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4

Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.33;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttccagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaangttccagatga 22

RESULT 2
US-09-802-518-6
; Sequence 6, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaangttccagatga 22

RESULT 3
US-09-802-359-4
; Sequence 4, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-4

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.33;
Matches 21; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 4
US-09-802-359-6
; Sequence 6, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-6

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaangttccagatga 22

RESULT 5
US-09-802-376-4
; Sequence 4, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-4

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.33;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
   |||||
DB 1 tgactgtgaacgttccagatga 22

RESULT 6
US-09-802-376-6
; Sequence 6, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-6
```

Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaangttccagatga 22

RESULT 7

US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaacgttcagatga 22

RESULT 8

US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaangttccagatga 22

RESULT 9

US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaacgttcagatga 22

RESULT 10

US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
|||||
DB 1 tgactgtgaangttccagatga 22

RESULT 11

```

US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match      88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred.No. 2.2;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
    ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 12
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

```

```

; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
; US-09-802-518-8
;
Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaangttngagatga 22

RESULT 14
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
; US-09-802-359-8
;
Query Match      83.6%; Score 18.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaangttngagatga 22

RESULT 15
US-09-802-376-8
; Sequence 8, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376

```

```

; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8

```

```

Query Match      83.6%;   Score 18.4;   DB 7;   Length 22;
Best Local Similarity 90.9%;
Pred. NO. 7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
    |||
Db 1 tgactgtgaangttngagatga 22
    |||

```

Search completed: October 9, 2001, 21:36:22
Job time: 21242 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:06 ; Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

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Title: US-09-713-136-6
Perfect score: 22
Sequence: 1 tqactgtgaangttccagatga 22

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length:	2000000000
Maximum DB seq length:	2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45

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Database :
Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/3A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/3B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	17.8	80.9	22	4	US-09-092-314-1	Sequence 1, Appli
2	17.8	80.9	22	4	US-09-092-314-2	Sequence 2, Appli
3	17.8	80.9	22	4	US-09-092-314-10	Sequence 10, Appl
4	16.8	76.4	913	2	US-08-975-316-61	Sequence 61, Appl
5	16.4	74.5	1166	1	US-08-121-063-7	Sequence 7, Appli
6	16.2	73.6	22	4	US-09-092-314-3	Sequence 3, Appli
7	16.2	73.6	22	4	US-09-092-314-4	Sequence 4, Appli
8	15.8	71.8	588	3	US-08-965-9048-1	Sequence 1, Appli
9	15.8	71.8	773	3	US-08-934-131-2	Sequence 2, Appli
10	15.4	70.0	1876	3	US-08-714-918-33	Sequence 33, Appl
11	15.4	70.0	1876	4	US-09-265-315-33	Sequence 33, Appl
12	15.4	70.0	1876	4	US-09-265-315-33	Sequence 33, Appl
13	15.4	70.0	1876	4	US-09-266-417-33	Sequence 33, Appl
14	15.4	70.0	10207	1	US-08-920-812-2	Sequence 2, Appli
15	15.4	70.0	10207	1	US-08-920-821-2	Sequence 2, Appli
16	15.4	70.0	10207	1	US-08-921-177-2	Sequence 2, Appli
17	15.4	70.0	10207	1	US-08-362-577C-2	Sequence 2, Appli
18	15.4	70.0	10207	2	US-08-920-828-2	Sequence 2, Appli
19	15.2	69.1	2694	3	US-08-975-703-5	Sequence 5, Appli
20	15.2	69.1	2694	4	US-09-515-884-5	Sequence 5, Appli
21	14.8	67.3	27	2	US-08-308-952-18	Sequence 18, Appl
22	14.8	67.3	27	2	US-09-124-141-27	Sequence 27, Appl
23	14.8	67.3	660	1	US-08-325-553-28	Sequence 28, Appl
24	14.8	67.3	660	2	US-08-394-152A-28	Sequence 28, Appl
25	14.8	67.3	2088	1	US-08-164-839-7	Sequence 7, Appli
26	14.8	67.3	2088	1	US-08-583-799-7	Sequence 7, Appli
27	14.8	67.3	2921	1	US-08-164-839-9	Sequence 9, Appli

ALIGNMENTS

```

RESULT      1
US-09-092-314-1
: Sequence 1, Application US/09092314
: Patent No. 6225292
: GENERAL INFORMATION:
: APPLICANT: Raz, Eyal
: APPLICANT: Roman, Mark
: TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
: TITLE OF INVENTION: Sequence Activity
: Patent No. 6225292
: FILE REFERENCE: 6510-173US1
: CURRENT APPLICATION NUMBER: US/09/092.314
: CURRENT FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/048,794
: PRIOR FILING DATE: 1997-06-06
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Oligonucleotide
: US-09-092-314-1

```

Query Match 80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1;
Matches 19; Conservative 0; Mismatches 3; Indels

Qy . 1 tgactgtgaangttccagatga 22
||||| ||| |||||

Dd 1 tgactgtgaagqtttaqaqatga 22

```

RESULT      2
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06

```

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttccagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 4
US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAYUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-975-316-61

Query Match      76.4%; Score 16.8; DB 2; Length 913;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccagatga 22
   ||||| ||||| |||||
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 5
US-08-121-063-7
; Sequence 7, Application US/08121063
; Patent No. 5446143
; GENERAL INFORMATION:
; APPLICANT: Simpson, Evan R.
; APPLICANT: Mahendroo, Mala
; APPLICANT: Mendelson, Carole R.
; TITLE OF INVENTION: Adipose-Specific Promoter Regions of
; TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,063
; FILING DATE: 14-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSD:351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-121-063-7

Query Match 74.5%; Score 16.4; DB 1; Length 1166;
Best Local Similarity 89.5%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaangttccagatga 22
||||| ||||| ||
DB 525 CTGTGAAGTTCAGAGA 543

RESULT 6
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
||||| ||||| ||
DB 1 tgactgtgaaccttagagatga 22

RESULT 7
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttccagatga 22
||||| ||||| ||
DB 1 tgactgtgaaccttagagatga 22

RESULT 8
US-08-965-904B-1
; Sequence 1, Application US/08965904B
; Patent No. 6030811
; GENERAL INFORMATION:
; APPLICANT: CHABOT-FLETCHER, MARIE
; APPLICANT: ANDERSON, KAREN M.
; TITLE OF INVENTION: A HUMAN MYOTROPHIN CLONE,
; TITLE OF INVENTION: HSABH01
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,904B
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,677
; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: ATG-50026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 588 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-965-904B-1

Query Match 71.8%; Score 15.8; DB 3; Length 588;
Best Local Similarity 85.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaangttccagatg 21
||||| ||||| ||
DB 341 GACTGTGAAGGCCCATG 360

RESULT 9
US-08-934-131-2
; Sequence 2, Application US/08934131

Patent No. 6153423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN MYOTROPHIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0387 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
LENGTH: 773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT22
CLONE: 2591910
US-08-934-131-2

Query Match 71.8%; Score 15.8; DB 3; Length 773;
Best Local Similarity 85.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccagatg 21
||||||| | |||||
Db 544 GACTGTGAAGCCCGAGATG 563

RESULT 10
US-08-714-918-33/C
Sequence 33, Application US/08714918
Patent No 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-714-918-33

Query Match 70.0%; Score 15.4; DB 3; Length 1876;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19
||||||| | |||||
Db 844 GACTGTAAATGTTCCAGA 827

RESULT 11
US-09-265-315-33/C
Sequence 33, Application US/09265315
Patent No. 6187341
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/265.315
;; FILING DATE: March 9, 1999
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/714, 918
;; FILING DATE: September 13, 1996
;; APPLICATION NUMBER: 60/009,102
;; FILING DATE: December 22, 1995
;; APPLICATION NUMBER: 60/003,798
;; FILING DATE: September 15, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 240/247
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-265-315-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19
||||| ||| |||||
Db 844 GACTGTAATGTTCCAGA 827

RESULT 12
US-09-265-315-33/c
; Sequence 33, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265.315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996

;; APPLICATION NUMBER: 60/009,102
;; FILING DATE: December 22, 1995
;; APPLICATION NUMBER: 60/003,798
;; FILING DATE: September 15, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 240/247
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-265-315-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttccaga 19
||||| ||| |||||
Db 844 GACTGTAATGTTCCAGA 827

RESULT 13
US-09-266-417-33/c
; Sequence 33, Application US/09266417
; Patent No. 6228588
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266.417
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714, 918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-33

Query Match 70.0%; Score 15.4; DB 4; Length 1876;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19
||||| || |||||
Db 844 GACTGTAATGTTCCAGA 827

RESULT 14
US-08-920-812-2/c
; Sequence 2, Application US/08920812
; Patent No. 5763188
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920.812
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus aureus
; STRAIN: Clinical Isolate SA-24
US-08-920-812-2

Query Match 70.0%; Score 15.4; DB 1; Length 10207;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19
||||| || |||||
Db 68 GACTGTAATGTTCCAGA 51

RESULT 15
US-08-920-827-2/c
; Sequence 2, Application US/08920827
; Patent No. 5770375
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920.827
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus aureus
; STRAIN: Clinical Isolate SA-24
US-08-920-827-2

Query Match 70.0%; Score 15.4; DB 1; Length 10207;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttccaga 19
||||| || |||||
Db 68 GACTGTAATGTTCCAGA 51

Search completed: October 9, 2001, 15:42:08
Job time: 298 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:15 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-7
Perfect score: 22
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl:*
- 1: gb_ba1:*
 - 2: gb_ba2:*
 - 3: gb_ba3:*
 - 4: gb_in1:*
 - 5: gb_in2:*
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 - 7: gb_ov:*
 - 8: gb_ov:*
 - 9: gb_pat1:*
 - 10: gb_pat2:*
 - 11: gb_ph:*
 - 12: gb_pl1:*
 - 13: gb_pl2:*
 - 14: gb_pl3:*
 - 15: gb_pl4:*
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 - 29: em_htg_hum8:*
 - 30: em_htg_inv1:*
 - 31: em_htg_inv2:*
 - 32: em_htg_other:*
 - 33: em_htg_rod:*
 - 34: em_hum1:*
 - 35: em_hum2:*
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 - 39: em_hum6:*
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 - 41: em_in:*
 - 42: em_ov:*
 - 43: em_or:*

- 44: em_ov:*
- 45: em_pat:*
- 46: em_ph:*
- 47: em_pl:*
- 48: em_ro:*
- 49: em_sts:*
- 50: em_sy:*
- 51: em_un:*
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- 90: gb_pr6:*
- 91: gb_pr7:*
- 92: gb_pr8:*
- 93: gb_pr9:*
- 94: gb_ro1:*
- 95: gb_ro2:*
- 96: gb_in4:*
- 97: gb_pr10:*
- 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	95.5	22	9	AX036945 Sequence
2	21	95.5	22	9	AX046993 Sequence
3	21	95.5	22	10	AX083675 Sequence
4	21	95.5	22	10	AX083681 Sequence
5	20	90.9	22	10	AX083682 Sequence
6	19.4	88.2	22	9	AX036944 Sequence
7	19.4	88.2	22	9	AX036946 Sequence
8	19.4	88.2	22	10	AX083676 Sequence

```

9 19.4 88.2 22 10 AX083678 Sequence
10 19.4 88.2 22 10 AX083680 Sequence
11 18.4 83.6 145939 79 AL158143 Homo sapi
12 18.4 83.6 165337 70 AC027442 Homo sapi
13 18.4 83.6 209777 69 AC024934 Homo sapi
14 17.8 80.9 12545 22 9 AX036952 Sequence
15 17.8 80.9 12545 22 9 CEFA42G10 Homo sapi
16 17.4 79.1 102798 78 AL138730 Homo sapi
17 17.4 79.1 135714 70 AL160037 Homo sapi
18 17.4 79.1 183869 73 AC068700 Homo sapi
19 16.8 76.4 929 53 CNS07553J clone BA0
20 16.8 76.4 992 53 CNS0740C clone BA0
21 16.8 76.4 2355 89 AK001312 Homo sapi
22 16.8 76.4 2442 89 AK001749 Homo sapi
23 16.8 76.4 2448 5 AF034078 Caenorhab
24 16.8 76.4 2502 91 BC002736 Homo sapi
25 16.8 76.4 2896 85 AB046637 Macaca fa
26 16.8 76.4 4334 85 AB033099 Homo sapi
27 16.8 76.4 13495 1 AE001805 Thermotog
28 16.8 76.4 29548 6 CE19B6 Caenorhabdi
29 16.8 76.4 49523 90 AL358135 Human DNA
30 16.8 76.4 82360 13 AP000606 Arabidops
31 16.8 76.4 85335 65 AC019557 Drosophil
32 16.8 76.4 85654 81 AL513169 Homo sapi
33 16.8 76.4 90287 61 AC010018 Drosophil
34 16.8 76.4 109120 79 AL157945 Homo sapi
35 16.8 76.4 110000 83 CEV111B2_4 Continuation (5 of
36 16.8 76.4 110762 81 AL391244 Homo sapi
37 16.8 76.4 122854 77 AC087581 Homo sapi
38 16.8 76.4 125590 6 CEV49E10 Caenorhabdi
39 16.8 76.4 136047 74 AC069470 Arabidops
40 16.8 76.4 139032 87 AC010656 Homo sapi
41 16.8 76.4 140907 80 AL162499 Human DNA
42 16.8 76.4 148984 92 HSI05D16 Human DNA
43 16.8 76.4 152842 73 AC067921 Homo sapi
44 16.8 76.4 157270 89 AF236874 Homo sapi
45 16.8 76.4 159958 91 AP000475 Homo sapi

ALIGNMENTS

RESULT 1
AX036945 22 bp DNA
LOCUS Sequence 2 from Patent FR2790955.
DEFINITION AX036945
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 t
BASE COUNT 6 a 3 c 7 g
ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangtcgagatga 22
|||||
Db 1 TGACTGTGAACGTCGAGATGA 22

RESULT 3
AX083675 22 bp DNA
LOCUS Sequence 1 from Patent WO0112223.
DEFINITION AX083675
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
equences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
6 t
BASE COUNT 6 a 3 c 7 g
ORIGIN

Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.67;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangtcgagatga 22
|||||
Db 1 TGACTGTGAACGTCGAGATGA 22

RESULT 4
AX083681 22 bp DNA
LOCUS Sequence 7 from Patent WO0112223.
DEFINITION
```

```

ACCESSION AX083681
VERSION AX083681.1 GI:13185413
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 7 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
modified_base 11
/mod_base=OTHER
6 a 2 c 7 g 6 t 1 others
BASE COUNT
ORIGIN
Query Match 95.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.67; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 5
LOCUS AX083682 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL Patent: WO 0112223-A 8 22-FEB-2001;
Dynamax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
modified_base 11
/mod_base=OTHER
6 a 1 c 7 g 6 t 2 others
BASE COUNT
ORIGIN
Query Match 90.9%; Score 20; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.4; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 6
LOCUS AX083694 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 1 from Patent FR2790955.
ACCESSION AX083694
VERSION AX083694.1 GI:11226372
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
TITLE Patent: FR 2790955-A 1 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
7 a 1 c 8 g 6 t
BASE COUNT
ORIGIN
Query Match 88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.1; Mismatches 2; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAAGGTAGATGA 22

RESULT 7
LOCUS AX083696 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION AX083696
VERSION AX083696.1 GI:11226374
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
TITLE Patent: FR 2790955-A 3 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
source
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 a 4 c 6 g 6 t
BASE COUNT
ORIGIN
Query Match 88.2%; Score 19.4; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.1; Mismatches 2; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 8
LOCUS AX083676 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)

```

```

AUTHORS
TITLE      van Nest,G.
METHODS    Methods of modulating an immune response using immunostimulatory s
SEQUENCES  sequences and compositions for use therein
PATENT     Patent: WO 011223-A 2 22-FEB-2001;
DYNAX      Dynavax Technologies Corporation (US)
FEATURES
SOURCE     Location/Qualifiers
1. .22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT      6 a 4 c 7 g 5 t
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||| ||||| ||||| |||||
DB 1 TGACCGTGAACGTTCCAGATGA 22

RESULT 9
AX083678
LOCUS      AX083678 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 4 from Patent WO011223.
ACCESSION AX083678
VERSION    AX083678.1 GI:13185410
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    van Nest,G.
TITLE      Methods of modulating an immune response using immunostimulatory s
JOURNAL    sequences and compositions for use therein
PATENT     Patent: WO 011223-A 4 22-FEB-2001;
DYNAX      Dynavax Technologies Corporation (US)
FEATURES
SOURCE     Location/Qualifiers
1. .22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT      6 a 4 c 6 g 6 t
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||| ||||| ||||| |||||
DB 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 10
AX083680
LOCUS      AX083680 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 6 from Patent WO011223.
ACCESSION AX083680
VERSION    AX083680.1 GI:13185412
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 22)
AUTHORS    van Nest,G.
TITLE      Methods of modulating an immune response using immunostimulatory s
JOURNAL    sequences and compositions for use therein
PATENT     Patent: WO 011223-A 6 22-FEB-2001;
DYNAX      Dynavax Technologies Corporation (US)

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```

FEATURES
SOURCE     Location/Qualifiers
1. .22
/organism="synthetic construct"
/db_xref="taxon:32630"
modified_base 11
/note="5-bromocytosine"
/mod_base=OTHER
BASE COUNT      6 a 3 c 6 g 6 t 1 others
ORIGIN

Query Match      88.2%; Score 19.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||| ||||| ||||| |||||
DB 1 TGACTGTGAANGTTCCAGATGA 22

RESULT 11
AL158143
LOCUS      AL158143 145939 bp DNA HTG 08-APR-2001
DEFINITION Homo sapiens chromosome X clone RP5-107418, *** SEQUENCING IN
PROGRESS ***, 17 unordered pieces.
ACCESSION    AL158143
VERSION      AL158143.12 GI:13567909
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 145939)
AUTHORS      Mclay,K.
TITLE        Direct Submission
JOURNAL      Submitted (07-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Apr 9, 2001 this sequence version replaced gi:9931672.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ107418
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
Dye-terminator Big Dye; 92% of reads
Consensus quality: 137464 bases at least Q40
Consensus quality: 141229 bases at least Q30
Consensus quality: 143037 bases at least Q20
Insert size: 144339; sum-of-contigs
Insert size: 111741; 30.4% error; agarose-fp
Quality coverage: 6.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.27x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3024: contig of 3024 bp in length
* 3025 3124: gap of 100 bp
* 3125 10834: contig of 7710 bp in length
* 10835 10934: gap of 100 bp
* 10935 13595: contig of 2661 bp in length
* 13596 13695: gap of 100 bp

```



```

Consensus quality: 150628 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 162337; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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```
* 151030 151129: gap of 100 bp
* 151130 165337: contig of 14208 bp in length.
FEATURES
    Location/Qualifiers
        1..165337
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="RP11-439K16"
            /clone_lib="RPC1-11 Human Male BAC"
        1..1105
            /note="assembly_fragment"
        1206..2479
            /note="assembly_fragment"
        2580..4211
            /note="assembly_fragment"
        4312..5781
            /note="assembly_fragment"
        5882..7830
            /note="assembly_fragment"
        7931..9913
            /note="assembly_fragment"
        10014..12486
            /note="assembly_fragment"
        12587..15592
            /note="assembly_fragment"
        15693..19721
            /note="assembly_fragment"
        19822..23269
            /note="assembly_fragment"
        23370..26785
            /note="assembly_fragment"
        26886..30363
            /note="assembly_fragment"
        30464..33964
            /note="assembly_fragment"
        34065..37794
            /note="assembly_fragment"
        37895..43354
            /note="assembly_fragment"
        43455..47839
            /note="assembly_fragment"
        47940..53326
            /note="assembly_fragment"
        53427..58576
            /note="assembly_fragment"
        58677..64554
            /note="assembly_fragment"
        64655..68538
            /note="assembly_fragment"
        clone_end:17
            vector_side:right"
        68639..74650
            /note="assembly_fragment"
        74751..80037
            /note="assembly_fragment"
        80138..85646
            /note="assembly_fragment"
        85747..92718
            /note="assembly_fragment"
        92819..101098
            /note="assembly_fragment"
        101199..108560
            /note="assembly_fragment"
        clone_end:SP6
            vector_side:right"
        108661..118118
            /note="assembly_fragment"
        118219..128612
            /note="assembly_fragment"
        128713..139860
            /note="assembly_fragment"
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Query Match 83.6%; Score 18.4; DB 70; Length 165337;
Best Local Similarity 90.5%; Pred. No. 33;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
|||||
Db 34792 GACTGTGAAGTTTGAGATGA 34812

AC024934 209777 bp DNA HTG 30-DEC-2000

Homo sapiens chromosome 12 clone RP11-329A19, WORKING DRAFT

SEQUENCE, 14 unordered pieces.

AC024934

AC024934.29 GI:11995487

HTG; HTGS-PHASE1; HTGS-DRAFT.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 209777)

Muzny,D.M., Adams,C., Adlo-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbara,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Honsl,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,I., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,C., Liu,W., Louissegh,H., Lorado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapue,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,S., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Picketts,R., Primus,E., Pu,L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shookshakar,N., Slismon,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleciyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 209777)

Worley,K.C.

Direct Submission

Submitted (03-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 29, 2000 this sequence version replaced gi:11992044.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: HAJA

Center clone name: RP11-329A19

Summary Statistics

Sequencing vector: M13; L08821

Chemistry: Dye-terminator Big Dye; 8% of reads

Chemistry: Dye-terminator Big Dye; version 0.990329

Assembly program: Phrap; version 0.990329

Consensus quality: 197273 bases at least Q40

Consensus quality: 202546 bases at least Q30

Consensus quality: 205790 bases at least Q20

Estimated insert size: 202671; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-gel estimation

Quality coverage: 5.5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 33513: contig of 33513 bp in length

33514 33613: gap of unknown length

33614 58205: contig of 24592 bp in length

58206 58305: gap of unknown length

58306 91615: contig of 33310 bp in length

91616 114617: gap of unknown length

114618 114717: contig of 22902 bp in length

114718 132860: contig of 18143 bp in length

132861 132961: gap of unknown length

132962 152339: contig of 19279 bp in length

152340 169844: contig of 17505 bp in length

169845 185351: contig of 15307 bp in length

185352 185358: gap of unknown length

185359 194559: contig of 9207 bp in length

194560 204081: contig of 9422 bp in length

204082 206129: contig of 1949 bp in length

206130 206229: gap of unknown length

206230 207330: contig of 1101 bp in length

207331 207430: gap of unknown length

207431 208674: contig of 1244 bp in length

208675 209777: gap of unknown length

209778 209779: contig of 1003 bp in length.

FEATURES

source

1. 209777

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="12"

/clone="RP11-329A19"

BASE COUNT 65720 a 39190 c 38969 g 64529 t 1369 others

ORIGIN

Query Match 83.6% Score 18.4; DB 69; Length 209777;

Best Local Similarity 90.5% Pred. No. 33;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
|||||
Db 76399 GACTGTGAAGTTTGAGATGA 76419

RESULT 14

AX036952

LOCUS AX036952 22 bp DNA 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES Location/Qualifiers
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="oligosoxynucleotide"
7 a 2 c 6 g 7 t
BASE COUNT 7 a 2 c 6 g 7 t
ORIGIN
1 tgactgtgaangttcgagatga 22
|||||
1 TGACTGTGAACGTTATAGATGA 22
|||||

Query Match 80.9%; Score 17.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 TGACTGTGAACGTTATAGATGA 22
|||||

RESULT 15
CER42G10/c
LOCUS CER42G10 12545 bp DNA INV 25-OCT-2000
DEFINITION Caenorhabditis elegans cosmid F42G10, complete sequence.
ACCESSION 248230
VERSION 248230.1 GI:668329
KEYWORDS HTG; Arg-tRNA; Mitogen activated protein kinase; Transfer RNA.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 12545)
none.

REFERENCE 1
AUTHORS Harris,B.R.
TITLE Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
JOURNAL Science 282 (5396), 2012-2018 (1998)
MEDLINE 99069613
REMARK Erratum: [published errata appear in Science 1999 Jan 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep 3;283(5433):1493]
2 (bases 1 to 12545)
Harris,B.R.

REFERENCE 2
AUTHORS Direct Submission
TITLE Submitted (12-FEB-1995) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
JOURNAL Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone F42G10.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone F42G10 is at 9861 in
sequence 248006.
The true right end of clone F42G10 is at 102 in

sequence 295122.
The true right end of clone F19C6 is at 104 in this sequence. The
start of this sequence (1..104) overlaps with the end of sequence
248006.
The end of this sequence (12448..12545) overlaps with the start of
sequence 295122.
For a graphical representation of this sequence and its analysis
see: http://wormbase.sanger.ac.uk/per1/ace/elegans/seq/sequence?
name=F42G10.

FEATURES Location/Qualifiers
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/clone="F42G10"
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4533..4658,5035..5087,5537..5600))
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cDNA EST yk24a6.5 comes from this gene"
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VAGLRMLLYVAQKTSDSOEIRDTVERSARFCTKRENLIHNPLOVDSINVAASEMPT
FNSLYNCKFGDMYVAPENYCKTLNMDIDVVEEYKSKIKIENDDLFLVTHFMDLEDTAV
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preliminary prediction
similar to tRNA-Arg"
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295122.1:554..639,295122.1:694..759,295122.1:809..905)
/genes="F42G10.2"
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CDS

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complement(268..327),complement(105),
complement(248006.1:36284..36493),
complement(248006.1:36093..36239),
complement(248006.1:35772..35885),
complement(248006.1:35359..35535),
complement(248006.1:35174..35317),
/gene="F19C6.4"
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complement(248006.1:35772..35885),
complement(248006.1:35359..35535),
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/gene="F19C6.4"
BASE COUNT      4001 a 2110 c 2008 g 4426 t
ORIGIN
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Query Match      80.9%  Score 17.8; DB 6; Length 12545;
Best Local Similarity 86.4%  Pred. No. 59;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  tgactgtgaangttcgagatga 22
      |||||  |||||  |||||
Db 10445 TGACTGTCAAGCTGGAGATGA 10424

Search completed: October 9, 2001, 16:20:28
Job time: 2598 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:24 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22

Sequence: 1 tgactgtgaangttcgagatga 22.

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	80.9	463	107	AU083559 AU083559
2	17.8	80.9	479	107	AU089685 AU089685
3	17.8	80.9	972	222	AL347814 Tetraodon
4	17.7	77.3	934	220	AL185061 Tetraodon
5	16.8	76.4	202	4	AA236074 zs05a04.f
6	16.8	76.4	236	127	BB183285 BB183285
7	16.8	76.4	236	171	BF922552 IL2-NT019
8	16.8	76.4	251	161	BB565758 BB565758
9	16.8	76.4	286	16	AI099019 uc02h08.f
10	16.8	76.4	297	7	AA445764 VC63b04.s
11	16.8	76.4	360	26	AV189436 AV189436
12	16.8	76.4	398	167	BE428418 BE428418
13	16.8	76.4	434	170	BF851024 IL5-EN008
14	16.8	76.4	441	22	AI597068 AI597068
15	16.8	76.4	474	167	BE419241 BE419241
16	16.8	76.4	479	142	BF475131 BF475131
17	16.8	76.4	479	142	BE946012 BE946012
18	16.8	76.4	490	116	AW493851 AW493851
19	16.8	76.4	514	240	AZ265882 AZ265882
20	16.8	76.4	516	118	AWG29719 AWG29719
21	16.8	76.4	527	149	BF487041 BF487041
22	16.8	76.4	537	118	AW610890 AW610890
23	16.8	76.4	537	173	BG085331 BG085331
24	16.8	76.4	542	107	AU017198 AU017198
25	16.8	76.4	547	122	AW966305 AW966305
26	16.8	76.4	548	228	AQ397925 AQ397925
27	16.8	76.4	555	165	BE284315 BE284315
28	16.8	76.4	558	245	AZ507714 AZ507714
29	16.8	76.4	561	249	AZ755668 AZ755668
30	16.8	76.4	563	173	BG070885 BG070885
31	16.8	76.4	564	239	AZ192394 AZ192394
32	16.8	76.4	572	248	AZ699837 AZ699837
33	16.8	76.4	579	251	AZ872651 AZ872651
34	16.8	76.4	583	141	BE895299 BE895299
35	16.8	76.4	592	142	BE949337 BE949337
36	16.8	76.4	603	16	AI121117 AI121117
37	16.8	76.4	612	32	AV653619 AV653619
38	16.8	76.4	620	162	BE060267 BE060267
39	16.8	76.4	646	244	AZ477578 AZ477578
40	16.8	76.4	650	147	BF305727 BF305727
41	16.8	76.4	667	149	BF484589 BF484589
42	16.8	76.4	668	250	AZ836523 AZ836523
43	16.8	76.4	672	251	AZ899331 AZ899331
44	16.8	76.4	679	107	AU126477 AU126477
45	16.8	76.4	681	175	BG295408 BG295408

ALIGNMENTS

RESULT 1					
AU083559		463 bp	mrna	EST	21-MAR-2000
LOCUS	AU083559	Rice green shoot Oryza sativa cdna clone SI4862, mrna			
DEFINITION	sequence.				
ACCESSION	AU083559				
VERSION	AU083559.1	GI:7274015			
KEYWORDS	EST.				
SOURCE	Oryza sativa.				
ORGANISM	Oryza sativa				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
TITLE	Ehrhartoideae; Oryzaceae; Oryza.				
JOURNAL	1 (bases 1 to 463)				
	Sasaki, T. and Yamamoto, K.				
	Rice cdna from green shoot (2000)				
	Unpublished (2000)				

COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = "RGP". SI4862_62.				
FEATURES	Location/Qualifiers 1..463 /organism="Oryza sativa" /strain="Nipponbare" /db_xref="taxon:4530" /clone="SI4862" /clone_lib="Rice green shoot" /note="Green shoot (8 days old)" 151 a 74 C 109 g 127 t 2 others				
BASE COUNT	151 a 74 C 109 g 127 t				
ORIGIN	Query Match 80.9%; Score 17.8; DB 107; Length 463; Best Local Similarity 86.4%; Pred. No. 98; Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 tgactgtgaagttcgagatga 22 				
DB	151 TGAGTGTGAATGTTAGAGATGA 172				
RESULT 2	AU089685 479 bp mrna EST 27-APR-2000 LOCUS AU089685 Rice callus Oryza sativa subsp. japonica cdna clone C40060 DEFINITION AU089685 . mRNA sequence.				
ACCESSION	AU089685				
VERSION	AU089685.1 GI:7652165				
KEYWORDS	EST.				
SOURCE	Oryza sativa subsp. japonica.				
ORGANISM	Oryza sativa subsp. japonica Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. 1 (bases 1 to 479) Sasaki, T. and Yamamoto, K. Rice cdna from callus (2000) Unpublished (2000)				
REFERENCE	1 (bases 1 to 479)				
AUTHORS	Sasaki, T. and Yamamoto, K.				
TITLE	Rice cdna from callus (2000)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = "RGP". C40060_32.				
FEATURES	Location/Qualifiers 1..479 /organism="Oryza sativa subsp. japonica" /strain="cultivar Nipponbare, sub_species Japonica" /db_xref="taxon:39947" /clone="C40060" /clone_lib="Rice callus" /note="Vector: pBluescript II SK+; Site 1: SalI; Site 2: NotI; CDNA prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the SalI-NotI site of pBluescript II SK+ phagemid." 149 a 96 C 104 g 130 t				
BASE COUNT	149 a 96 C 104 g 130 t				
ORIGIN					

[illegible]

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Trace considered overall poor quality. Possible reversed clone: similarity on wrong strand. Insert Length: 2064 Std Error: 0.00 Seq primer: -28ml3 rev2 Et from Amersham High quality sequence stop: 1.

FEATURES

source

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Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD+), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3', (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
```

BASE COUNT 45 a 42 c 57 g 58 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 4; Length 202;

Best Local Similarity 85.7%; Pred. No. 2.7e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22

||||| | ||||| |||

Db 46 GACTGTGAACCTTCGAGCTCA 66

RESULT 6

BB183285

LOCUS

DEFINITION

musculus cDNA clone A230106B04 3', mRNA sequence.

ACCESSION

BB183285

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 236)

P., Endo, T., Fukuda, S., Akahira, S., Akiyama, J., Arakawa, T., Carninci

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.

Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata

Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.

T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yananaka, I.

Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino

M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

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Science Laboratory

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Sciences Center

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Fax: +81-298-36-9098

Email: genome-res@rtc.riken.go.jp,

URL: http://genome.rtc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki

N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki

Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.

FEATURES

source

Location/Qualifiers

1..236

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone_lib="A230106B04"

/clone_lib="RIKEN full-length enriched, adult male

hypothalamus"

/sex="male"

/tissue_type="hypothalamus"

/dev_stage="adult"

/lab_host="DH10B"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 20.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCTCCCTCC

3']. cDNA was cleaved with XhoI and BamHI. Vector: a

modified pBluescript KS(+) after bulk excision from Lambda

FLC 1."

BASE COUNT 54 a 51 c 67 g 64 t

ORIGIN

Query Match 76.4%; Score 16.8; DB 127; Length 236;

Best Local Similarity 85.7%; Pred. No. 2.8e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22

||||| | ||||| |||

Db 1 GACTGTTCAGCTTCGAGATGA 21

RESULT 7

BF932252/c

LOCUS

DEFINITION

IL2-NT0196-181200-281-D08 NT0196 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF932252

VERSION

BF932252.1 GI:12349576

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS
1 (bases 1 to 236)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,C.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&tl2=IL2-NT0196-
191200-281-D08&tl3=2000-12-18&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 236.
FEATURES
source
1..236
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0196"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
50 a 74 c 65 g 47 t
ORIGIN
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, ES cells"
/cell_type="ES cells"
/lab_host="SOLR"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 25.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCC 3'].
BASE COUNT
73 a 65 c 63 g 50 t
ORIGIN
Query Match 76.4%; Score 16.8; DB 161; Length 251;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 gactgtgaangttcgagatg 22
Db 203 GACTGTGAAACTTCGGGATGA 223
RESULT 9
LOCUS
AI099019 286 bp mRNA EST 20-AUG-1998
DEFINITION
uc02h08.r1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
IMAGE:1396863 5' similar to WP:C47D12.7 CE05435 RING CANAL PROTEIN .
LIKE ;, mRNA sequence.
ACCESSION
AI099019
VERSION
AI099019.1 GI:3448544
KEYWORDS
EST.
TITLE
JOURNAL
COMMENT
Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..251
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, ES cells"
/cell_type="ES cells"
/lab_host="SOLR"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 25.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCC 3'].
BASE COUNT
73 a 65 c 63 g 50 t
ORIGIN
Query Match 76.4%; Score 16.8; DB 161; Length 251;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 gactgtgaangttcgagatg 22
Db 203 GACTGTGAAACTTCGGGATGA 223
RESULT 9
LOCUS
AI099019 286 bp mRNA EST
DEFINITION
uc02h08.r1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
IMAGE:1396863 5' similar to WP:C47D12.7 CE05435 RING CANAL PROTEIN .
LIKE ;, mRNA sequence.
ACCESSION
AI099019
VERSION
AI099019.1 GI:3448544
KEYWORDS
EST.

```

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 286)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:908579
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 273.

FEATURES
source
1..286
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1396863"
/clone_lib="Soares_mammary_gland_NBMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
RI) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer (5'
TGTTACCAATCTGAAGTGGGAGCGCGGGAATGTTTTTTTTTTTTTTTTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru KO, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 68 a 57 c 80 g 71 t
ORIGIN
Query Match 76.4%; Score 16.8; DB 16; Length 286;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
|||||
Db 105 GACTGTGAAACTTCGAGCTGA 125

RESULT 10
LOCUS AA445764 297 bp mRNA EST 04-AUG-1997
DEFINITION vc63b04.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:779215 5', mRNA sequence.
ACCESSION AA445764
VERSION AA445764.1 GI:2158447
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 297)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
Unpublished (1996)
The WashU-HMI Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:472071
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
Location/Qualifiers
1..297
/organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:779215"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: phuescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos; Primer:
SalI(dT): 5'-CGTCCAGCGTCGACCGTTTTTTTTTTT-3', cDNAs
were cloned into the MluI/SalI sites of a modified
phuescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
BASE COUNT 84 a 73 c 76 g 64 t
ORIGIN

Query Match 76.4%; Score 16.8; DB 7; Length 297;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
|||||
Db 219 GAATGTGAAGTCTTAGATCA 239

RESULT 11
LOCUS AV189436 360 bp mRNA EST 22-JUL-1999
DEFINITION AV189436 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk536b7 5', mRNA sequence.
AV189436
ACCESSION AV189436.1 GI:5571419
VERSION AV189436.1
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida
; Rhabditidae; Peleoderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,
Nishigaki, A., Mochizuki, T., Zeng, O., Watanabe, H., Sugimoto, A., Sano
M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
Nomoto, H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

```

FEATURES
  source
    Location/Qualifiers
      1. 360
        /organism="Caenorhabditis elegans"
        /strain="N2"
        /db_xref="taxon:6239"
        /clone="yK536b7"
        /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
        hermaphrodite embryo"
        /sex="hermaphrodite"
        /dev_stage="embryo"
      111 a 68 c 89 g 92 t
BASE COUNT
ORIGIN

Query Match 76.4%; Score 16.8; DB 26; Length 360;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 151 TCAGTGTGATAGTCGAGATG 171

RESULT 12
BE428418 398 bp mRNA EST 26-JUL-2000
LOCUS MTD006.G10F990616 ITEC MTD Durum Wheat Root Library Triticum
DEFINITION turgidum subsp. durum cDNA clone MTD006.G10, mRNA sequence.
ACCESSION BE428418
VERSION BE428418.1 GI:9426261
KEYWORDS EST.
SOURCE turgidum wheat.
ORGANISM Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
  1 (bases 1 to 398)
  Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
  ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
  Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
  Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,T.,
  Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
  Sorrells,M., Warburton,M. and Wenzel,G.
  International Triticeae EST Cooperative (ITEC): Production of
  Expressed Sequence Tags for Species of the Triticeae
  Unpublished (2000)
  Contact: Joudrier P
  INRA, Unite de Biochimie et Biologie Moleculaire des Cereales
  2, place VIAUA, 34060 Montpellier cedex 01 FRANCE
  Tel: 33 4 99 61 23 84
  Fax: 33 4 99 61 23 48
  Email: joudrier@enscm.inra.fr
  International Triticeae EST Cooperative (ITEC)
  http://wheat.pw.usda.gov/genome.
FEATURES
  source
    Location/Qualifiers
      1. 398
        /organism="Triticum turgidum subsp. durum"
        /cultivar="Silliana"
        /db_xref="taxon:4567"
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        /tissue_type="root"
        /dev_stage="3-day-old seedling, water-stressed"
        /note="vector: pSPORT1; T7 primers used. See pSPORT1
        polylinker site. 0.3-2.0 kbp average insert size."
      99 a 77 c 104 g 118 t
BASE COUNT
ORIGIN

Query Match 76.4%; Score 16.8; DB 167; Length 398;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 147 TCAGTGTGATAGTCGAGATG 167

FEATURES
  source
    Location/Qualifiers
      1. 434
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="EN0086"
        /dev_stage="Adult"
        /note="Organ: lung_normal; vector: puc18; Site_1: Sma1;
        Site_2: Sma1; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
      85 a 117 c 135 g 97 t
BASE COUNT
ORIGIN

Query Match 76.4%; Score 16.8; DB 170; Length 434;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatg 21
    ||| ||||| ||||| |||||
Db 147 TCAGTGTGATAGTCGAGATG 167

RESULT 14
AI597068/c 441 bp mRNA EST 21-APR-1999
LOCUS AI597068
DEFINITION VJ44e09.xl Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:931912 3', mRNA sequence.
ACCESSION AI597068

```

Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
 Sorrells, M., Warburton, M. and Wenzel, G.
 International Triticeae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)
 Contact: Schuch W
 Zeneca Wheat Improvement Centre, Norwich Research Park
 Colney Lane, Norwich NR4 7UH UNITED KINGDOM
 Tel: 44 1603 250 2600
 Fax: 44 1603 250 699
 Email: wolfgang.schuch@zeneca.com
 International Triticeae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 Location/Qualifiers
 1. 474
 /organism="Triticum aestivum"
 /cultivar="Novosibirskaya 67"
 /db_xref="taxon:4565"
 /clone="WNR021.G5"
 /clone_lib="ITEC WMR Wheat Root Library"
 /tissue_type="root"
 /note="W13 Reverse sequencing primer used for 5' end of
 clone."
 BASE COUNT 119 a 87 c 127 g 141 t
 ORIGIN
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 Best Local Similarity 85.7%; Pred. No. 3.2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 gactgtgaangttcgagatga 22
 ||| ||||| ||| |||||
 Db 350 GACGGTGAAGTTAGAGATGA 370

Search completed: October 9, 2001, 18:20:25
 Job time: 9795 sec

AT597068.1 GI:4606116
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 441)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, F., Person
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999.
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:536832
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 High quality sequence stop: 427.
 Location/Qualifiers
 1. 441
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:931912"
 /clone_lib="Stratagene mouse skin (#937313)"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
 ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
 adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"
 BASE COUNT 103 a 144 c 111 g 82 t 1 others
 ORIGIN
 Query Match 76.4%; Score 16.8; DB 22; Length 441;
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 gactgtgaangttcgagatga 22
 ||| ||||| ||||| |||||
 Db 116 GGCTGTGATGTTCCACAGATGA 96

BE419241 474 bp mRNA EST 24-JUL-2000
 LOCUS WNR021.G5R000101 ITEC WMR Wheat Root Library Triticum aestivum CDNA
 clone WNR021.G5, mRNA sequence.
 BE419241
 ACCESSION BE419241.1 GI:9417087
 VERSION
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 474)
 Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22
Sequence: 1 tgactgtgaangtcgagatga 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601:*

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2: /SID88/gcgdata/geneseq/geneseqn/NA1981.DAT:*

3: /SID88/gcgdata/geneseq/geneseqn/NA1982.DAT:*

4: /SID88/gcgdata/geneseq/geneseqn/NA1983.DAT:*

5: /SID88/gcgdata/geneseq/geneseqn/NA1984.DAT:*

6: /SID88/gcgdata/geneseq/geneseqn/NA1985.DAT:*

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9: /SID88/gcgdata/geneseq/geneseqn/NA1988.DAT:*

10: /SID88/gcgdata/geneseq/geneseqn/NA1989.DAT:*

11: /SID88/gcgdata/geneseq/geneseqn/NA1990.DAT:*

12: /SID88/gcgdata/geneseq/geneseqn/NA1991.DAT:*

13: /SID88/gcgdata/geneseq/geneseqn/NA1992.DAT:*

14: /SID88/gcgdata/geneseq/geneseqn/NA1993.DAT:*

15: /SID88/gcgdata/geneseq/geneseqn/NA1994.DAT:*

16: /SID88/gcgdata/geneseq/geneseqn/NA1995.DAT:*

17: /SID88/gcgdata/geneseq/geneseqn/NA1996.DAT:*

18: /SID88/gcgdata/geneseq/geneseqn/NA1997.DAT:*

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21: /SID88/gcgdata/geneseq/geneseqn/NA2000.DAT:*

22: /SID88/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	19	AAV32079
2	21	95.5	22	20	AAV36624
3	21	95.5	22	20	AAV80097
4	21	95.5	22	20	AAV80102
5	21	95.5	22	20	AAV80103
6	21	95.5	22	21	AAAC64051
7	21	95.5	22	21	AAV80103
8	21	95.5	22	21	AAV80103
9	21	95.5	22	21	AAV80103
10	21	95.5	22	21	AAV80103
11	21	95.5	22	21	AAV80103

12	21	95.5	22	21	AAA38072	Immunostimulatory
13	21	95.5	22	21	AAV55876	Immunomodulatory o
14	21	95.5	22	21	AAV55880	Immunomodulatory o
15	21	95.5	22	22	AAV77040	Immunostimulatory
16	21	95.5	22	22	AAV77046	Cholera toxin immu
17	21	95.5	22	22	AAV29800	Oligonucleotide OD
18	21	95.5	22	22	AAV82107	CG motif and CFA c
19	21	95.5	22	22	AAV77047	Immunostimulatory
20	20.2	91.8	22	22	AAV55881	Immunomodulatory o
21	20	90.9	22	21	AAV32080	Nucleotide sequenc
22	19.4	88.2	22	19	AAV36625	ISS-ODN mutant DY1
23	19.4	88.2	22	20	AAV55797	Immunostimulatory
24	19.4	88.2	22	20	AAV55788	Immunostimulatory
25	19.4	88.2	22	20	AAV80105	Oligo used in expe
26	19.4	88.2	22	20	AAV80096	Immunomodulatory o
27	19.4	88.2	22	20	AAV80099	Immunomodulatory o
28	19.4	88.2	22	20	AAV80101	Immunomodulatory o
29	19.4	88.2	22	20	AAV80104	Oligo used in expe
30	19.4	88.2	22	21	AAV64052	Non-Cpg control ph
31	19.4	88.2	22	21	AAV64052	Sequence of a stab
32	19.4	88.2	22	21	AAV62524	Inactive immunosti
33	19.4	88.2	22	21	AAV14468	Immunostimulatory
34	19.4	88.2	22	21	AAV38066	Immunostimulatory
35	19.4	88.2	22	21	AAV38068	Immunostimulatory
36	19.4	88.2	22	21	AAV38070	Immunostimulatory
37	19.4	88.2	22	21	AAV55877	Immunostimulatory
38	19.4	88.2	22	22	AAV77041	Immunostimulatory
39	19.4	88.2	22	22	AAV77043	Immunostimulatory
40	19.4	88.2	22	22	AAV77045	Immunostimulatory
41	19.4	88.2	22	22	AAV55790	Immunostimulatory
42	17.8	80.9	22	20	AAV55791	Immunostimulatory
43	17.8	80.9	22	20	AAV80106	Oligo used in expe
44	17.8	80.9	22	20	AAV80106	CG motif and CFA c
45	17.8	80.9	22	22	AAV92378	

ALIGNMENTS

RESULT 1

AAV32079

ID AAV32079 standard; DNA; 22 BP.

XX

AC AAV32079;

XX

DT 09-SEP-1998 (first entry)

XX

DE Nucleotide sequence of DY1018.

XX

DY1018: beta-gal; ISS-PN/IMM; antigen; immune response; antibody;

KW immunisation; anaphylaxis; IgE; retinopathies; ss.

XX

OS synthetic.

XX

Key Location/Qualifiers

FH modified_base 1..22

FT /*tag= a

FT /*note= "phosphothioate backbone"

XX

XX WO9816247-A1.

XX

XX 23-APR-1998.

XX

XX 09-OCT-1997; 97NO-US19004.

XX

XX 11-OCT-1996; 96US-0028118.

XX

XX (REGC) UNIV CALIFORNIA.

XX

XX Carson DA, Raz E, Roman M;

XX WPI, 1998-261028/23.

XX

PT New Immunomodulatory compositions - comprising an antigen conjugated
 PT to a polynucleotide that contains an immunostimulatory sequence

XX-
 PS Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1018, which is conjugated to
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
 CC (IMM), which comprises an antigen conjugated to a polynucleotide
 CC (PN) that contains at least one immunostimulatory nucleotide sequence
 CC (ISS). The conjugate synergistically boost the magnitude of the host
 CC immune response against an antigen to a level greater than the host
 CC immune response to either the IMM, antigen or ISS-PN alone. These
 CC responses to ISS-PN/IMM conjugates are particularly acute during
 CC the important early phase of the host immune response to an antigen.
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular
 CC (Th1 type) immune responses of the host. Thus, use of the method to
 CC boost the immune responsiveness of a host to subsequent challenge by a
 CC sensitising antigen without immunisation avoids the risk of
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE
 CC production in response to the antigen challenge. The conjugates can
 CC also be used to combat pathogenic infection and to stimulate
 CC therapeutic angiogenesis to treat conditions in which localised blood
 CC flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ

Query Match 95.5%; Score 21; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 2

AAX36624
 ID AAX36624 standard; DNA; 22 BP.

XX
 AC AAX36624;

XX 09-JUL-1999 (first entry)

XX ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

XX Example 2; Page 30; 69pp; English.

XX

CC This is the ISS-ODN DY1018 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ

Query Match 95.5%; Score 21; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 3

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX
 AC AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
 CC GACGTTC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14; Mismatches 1; Indels 0; Gaps 0;
 Matches 21; Conservative 0;

OY 1 tgactgtgaangttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
 AAV80102
 ID AAV80102 standard; DNA; 22 BP.
 XX
 AC AAV80102;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 11
 FT /*tag= a
 FT /*note= "5-bromocytosine"

XX WO9855495-A2.
 XX 10-DEC-1998.
 XX 05-JUN-1998; 98WO-US11578.
 XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 23; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14; Mismatches 1; Indels 0; Gaps 0;
 Matches 21; Conservative 0;

OY 1 tgactgtgaangttcgagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
 AAV80103
 ID AAV80103 standard; DNA; 22 BP.

XX
 AC AAV80103;

XX
 DT 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 11
 FT /*tag= a
 FT /*note= "5-bromocytosine"

XX WO9855495-A2.
 XX 10-DEC-1998.
 XX 05-JUN-1998; 98WO-US11578.
 XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;
 XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

XX Claim 24; Page 30; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCCG,
 CC GACGTTCC, and GACGTTCCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 Query Match 95.5%; Score 21; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaangttcagatga 22
 Db 1 tgactgtgaacgttcagatga 22
 RESULT 6
 AAC64051
 ID AAC64051 standard; DNA; 22 BP.
 AC AAC64051;
 DT 15-FEB-2001 (first entry)
 DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
 KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
 KW enhanced antigen presentation; antigen-presenting cell; APC;
 KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
 KW vaccine; ss.
 OS Synthetic.
 PN WO200062787-A1.
 PD 26-OCT-2000.
 PP 11-APR-2000; 2000WO-US09664.
 PR 15-APR-1999; 99US-0292278.
 PA (REGC) UNIV CALIFORNIA.
 PI Raz E, Martin-Orozco E;
 DR WPI; 2000-679548/66.
 PT Enhancing antigen-presentation capabilities of T-cells for cancer
 PT immunotherapy, by contacting cells with an immunostimulatory
 PT oligonucleotide.
 PS Example 1; Page 18; 42pp; English.
 XX The invention relates to a method of inducing activation of T-cells
 CC to respond to an antigen, comprising contacting antigen-presenting cells
 CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
 CC thus treated have enhanced antigen presenting capabilities compared to
 CC antigen-activated APCs. APCs with enhanced antigen-presentation
 CC capabilities then present the antigen to T-cells. The method is useful
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell
 CC activation, and is therefore useful for treating tumours. Additionally,
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation
 CC of Fc-receptor expression, to present antigen through upregulation of
 CC major histocompatibility complex (MHC) Class I and II expression and
 CC CD1d expression, to produce co-stimulatory factors (B7 and CD40), to
 CC provide cell-to-cell adhesion through upregulation of intercellular
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
 CC cytokine production, all at levels greater than that achieved through
 CC contact of APC with antigen alone. The present sequence represents
 CC a phosphorothioate CpG ISS-ODN used in the exemplifications of the
 XX invention.
 XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 Query Match 95.5%; Score 21; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaangttcagatga 22
 Db 1 tgactgtgaacgttcagatga 22
 RESULT 7
 AAA96253
 ID AAA96253 standard; DNA; 22 BP.
 AC AAA96253;
 DT 08-FEB-2001 (first entry)
 DE Sequence of a stabilised oligonucleotide with antitumour activity.
 KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
 KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.
 OS Synthetic.
 PN WO200056342-A2.
 PD 28-SEP-2000.
 PP 17-MAR-2000; 2000WO-FR00676.
 PR 19-MAR-1999; 99FR-0003433.
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX Carpentier A;
 DR WPI; 2000-602192/57.
 PT Use of stabilised oligonucleotides as antitumor agents, particularly
 PT against nervous system tumors, have optimal activity and are not toxic
 PT .
 PS Example 2; Page 16; 57pp; French.
 CC The present sequence represents a stabilised oligonucleotide which has
 CC antitumour activity. The oligonucleotide comprises an octamer motif
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
 CC immunostimulatory, and are not toxic. They may be adapted for use in
 CC animals or humans. The stabilised oligonucleotides are used for
 CC treating tumours, of any type and any degree of anaplasia, particularly
 CC human tumours in the peripheral or central nervous systems, specifically
 CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 Query Match 95.5%; Score 21; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.14;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 tgactgtgaangttcagatga 22
 Db 1 tgactgtgaacgttcagatga 22
 RESULT 8
 AAA90458
 ID AAA90458 standard; DNA; 22 BP.
 XX AAA90458;
 AC AAA90458;

Wed Oct 10 05:59:22 2001

us-09-713-136-7.rng

XX DT 10-JAN-2001 (first entry)

XX DE CpG adjuvant oligonucleotide, SEQ ID NO:19.

XX CPg oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;

KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;

KW viral infection; bacterial infection; parasitic infection; HCV; HBV;

KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;

KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;

KW rabies virus; cholera; diphtheria; tetanus; pertussis;

KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.

XX OS Synthetic.

XX PN WO200050006-A2.

XX PD 31-AUG-2000.

XX PF 09-FEB-2000; 2000WO-US03331.

XX PR 26-FEB-1999; 99US-0121858.

XX PR 29-JUL-1999; 99US-0146391.

XX PR 28-OCT-1999; 99US-0161997.

XX CHIR) CHIRON CORP.

XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Uguzzoli M, Singh M;

PI Barackman J;

XX WPI; 2000-587123/55.

XX Microemulsion having an adsorbent surface comprising a microdroplet

PT emulsion consisting of a metabolizable oil and an emulsifying agent

PT which is a detergent, useful as a vaccine to treat bacterial, viral,

PT and parasitic infection

XX Claim 17; Page 40; 95pp; English.

XX The invention relates to a microdroplet emulsion (microemulsion) with an

CC adsorbent surface, and which comprises a metabolizable oil and an

CC emulsifying agent (a detergent). It also relates to a composition

CC comprising the microemulsion and a microparticle with an adsorbent

CC surface, where the microparticle comprises a polymer selected from a

CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a

CC polycaprolactone, a polyorthoester, a polyanhydride, and a

CC polycyanoacrylate, and a second detergent. The surface of the

CC microparticles efficiently adsorb biologically active macromolecules such

CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,

CC mediators of transcription or translation, metabolic intermediates and

CC adjuvants. Additionally, a second biologically active molecule may be

CC encapsulated within the microparticle. The microemulsion can be used in

CC methods of immunising a host animal, particularly a human, against a

CC viral, bacterial or parasitic infection, and in methods of increasing a

CC Th1 immune response. The microemulsions (having the appropriate antigens

CC adsorbed) may be particularly used as vaccines for hepatitis C virus

CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human

CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and

CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and

CC pertussis; Helicobacter pylori and Haemophilus influenzae; and

CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1

CC lymphocyte stimulating oligonucleotides containing at least one CpG motif

CC which are claimed for use as adjuvants in the compositions of the

CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Db 1 tgactgtgaacgttcgagatga 22

RESULT 9

AAAL4467

ID AAA14467 standard; DNA; 22 BP.

XX AAAL4467;

AC AAAL4467;

XX 21-AUG-2000 (first entry)

DT

XX Immunostimulatory oligonucleotide (ISS-ODN) DY1018.

DE

XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;

XX secretory immunoglobulin A production; sigA; Th1 phenotype; ds.

KW

XX Synthetic.

OS

XX WO200020039-A1.

XX PN

XX 13-APR-2000.

XX PD

XX 15-SEP-1999; 99WO-US21203.

XX PF

XX 05-OCT-1998; 98US-0167039.

XX PR

XX (REGC) UNIV CALIFORNIA.

XX PA

XX Raz E, Horner AA, Carson DA;

XX PI

XX WPI; 2000-303647/26.

XX DR

XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to

PT an antigen in a mammalian host through production of secretory

PT immunoglobulin A

PT

XX Claim 8; Page 21; 64pp; English.

PS

XX The invention relates to a method of inducing mucosal immunity to an

CC antigen in a mammalian host, including the production of secretory

CC immunoglobulin A (sigA). Immune protection in the mucosa (the principal

CC site of entry of most foreign antigens) is mediated by mucosa-associated

CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory

CC cell sub-populations. The primary immune response which characterises

CC the induction of mucosal immunity to an antigen is sigA production by

CC activated B-cells. The method comprises introducing an immunostimulatory

CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the

CC ISS-ODN includes a core nucleotide sequence. The core nucleotide

CC sequence is 5'-purine-purine-C-G-Pyrimidine-Pyrimidine-3', specific

CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A

CC specific example of an ISS-ODN is DY1018 (AAAL4467). The ISS-ODN is used

CC as an adjuvant with an antigen for stimulating mucosal immunity. The

CC level of sigA production induced in the host is at least 3 times the

CC magnitude of sigA production achievable in response to introduction of

CC antigen alone into the mucosal tissue and is equivalent or greater than

CC the magnitude of sigA production achievable in response to introduction

CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The

CC host immune response is stimulated to antigen specific IgA production,

CC biased towards the Th1 phenotype while antigen-induced IgE production is

CC avoided. The adjuvant has little or no known toxicity in mammals and its

CC efficacy is comparable to that of cholera toxin which is used as a

CC mucosal adjuvant. The present sequence represents the immunostimulatory

CC oligonucleotide DY1018.

XX

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.14;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcagatga 22

Query Match 95.5%; Score 21; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.14;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 10

AAA38065

ID AAA38065 standard; DNA; 22 BP.

XX AC AAA38065;

XX AC AAA38065;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #1.

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

XX gp120; human immunodeficiency virus; HIV; immune response; infection;

XX development; ss.

XX Synthetic.

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

XX HIV glycoprotein gp120 useful for modulating, stimulating an immune

XX response against HIV in an HIV infected individual

XX Claim 3; Page 16; 65pp; English.

XX The present invention relates to an immunostimulatory composition

XX comprising a human immunodeficiency virus (HIV) antigen, and an

XX immunostimulatory polynucleotide comprising an immunostimulatory sequence

XX (ISS). This sequence represents an ISS that can be used in the

XX composition. An immunostimulatory composition which comprises a gp120

XX conjugated to an immunostimulatory polynucleotide, or is proximately

XX associated to it and not conjugated, is used for modulating or

XX stimulating a specific immune response against gp120 in an individual by

XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

XX is also used for suppressing or delaying development of HIV infection in

XX an individual infected with HIV or an individual at risk of infection

XX with HIV, respectively. It is also used for treating an individual

XX infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.14;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAA38071

ID AAA38071 standard; DNA; 22 BP.

XX AC AAA38071;

XX AC AAA38071;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX DE Immunostimulatory sequence (ISS) #7.

DT 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;

XX gp120; human immunodeficiency virus; HIV; immune response; infection;

XX development; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 11

XX /tag- a

XX /mod_base- OTHER

XX /note- "5-Bromocytosine"

XX WO200021556-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23677.

XX 09-OCT-1998; 98US-0103733.

XX 07-OCT-1999; 99US-0415186.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

XX Anti-HIV composition comprises immunostimulatory polynucleotides and

XX HIV glycoprotein gp120 useful for modulating, stimulating an immune

XX response against HIV in an HIV infected individual

XX Disclosure; Page 17; 65pp; English.

XX The present invention relates to an immunostimulatory composition

XX comprising a human immunodeficiency virus (HIV) antigen, and an

XX immunostimulatory polynucleotide comprising an immunostimulatory sequence

XX (ISS). This sequence represents an ISS that can be used in the

XX composition. An immunostimulatory composition which comprises a gp120

XX conjugated to it and not conjugated, is used for modulating or

XX stimulating a specific immune response against gp120 in an individual by

XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It

XX is also used for suppressing or delaying development of HIV infection in

XX an individual infected with HIV or an individual at risk of infection

XX with HIV, respectively. It is also used for treating an individual

XX infected with HIV in need of immune modulation.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.14;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAA38072

ID AAA38072 standard; DNA; 22 BP.

XX AC AAA38072;

XX AC AAA38072;

XX 24-AUG-2000 (first entry)

XX Immunostimulatory sequence (ISS) #7.

XX DE Immunostimulatory sequence (ISS) #7.

Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120; gp120; human immunodeficiency virus; HIV; immune response; infection; development; ss.

Synthetic.

Key Location/Qualifiers
modified_base 11
/tag= a
/mod_base= OTHER
/note= "5-Bromocytosine"
modified_base 15
/tag= b
/mod_base= OTHER
/note= "5-Bromocytosine"

WO200021556-A1.

20-APR-2000.

08-OCT-1999; 99WO-US23677.

09-OCT-1998; 98US-010733.

07-OCT-1999; 99US-0415186.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Tighe H, Raz E, Schwartz D, Takabayashi K;

WPI; 2000-317846/27.

Anti-HIV composition comprises immunostimulatory polynucleotides and HIV glycoprotein gp120 useful for modulating, stimulating an immune response against HIV in an HIV infected individual

Disclosure; Page 17; 65pp; English.

The present invention relates to an immunostimulatory composition comprising a human immunodeficiency virus (HIV) antigen, and an immunostimulatory polynucleotide comprising an immunostimulatory sequence (ISS). This sequence represents an ISS that can be used in the composition. An immunostimulatory polynucleotide, or is proximately conjugated to it and not conjugated, is used for modulating or associating a specific immune response against gp120 in an individual by stimulating anti-gp120 antibodies or gp120 specific cytotoxic T cells. It is also used for suppressing or delaying development of HIV infection in an individual infected with HIV or an individual at risk of infection with HIV, respectively. It is also used for treating an individual infected with HIV in need of immune modulation.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 13

AAZ55876

ID AAZ55876 standard; DNA: 22 BP.

XX AAZ55876;

DT 10-APR-2000 (first entry)

XX Immunomodulatory oligonucleotide SEQ ID NO: 1.

DE

XX

Immunomodulation; immunostimulatory sequence; adjuvant; Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy; asthma; immunosuppression; ss.

Mus musculus.
OS Synthetic.

Key Location/Qualifiers
modified_base 1..22
/tag= a
/note= "Phosphorothioate linkages"
misc_feature 9..16
/tag= b
/note= "Immunostimulatory sequence (ISS)"

WO9962923-A2.

09-DEC-1999.

04-JUN-1999; 99WO-US12538.

05-JUN-1998; 98US-0088310.

01-JUN-1999; 99US-0324191.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Schwartz D;

WPI; 2000-105687/09.

Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens

Example 1; Page 35; 54pp; English.

Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory oligonucleotides comprising an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT, AGCGTC, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTCC and GACGTTCC). The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55886 contain ISSs comprising an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect; when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells). While simultaneously downregulating the Th2-type response. The Th1 response is particularly effective for control of viruses and intracellular parasites. The immunomodulatory oligonucleotides are used, particularly when formulated with an antigen or a facilitator, for modulating immune responses. Such compositions may be used in tumour therapy, in treatment of allergy (including asthma), for inducing a vigorous cellular response (against a virus, bacterium, fungus or protozoan), and also in contraceptive vaccines based on sperm antigens.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 95.5%; Score 21; DB 21; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.14;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttcgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 14

AAZ55880

ID AAZ55880 standard; DNA: 22 BP.

XX

AC

```
XX 10-APR-2000 (first entry)
XX Immunomodulatory oligonucleotide SEQ ID NO: 5.
XX
XX Immunomodulation; immunostimulatory sequence; adjuvant;
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
KW asthma; immunosuppression; 5-bromocytosine; ss.
XX
XX Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
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FT /*tag= a
FT /note= "Phosphorothioate linkages"
FT misc_feature 9..16
FT /*tag= b
FT /note= "Immunostimulatory sequence (ISS)"
FT modified_base 11
FT /*tag= c
FT /mod_base= OTHER
FT /note= "5-bromocytosine"
XX
XX WO9962923-A2.
XX
XX 09-DEC-1999.
XX
XX 04-JUN-1999; 99WO-US12538.
XX
XX 05-JUN-1998; 98US-0088310.
XX 01-JUN-1999; 99US-0324191.
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Schwartz D;
XX
XX WPI; 2000-105687/09.
XX
XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
XX response, e.g. to tumor antigens.
XX
XX Claim 30; Page 35; 54pp; English.
XX
XX Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory
XX oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
XX AACGTC, AACGTT, AGCGTC, AGCGTT, AGCGTT, GACGTC, GACGTT, GCGGTT,
XX ACAGTCC and GACGTTCC). The invention relates to oligonucleotides
XX comprising one or more ISSs, where the ISS comprises at least
XX one modified cytosine with an electron-withdrawing moiety at
XX position C-5 or C-6 of the base. Sequences AA255877 and AA255886
XX contain ISSs comprising at least one bromocytosine, whereas sequence
XX AA255876 contains an unmodified ISS. The immunomodulatory
XX oligonucleotides have an adjuvant-like effect; when formulated with an
XX antigen, the oligonucleotides stimulate production of Th1-type cytokines,
XX and induce a Th1-type immune response (activation of cytotoxic T cells),
XX while simultaneously downregulating the Th2-type response. The Th1
XX response is particularly effective for control of viruses and
XX intracellular parasites. The immunomodulatory oligonucleotides are used,
XX particularly when formulated with an antigen or a facilitator, for
XX modulating immune responses. Such compositions may be used in tumour
XX therapy, in treatment of allergy (including asthma), for inducing a
XX vigorous cellular response (against a virus, bacterium, fungus or
XX protozoan), and also in contraceptive vaccines based on sperm antigens.
XX
XX Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;
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XX Best Local Similarity 100.0%; Pred. No. 0.14;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 tgcgtggaangttcgagatga 22
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Db 1 tgcgtggaangttcgagatga 22
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RESULT 15
AAF77040
ID AAF77040 standard; DNA; 22 BP.
XX
XX AAF77040;
XX
XX 15-MAY-2001 (first entry)
XX Immunomodulatory DNA.
XX Modulate; immune; antigen; immunostimulatory; ds.
XX Synthetic.
XX WO200112223-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000WO-US22835.
XX 19-AUG-1999; 99US-0149768.
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX Van Nest G;
XX WPI; 2001-211136/21.
XX Modulating immune response to a second antigen in humans involves
XX administering an immunostimulatory polynucleotide comprising an
XX immunostimulatory sequence and a first antigen.
XX Claim 31; Page 15; 63pp; English.
XX
XX The present invention relates to modulating an immune response to
XX a second antigen in an individual, involving
XX administering to the individual an immunomodulatory polynucleotide
XX comprising an immunostimulatory sequence (ISS) and a first antigen.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
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GenCore version 4.5
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SUMMARIES

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9	21	95.5	22	1	PCT-US01-10118-1
10	21	95.5	22	1	PCT-US01-11290-1
11	21	95.5	22	1	PCT-US01-11290-2
12	21	95.5	22	1	PCT-US01-14508-1
13	21	95.5	22	1	PCT-US99-21203-19
14	21	95.5	22	13	US-08-927-120-19
15	21	95.5	22	15	US-09-167-039-19
16	21	95.5	22	16	US-09-235-742-19
17	21	95.5	22	16	US-09-298-477-2
18	21	95.5	22	16	US-09-298-477-15
19	21	95.5	22	17	US-09-308-036A-1
20	21	95.5	22	17	US-09-324-191A-1
21	21	95.5	22	17	US-09-324-191A-5
22	21	95.5	22	17	US-09-347-343-32
23	21	95.5	22	17	US-09-397-188-1
24	21	95.5	22	18	US-09-415-186-1
25	21	95.5	22	18	US-09-415-186-7
26	21	95.5	22	18	US-09-470-382-69
27	21	95.5	22	22	US-09-565-906-2
28	21	95.5	22	22	US-09-570-325-19
29	21	95.5	22	25	US-09-642-492-1
30	21	95.5	22	25	US-09-642-492-7
31	21	95.5	22	28	US-09-700-354-1
32	21	95.5	22	28	US-09-713-136-1
33	21	95.5	22	28	US-09-713-136-7
34	21	95.5	22	29	US-09-746-130-1
35	21	95.5	22	29	US-09-746-130-2
36	21	95.5	22	30	US-09-774-403-1
37	21	95.5	22	30	US-09-774-403-2
38	21	95.5	22	30	US-09-791-500-1
39	21	95.5	22	30	US-09-791-500-4
40	21	95.5	22	31	US-09-820-484-1
41	21	95.5	22	31	US-09-820-484-3
42	21	95.5	22	31	US-09-828-505-1
43	21	95.5	22	31	US-09-828-505-2
44	20.2	91.8	22	18	US-09-415-186-8
45	20.2	91.8	22	28	US-09-713-136-8

ALIGNMENTS

RESULT 1
PCT-US00-18229-32
; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR FILING DATE: 09/347,343
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32

Query Match 95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1

Query Match 95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
PCT-US00-35064-2
; Sequence 2, Application PC/TUS0035064
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; FILE REFERENCE: 06510/201W01
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant
PCT-US00-35064-2

Query Match 95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaaggttcgagatga 22

RESULT 4
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
PCT-US01-03029-1

Query Match 95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttcgagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
PCT-US01-03029-2
; Sequence 2, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi

```
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaagggttcgagatga 22

RESULT 6
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacggttcgagatga 22

RESULT 7
PCT-US01-06034-4
; Sequence 4, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-4

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaagggttcgagatga 22

RESULT 8
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacggttcgagatga 22

RESULT 9
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
```



```
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 10
PCT-US01-11290-1
; Sequence 1, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE REFERENCE: Polynucleotide Vaccines
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 11
PCT-US01-11290-2
; Sequence 2, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE REFERENCE: Polynucleotide Vaccines
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-2

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
PCT-US01-14508-1
; Sequence 1, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE REFERENCE: Methods of Use Thereof
; FILE REFERENCE: 06510/168W01
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-1

Query Match          95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||||||| |||||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
PCT-US99-21203-19
; Sequence 19, Application PC/TUS9921203
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 865 S. Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: US
; ZIP: 90017
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/21203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-892-9200
TELEFAX: 213-680-4518
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
PCT-US99-21203-19

Query Match 95.5%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 TGACTGTGAACGTTCCGAGATGA 22

RESULT 14
US-08-927-120-19
Sequence 19, Application US/08927120
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: IMMUNIZATION-FREE METHODS
FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING
INFLAMMATION IN A HOST
TITLE OF INVENTION: INFLAMMATION IN A HOST
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,120
FILING DATE: 22-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/054001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
US-08-927-120-19

Query Match 95.5%; Score 21; DB 13; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 TGACTGTGAACGTTCCGAGATGA 22

RESULT 15
US-09-167-039-19
Sequence 19, Application US/09167039
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: METHODS AND ADJUVANTS
FOR STIMULATING MUCOSAL IMMUNITY
TITLE OF INVENTION: FOR STIMULATING MUCOSAL IMMUNITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 402 West Broadway, Suite 2300
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,039
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/063001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-234-6655
TELEFAX: 619-234-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
US-09-167-039-19

Query Match 95.5%; Score 21; DB 15; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 TGACTGTGAACGTTCCGAGATGA 22

Search completed: October 9, 2001, 21:12:47
Job time: 20072 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:22 ; Search time 1391.6 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-713-136-7
Perfect score: 22
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2049885 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4099770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq1:*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	22	7 US-09-802-518-1	Sequence 1, Appli
2	21	95.5	22	7 US-09-802-518-7	Sequence 7, Appli
3	21	95.5	22	7 US-09-802-359-1	Sequence 1, Appli
4	21	95.5	22	7 US-09-802-359-7	Sequence 7, Appli
5	21	95.5	22	7 US-09-802-376-1	Sequence 1, Appli
6	21	95.5	22	7 US-09-802-376-7	Sequence 7, Appli
7	20	90.9	22	7 US-09-802-518-8	Sequence 8, Appli
8	20	90.9	22	7 US-09-802-359-8	Sequence 8, Appli
9	20	90.9	22	7 US-09-802-376-8	Sequence 8, Appli
10	19.4	88.2	22	6 US-09-770-943-1	Sequence 2, Appli
11	19.4	88.2	22	6 US-09-770-943-2	Sequence 2, Appli
12	19.4	88.2	22	6 US-09-770-943-10	Sequence 10, Appli
13	19.4	88.2	22	7 US-09-802-518-2	Sequence 2, Appli
14	19.4	88.2	22	7 US-09-802-518-4	Sequence 4, Appli
15	19.4	88.2	22	7 US-09-802-518-6	Sequence 6, Appli
16	19.4	88.2	22	7 US-09-802-518-10	Sequence 10, Appli
17	19.4	88.2	22	7 US-09-802-359-2	Sequence 2, Appli
18	19.4	88.2	22	7 US-09-802-359-4	Sequence 4, Appli
19	19.4	88.2	22	7 US-09-802-359-6	Sequence 6, Appli
20	19.4	88.2	22	7 US-09-802-359-9	Sequence 9, Appli
21	19.4	88.2	22	7 US-09-802-376-2	Sequence 2, Appli
22	19.4	88.2	22	7 US-09-802-376-4	Sequence 4, Appli
23	19.4	88.2	22	7 US-09-802-376-6	Sequence 6, Appli
24	19.4	88.2	22	7 US-09-802-376-9	Sequence 9, Appli
25	17.8	80.9	22	6 US-09-770-943-3	Sequence 3, Appli

26	17.8	80.9	22	6 US-09-770-943-4	Sequence 4, Appli
27	17.8	80.9	22	7 US-09-802-518-11	Sequence 11, Appli
28	17.8	80.9	22	7 US-09-802-359-10	Sequence 10, Appli
29	17.8	80.9	22	7 US-09-802-376-10	Sequence 10, Appli
30	16.8	76.4	442	6 US-09-836-472-216	Sequence 216, Appli
31	16.8	76.4	448	6 US-09-904-703-14097	Sequence 14097, A
32	16.8	76.4	448	6 US-09-909-627-7849	Sequence 7849, A
33	16.8	76.4	469	6 US-09-909-627-19415	Sequence 19415, A
34	16.8	76.4	606	5 US-09-921-378-10527	Sequence 10527, A
35	16.8	76.4	668	6 US-09-836-472-1014	Sequence 1014, A
36	16.8	76.4	3713	8 US-60-278-232-10258	Sequence 10258, A
37	16.8	76.4	82360	6 US-09-803-736-484	Sequence 484, App
38	16.4	74.5	24853	7 US-09-764-874-10235	Sequence 10235, A
39	16.4	74.5	32212	7 US-09-764-874-10236	Sequence 10236, A
40	16.2	73.6	22	6 US-09-770-943-7	Sequence 7, Appli
41	16.2	73.6	22	6 US-09-770-943-8	Sequence 8, Appli
42	16.2	73.6	239	7 US-09-540-213-25987	Sequence 25987, A
43	16.2	73.6	252	5 US-09-825-790-331	Sequence 331, App
44	16.2	73.6	284	7 US-09-540-213-29122	Sequence 29122, A
45	16.2	73.6	445	6 US-09-909-629-31699	Sequence 31699, A

ALIGNMENTS

RESULT 1
US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||||| |||||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 2
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 3
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-7
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 5
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match          95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaacgttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7
```

Query Match 95.5%; Score 21; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 7
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 8
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.65;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 9
US-09-802-376-8
; Sequence 8, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.65;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22
Db 1 tgactgtgaangttcgagatga 22

RESULT 10
US-09-770-943-1
; Sequence 1, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-1

Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttcgagatga 22

```
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 11
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttcgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 12
US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10

Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttcgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 13
US-09-802-518-2
; Sequence 2, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-2

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 14
US-09-802-518-4
; Sequence 4, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-4

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgaccgtgaacgttcgagatga 22

RESULT 15
US-09-802-518-6
; Sequence 6, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
```

Wed Oct 10 05:59:25 2001

; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE

; FILE REFERENCE: SEQUENCES

; CURRENT APPLICATION NUMBER: US/09/802,518

; CURRENT FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: 60/188,556

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G

; NAME/KEY: misc-feature

; LOCATION: (1)...(22)

; OTHER INFORMATION: n = 5-bromocytosine

; US-09-802-518-6

Query Match 88.2%; Score 19.4; DB 7; Length 22;

Best Local Similarity 95.5%; Pred. No. 1.3;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy .1 tgactgtgaangttcgagatga 22

|||||

Db .1 tgactgtgaangttccagatga 22

Search completed: October 9, 2001, 21:36:22

Job time: 21242 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:08 : Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

Title: US-09-713-136-7

Perfect score: 22
Sequence: 1 tgactgtgaangttcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:**

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	88.2	22	4	US-09-092-314-1
2	19.4	88.2	22	4	US-09-092-314-2
3	19.4	88.2	22	4	US-09-092-314-10
4	17.8	80.9	22	4	US-09-092-314-3
5	17.8	80.9	22	4	US-09-092-314-4
6	16.2	73.6	22	4	US-09-092-314-7
7	16.2	73.6	22	4	US-09-092-314-8
8	15.8	71.8	1892	2	US-08-933-750C-66
9	15.8	71.8	1892	3	US-09-234-613-66
10	15.8	71.8	6638	2	US-08-070-301-2
11	15.2	69.1	913	2	US-08-975-316-61
12	15.2	69.1	2694	3	US-08-975-703-5
13	15.2	69.1	2694	4	US-09-515-884-5
14	14.8	67.3	864	4	US-08-998-416-297
15	14.8	67.3	1166	1	US-08-121-083-7
16	14.6	66.4	22	4	US-09-092-314-5
17	14.6	66.4	95	5	PCT-US96-09455A-258
18	14.6	66.4	1418	1	US-08-391-615-7
19	14.6	66.4	1830	4	US-09-019-931-2
20	14.6	66.4	2505	1	US-08-391-615-1
21	14.6	66.4	2971	1	US-07-718-575-7
22	14.6	66.4	2971	1	US-08-481-206-7
23	14.6	66.4	2971	2	US-08-486-269A-7
24	14.6	66.4	6909	2	US-08-804-196-1
25	14.6	66.4	6909	2	US-08-658-340-1
26	14.6	66.4	6909	3	US-08-746-111-26
27	14.2	64.5	588	3	US-08-965-904B-1

Sequence 5, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 12, Appli
Sequence 4, Appli
Sequence 10, Appli
Sequence 16, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 24, Appli
Sequence 7, Appli

28 14.2 64.5 618 1 US-08-155-171B-5
29 14.2 64.5 618 2 US-08-435-998-5
30 14.2 64.5 773 3 US-08-934-131-2
31 14 63.6 8543 3 US-08-496-944-1
32 13.8 62.7 36 4 US-09-386-607-6
33 13.8 62.7 492 3 US-08-729-416C-12
34 13.8 62.7 882 1 US-08-622-354-4
35 13.8 62.7 1425 3 US-08-729-416C-10
36 13.8 62.7 1785 3 US-08-729-416C-16
37 13.8 62.7 1876 3 US-08-714-918-33
38 13.8 62.7 1876 4 US-09-365-315-33
39 13.8 62.7 1876 4 US-09-365-315-33
40 13.8 62.7 1876 4 US-09-366-417-33
41 13.8 62.7 2333 1 US-08-392-678-33
42 13.8 62.7 2334 1 US-08-457-304A-33
43 13.8 62.7 2334 1 US-08-456-701A-33
44 13.8 62.7 3456 1 US-08-190-687B-24
45 13.8 62.7 4307 1 US-08-190-687B-7

ALIGNMENTS

RESULT 1
US-09-092-314-1
Sequence 1, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048.794
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match 88.2%; Score 19.4; DB 4; Length 22;

Best Local Similarity 90.9%; Pred No. 0.099; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0;

Qy 1 tgactgtgaangttcgagatga 22
|||||
Db 1 tgactgtgaagtttagagatga 22

RESULT 2
US-09-092-314-2
Sequence 2, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048.794
PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 4
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 0.68;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 6
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173051
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-092-314-7

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||||| | | | | | | | |
Db 1 tgactgtgagggtcagagatga 22

RESULT 7
US-09-092-314-8
Sequence 8, Application US/09092314
Patent No. 6225292
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
APPLICANT: Roman, Mark
TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
TITLE OF INVENTION: Sequence Activity
Patent No. 6225292
FILE REFERENCE: 6510-173US1
CURRENT APPLICATION NUMBER: US/09/092.314
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,794
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-092-314-8

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagatga 22
||||||| | | | | | | | |
Db 1 tgactgtgagggtcagagatga 22

RESULT 8
US-08-933-750C-66/c
Sequence 66, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT03
CLONE: 641127
US-08-933-750C-66

Query Match 71.8%; Score 15.8; DB 2; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
||||||| | | | | | | | |
Db 1278 TGAATGTGAAGGTCGAGCT 1259

RESULT 9
US-09-234-613-66/c
Sequence 66, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-09-234-613-66

Query Match 71.8%; Score 15.8; DB 3; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
||| ||||| ||||| |||
Db 1278 TGAATGTGAAGGTTGCGAGCT 1259

RESULT 10
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Onji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; APPLICATION NUMBER: JP 2-106412
;

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127
; US-09-234-613-66

Query Match 71.8%; Score 15.8; DB 3; Length 1892;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttcgagat 20
||| ||||| ||||| |||
Db 1278 TGAATGTGAAGGTTGCGAGCT 1259

RESULT 10
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KAMINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Onji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; APPLICATION NUMBER: JP 2-106412
;

; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Horse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11...3070
; US-08-070-301-2

Query Match 71.8%; Score 15.8; DB 2; Length 6638;
Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaangttcgagatg 21
||||| ||| |||||
Db 2380 GACTGTGTATGTTGGAGATG 2399

RESULT 11
US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:

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; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-975-316-61
Query Match          69.1%; Score 15.2; DB 2; Length 913;
Best Local Similarity 81.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
||||| ||| ||| ||| |||
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 12
US-08-975-703-5
; Sequence 5, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,703
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2691
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-975-703-5
Query Match          69.1%; Score 15.2; DB 3; Length 2694;
Best Local Similarity 81.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGTGAATGTTTAGATGA 1805

US-09-515-884-5
; Sequence 5, Application US/09515884
; Patent No. 6235263
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,884
; FILING DATE: 29-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,703
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2691
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-515-884-5
Query Match          69.1%; Score 15.2; DB 4; Length 2694;
Best Local Similarity 81.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttcgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGTGAATGTTTAGATGA 1805
```

RESULT 14
US-08-998-416-297/c
; Sequence 297, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgin
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/GC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1245UP
US-08-998-416-297

Query Match 67.3%; Score 14.8; DB 4; Length 864;
Best Local Similarity 84.2%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 ctgtgaangttcagatga 22
||||| ||||| |||
Db 191 CTGTGAATGATCGAGTTGA 173

RESULT 15
US-08-121-063-7
; Sequence 7, Application US/08121063
; Patent No. 5446143
; GENERAL INFORMATION:
; APPLICANT: Simpson, Evan R.
; APPLICANT: Mahendroo, Mala
; APPLICANT: Mendelson, Carole R.
; TITLE OF INVENTION: Adipose-Specific Promoter Regions of
; TITLE OF INVENTION: Human Aromatase Cytochrome P450 gene
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,063
; FILING DATE: 14-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: UTSD:351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-121-063-7

Query Match 67.3%; Score 14.8; DB 1; Length 1166;
Best Local Similarity 84.2%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ctgtgaangttcagatga 22
||||| ||||| |||
Db 525 CTGTGAAGTTCAGAGA 543

Search completed: October 9, 2001, 15:42:09
Job time: 299 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:28 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-8
Perfect score: 22
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_bal: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
7: gb_om: *
8: gb_ov: *
9: gb_pat1: *
10: gb_pat2: *
11: gb_ph: *
12: gb_pl1: *
13: gb_pl2: *
14: gb_pl3: *
15: gb_pl4: *
16: em_bal: *
17: em_ba2: *
18: em_fun: *
19: em_htgo_hum: *
20: em_htgo_inv: *
21: em_htgo_rod: *
22: em_htg_hum1: *
23: em_htg_hum2: *
24: em_htg_hum3: *
25: em_htg_hum4: *
26: em_htg_hum5: *
27: em_htg_hum6: *
28: em_htg_hum7: *
29: em_htg_hum8: *
30: em_htg_inv1: *
31: em_htg_inv2: *
32: em_htg_other: *
33: em_htg_rod: *
34: em_hum1: *
35: em_hum2: *
36: em_hum3: *
37: em_hum4: *
38: em_hum5: *
39: em_hum6: *
40: em_hum7: *
41: em_in: *
42: em_om: *
43: em_or: *

44: em_ov: *
45: em_pat: *
46: em_ph: *
47: em_pl: *
48: em_ro: *
49: em_sts: *
50: em_sy: *
51: em_un: *
52: em_vl: *
53: gb_sts1: *
54: gb_sts2: *
55: gb_sts3: *
56: gb_sy: *
57: gb_un: *
58: gb_vl: *
59: gb_vl2: *
60: gb_htg1: *
61: gb_htg2: *
62: gb_htg3: *
63: gb_htg4: *
64: gb_htg5: *
65: gb_htg6: *
66: gb_htg7: *
67: gb_htg8: *
68: gb_htg9: *
69: gb_htg10: *
70: gb_htg11: *
71: gb_htg12: *
72: gb_htg13: *
73: gb_htg14: *
74: gb_htg15: *
75: gb_htg16: *
76: gb_htg17: *
77: gb_htg18: *
78: gb_htg19: *
79: gb_htg20: *
80: gb_htg21: *
81: gb_htg22: *
82: gb_htg23: *
83: gb_htg24: *
84: gb_htg25: *
85: gb_pr1: *
86: gb_pr2: *
87: gb_pr3: *
88: gb_pr4: *
89: gb_pr5: *
90: gb_pr6: *
91: gb_pr7: *
92: gb_pr8: *
93: gb_pr9: *
94: gb_rol: *
95: gb_rod: *
96: gb_in4: *
97: gb_pr10: *
98: em_ba3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	91.8	22	9	AX036945 Sequence
2	20.2	91.8	22	9	AX046993 Sequence
3	20.2	91.8	22	10	AX083675 Sequence
4	20.2	91.8	22	10	AX083681 Sequence
5	20	90.9	22	10	AX083682 Sequence
6	19.4	88.2	22	9	AX036944 Sequence
7	19.2	87.3	165337	70	AC027442 Homo sapi
8	19.2	87.3	209777	69	AC024934 Homo sapi

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9 18.6 84.5 22 9 AX036946
10 18.6 84.5 22 10 AX083676
11 18.6 84.5 22 10 AX083678
12 18.6 84.5 22 10 AX083680
13 18.6 84.5 12545 6 CEP42610
14 17.8 80.9 22 9 AX036952
15 17.6 80.0 49523 90 AL358135
16 17.6 80.0 85535 65 AX019557
17 17.6 80.0 85654 81 AL513169
18 17.6 80.0 90287 61 AC010018
19 17.6 80.0 122854 80 AC087581
20 17.6 80.0 139032 87 AC010656
21 17.6 80.0 140907 90 AL162499
22 17.6 80.0 145939 79 AL158143
23 17.6 80.0 152842 73 AC067921
24 17.6 80.0 168247 85 AC005014
25 17.6 80.0 172346 64 AC016349
26 17.6 80.0 178353 62 AC012334
27 17.6 80.0 182703 74 AC073117
28 17.6 80.0 304633 4 AE003477
29 17.4 79.1 183869 73 AC068700
30 17.2 78.2 42726 5 CBRG45N02
31 17 77.3 552 14 RCSINE04
32 17 77.3 2234 89 AK023935
33 17 77.3 32919 83 CER37L19
34 17 77.3 35503 6 CEM09D6
35 17 77.3 36949 77 AC087340
36 17 77.3 63807 77 AC087299
37 17 77.3 140530 76 AC079837
38 17 77.3 143747 92 HS370M22
39 17 77.3 144778 84 CNS07EFR
40 17 77.3 148170 76 AC087821
41 17 77.3 153019 76 AC079323
42 17 77.3 155323 22 AC009824
43 17 77.3 156375 83 AP002859
44 17 77.3 159485 62 AC012435
45 17 77.3 160437 79 AL355805

ALIGNMENTS

RESULT 1
LOCUS AX036945 22 bp DNA
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR).
FEATURES
source
Location/Qualifiers
1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
6 t
3 c
7 g
6 t

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 91.8%; Score 20.2; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 3.3;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 4
LOCUS AX083681 22 bp DNA
DEFINITION Sequence 7 from Patent WO0112223.

```


[illegible]

Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L8145
 Center clone name: 439_K_16
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 149010 bases at least Q40
 Consensus quality: 157303 bases at least Q30
 Consensus quality: 160828 bases at least Q20
 Insert size: 170000; agarose-fp
 Insert size: 162337; sum-of-contigs
 Quality coverage: 3.6 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 31 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1105: contig of 1105 bp in length
 * 1106 1205: gap of 100 bp
 * 1206 2479: contig of 1274 bp in length
 * 2480 2579: gap of 100 bp
 * 2580 4311: contig of 1632 bp in length
 * 4212 4311: gap of 100 bp
 * 4312 5781: contig of 1470 bp in length
 * 5782 5881: gap of 100 bp
 * 5882 7830: contig of 1949 bp in length
 * 7831 7930: gap of 100 bp
 * 7931 9913: contig of 1983 bp in length
 * 9914 10013: gap of 100 bp
 * 10014 12486: contig of 2473 bp in length
 * 12487 12586: gap of 100 bp
 * 12587 15592: contig of 3006 bp in length
 * 15593 15692: gap of 100 bp
 * 15693 19721: contig of 4029 bp in length
 * 19722 19821: gap of 100 bp
 * 19822 23369: contig of 3448 bp in length
 * 23370 23369: gap of 100 bp
 * 23370 26785: contig of 3416 bp in length
 * 26786 26885: gap of 100 bp
 * 26886 30363: contig of 3478 bp in length
 * 30364 30463: gap of 100 bp
 * 30464 33964: contig of 3501 bp in length
 * 33965 34064: gap of 100 bp
 * 34065 37794: contig of 3730 bp in length
 * 37795 37894: gap of 100 bp
 * 37895 43354: contig of 5460 bp in length
 * 43355 43454: gap of 100 bp
 * 43455 47839: contig of 4385 bp in length
 * 47840 47939: gap of 100 bp
 * 47940 53326: contig of 5387 bp in length
 * 53327 53426: gap of 100 bp
 * 53427 58576: contig of 5150 bp in length
 * 58577 58676: gap of 100 bp
 * 58677 64554: contig of 5878 bp in length
 * 64555 64654: gap of 100 bp
 * 64655 68538: contig of 3884 bp in length
 * 68539 68639: gap of 100 bp
 * 68639 74650: contig of 6012 bp in length
 * 74651 74750: gap of 100 bp
 * 74751 80037: contig of 5287 bp in length

* 80038 80137: gap of 100 bp
 * 80138 85646: contig of 5509 bp in length
 * 85647 85746: gap of 100 bp
 * 85747 92718: contig of 6972 bp in length
 * 92719 92818: gap of 100 bp
 * 92819 101098: contig of 8280 bp in length
 * 101099 101198: gap of 100 bp
 * 101199 108560: contig of 7362 bp in length
 * 108561 108660: gap of 100 bp
 * 108661 118118: contig of 9458 bp in length
 * 118119 118218: gap of 100 bp
 * 118219 128612: contig of 10394 bp in length
 * 128613 128712: gap of 100 bp
 * 128713 139860: contig of 11148 bp in length
 * 139861 139960: gap of 100 bp
 * 139961 151029: contig of 11069 bp in length
 * 151030 151129: gap of 100 bp
 * 151130 165337: contig of 14208 bp in length.
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 1..165337
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="RP11-439K16"
 /clone_lib="RPC1-11 Human Male BAC"
 1..1105
 /note="assembly_fragment"
 1206..2479
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 2580..4211
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 4312..5781
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 5882..7830
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 19822..23369
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 34065..37794
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 /note="assembly_fragment"
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 47940..53326
 /note="assembly_fragment"
 53427..58576
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 58677..64554
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 74751..80037
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BASE COUNT      65720 a 39190 c 38969 g 64529 t 1369 others
ORIGIN

Query Match      87.3%; Score 19.2; DB 69; Length 209777;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 gactgtgaangttbgagatga 22
||||| ||||| ||||| ||||| |||||
Db  76399 GACTGTGAAGTTTGAGATGA 76419

RESULT 9
AX036946
LOCUS      AX036946      22 bp      DNA
DEFINITION Sequence 3 from Patent FR2790955.
ACCESSION  AX036946
VERSION     AX036946.1 GI:11226374
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Carpentier,A.
JOURNAL     Patent: FR 2790955-A 3 22-SEP-2000;
            ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES   Location/Qualifiers
            source
            1..22
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            /db_xref="taxon:32630"
            /note="oligodesoxynucleotide"
BASE COUNT      6 a 4 c 6 g 6 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

RESULT 10
AX03676
LOCUS      AX03676      22 bp      DNA
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION  AX03676
VERSION     AX03676.1 GI:13185408
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 22)
AUTHORS     van Nest,G.
JOURNAL     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
            Patent: WO 0112223-A 2 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic construct"
BASE COUNT      6 a 4 c 7 g 5 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

RESULT 12
AX03680
LOCUS      AX03680      22 bp      DNA
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION  AX03680
VERSION     AX03680.1 GI:13185412
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 22)
AUTHORS     van Nest,G.
JOURNAL     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
            Patent: WO 0112223-A 6 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="5-bromocytosine"
            /mod_base=OTHER
BASE COUNT      6 a 3 c 6 g 6 t 1 others
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACCGTGAACGTTCCAGATGA 22

RESULT 11
AX083678
LOCUS      AX083678      22 bp      DNA
DEFINITION Sequence 4 from Patent WO0112223.
ACCESSION  AX083678
VERSION     AX083678.1 GI:13185410
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 22)
AUTHORS     van Nest,G.
JOURNAL     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
            Patent: WO 0112223-A 4 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic construct"
BASE COUNT      6 a 4 c 6 g 6 t
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

RESULT 12
AX083680
LOCUS      AX083680      22 bp      DNA
DEFINITION Sequence 6 from Patent WO0112223.
ACCESSION  AX083680
VERSION     AX083680.1 GI:13185412
KEYWORDS   synthetic construct.
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 22)
AUTHORS     van Nest,G.
JOURNAL     Methods of modulating an immune response using immunostimulatory s
            equences and compositions for use therein
            Patent: WO 0112223-A 6 22-FEB-2001;
            Dynavax Technologies Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="5-bromocytosine"
            /mod_base=OTHER
BASE COUNT      6 a 3 c 6 g 6 t 1 others
ORIGIN

Query Match      84.5%; Score 18.6; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 tgactgtgaangttbgagatga 22
||||| ||||| ||||| |||||
Db  1 TGACTGTGAACGTTCCAGATGA 22

```

|||||TGACTGTGAAGTTCCAGATGA 22

Db 1

RESULT 13

CEFA2G10/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CEFA2G10 12545 bp DNA INV 25-OCT-2000

Caenorhabditis elegans cosmid F42G10, complete sequence.

248230

248230.1 GI:668329

HTG: Arg-tRNA; Mitogen activated protein kinase; Transfer RNA.

Caenorhabditis elegans.

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 12545)

none.

Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium

Science 282 (5396), 2012-2018 (1998)

95069613

The C.elegans Sequencing Consortium.

Erratum: [[published errata appear in Science 1999 Jan 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep 3;285(5433):1493]]

2 (bases 1 to 12545)

Harris,B.R.

Direct Submission

Submitted (12-FEB-1995) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rvnematode.wustl.edu

Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone F42G10. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F42G10 is at 9861 in sequence 248006.

The true right end of clone F42G10 is at 102 in sequence 295122.

The true right end of clone F19C6 is at 104 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence 248006.

The end of this sequence (12448..12545) overlaps with the start of sequence 295122.

For a graphical representation of this sequence and its analysis see: - <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=F42G10>.

Location/Qualifiers

1..12545

/organism="Caenorhabditis elegans"

/db_xref="taxon:6239"

/chromosome="X"

/clone="F42G10"

complement(join(1923..1983,2244..2767,2819..2932,3209..3352,3396..3609,3875..4179,4227..4404,4451..4488,4533..4658,5035..5087,5537..5600))

/gene="F42G10.1"

complement(join(1923..1983,2244..2767,2819..2932,3209..3352,3396..3609,3875..4179,4227..4404,4451..4488,4533..4658,5035..5087,5537..5600))

/gene="F42G10.1"

/note="contains similarity to Pfam domain: PF01431 (Peptidase family M13, Score=215.9, E-value=2e-61, N=1)

CDNA EST yk24a6.5 comes from this gene"

/codon_start=1

/protein_id="CAA88262.1"

/db_xref="GI:3877041"

/db_xref="SPTREMBL:Q09393"

/translation="MKLYFLSPALWAVFGNGDOVILRLKHSCTFTVGVQHAQKLSLSEHPICNNEYETICHKNITRVSRLDRVAMEVSDDDIDQYEVVPHASNKQRLWQSVNPDIVSKWLVQFNTYKGVGNWNEHQKHESFLNLDAHEKYKNLENSEFEGYDFOILLTKFYKSLKLSVEYLTELKIPISRNHFYHGLFDEIRDIHILNITRMSKFSKDRKNELIENVRNLIKIIPEYLEYNDKVKVRDAKTAYEKEYRLKIMIEPNLSPILVDDKIIIRVAANPAMEIFEKYITSTSRVDFQHITAAASGLSFNYQNDIHISVFTMENPIADPKSVYDOFLYVLCHLOHVIYVNAQKTSDOEIRDTVERSARECTKNRNLHNPLDVSINVAASEMPTVAGLRMLLYVAPENYCKTLNMDIDVEYKSKQK TENDDLFLVLTFMVDLEDTAVFNSLYNCKPGDMRYAPENYCKTLNMDIDVEYKSKQK TENDDLFLVLTFMVDLEDTAVELDAANITTFEGLFEDITVEEVEEESKEGSAESSSSSESSSESSSESSVERELDEVSDGUDDSENTELKSEIATSRSSFIWPAFTVFTLLIKYIKF"

complement(2120..2192)

/gene="F42G10.tl"

/note="ACG Arg R-tRNA

predicted using tRNAscan-SE-1.11

preliminary prediction

similar to tRNA-Arg

complement(2120..2192)

/gene="F42G10.tl"

join(11556..11680,11734..11893,11938..12060,12174..12293,12340..12519,295122.1:325..393,295122.1:438..503,295122.1:554..639,295122.1:694..759,295122.1:809..905)

/gene="F42G10.2"

join(11556..11680,11734..11893,11938..12060,12174..12293,12340..12519,295122.1:325..393,295122.1:438..503,295122.1:554..639,295122.1:694..759,295122.1:809..905)

/gene="F42G10.2"

/note="contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=196.8, E-value=1.1e-55, N=1"

/codon_start=1

/protein_id="CAA88264.1"

/db_xref="GI:3877043"

/db_xref="SWISS-PROT:Q20347"

/translation="MVQEDDENLRNMSLRPTSLSTRPTSLVNGNEKTLPEESVLRSLSQTKYDPDEHLYTFSSALADLGAINGNFTVYKMRKTKGLIAVKRIRCNRI GHREQLRLLEHDTIVKSEGNIVKFGALFSEGDCWICMELMDISMLLYKRVYVKNRNLNENYVGHITVCTVDALDYLLKDIHRDVKPSNILLVDGTGAVKLCDFGICGO LEESFARKHDAGCQYLAPEIRTSDDIKYRSDVNSLGLITLYELATGKFPYQMSNLSL DQIATVVGDPPIIHPDSDDFHYSLPKFNTCLTKDRHRPRKYDTLAKSDFRYIYA VAGTEAEAKRILGVEADIRNHPVDHRG"

join(complement(1308..1367),complement(1111..1227),complement(851..1066),complement(502..803),complement(268..327),complement(105),complement(248006.1:36284..36493),complement(248006.1:36093..36239),complement(248006.1:35772..35885),complement(248006.1:35359..35355),complement(248006.1:35174..35317))

/gene="F19C6.4"

/note="contains similarity to Pfam domain: PF01431 (Peptidase family M13), Score=268.8, E-value=2.4e-77, N=1"

/codon_start=1

/protein_id="CAA88263.1"

/db_xref="GI:3877042"

/db_xref="SPTREMBL:Q09539"

/translation="MKGFIFIVLTIVTSQSFHKSIDISKSPCNDYDYVCAKDRSISNLTFTKMOLEILKPNVTIENNGTFLADKIVKTRVMKCTEIEVLTGFTVFDYFGDLHSEKMTIHSRYTAVSVRLKEINTMANIFYNALHANTEIQQMEIPISSKNKFLHLFNTLKTNAIIELETTTISEAKSKMKGIEMSKYVFAFYFNITVYKAKLVITYEYRLKLSLSPKPPKNNLHIFIQNLNMRVRLTNPIAEKILRIGAIASMTLPAKTISEYDITRFLFOAIVANPANDGFQYLNHNTITVITNDLNOPEKAIDTFTVETHEIMHRVYVYCNFLNNSVNTVAQCARREYQMLGDTDAVKPIISGFWKNKVDVWVNIAMRMVTKMIIKSTNEKOLKEALTIVGLGCKSEKRNELIPIHNPILSLCAVRQYLFKTLIYCGRIDRMEFAKHEEFCCKPGDDVKVEDYAVKSSSKADKVGKFKLLAKTSKSNFTYGI"

join(complement(1308..1367),complement(1111..1227),complement(851..1066),complement(502..803),complement(268..327),complement(105),complement(248006.1:36284..36493),complement(248006.1:36093..36239),complement(248006.1:35772..35885),complement(248006.1:35359..35355),complement(248006.1:35174..35317))

/gene="F19C6.4"

/note="contains similarity to Pfam domain: PF01431 (Peptidase family M13), Score=268.8, E-value=2.4e-77, N=1"

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join(complement(1308..1367),complement(1111..1227),complement(851..1066),complement(502..803),complement(268..327),complement(105),complement(248006.1:36284..36493),complement(248006.1:36093..36239),complement(248006.1:3577

complement(268...327),complement(105),
complement(248006.1:36284...36493),
complement(248006.1:36093...36239),
complement(248006.1:35772...35885),
complement(248006.1:35359...35535),
complement(248006.1:35174...35317))
/gene="P19C6.4"

BASE COUNT 4001 a 2110 c 2008 g 4426 t
ORIGIN

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Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
||||||| || ||||| |||||
Db 10445 TGACTGTCAAAGTTGGAGATGA 10424

RESULT 14
AX036952 AX036952 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier A.
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
ASSIST PUBL HOPIAUX DE PARIS (FR)

FEATURES
Location/Qualifiers
1..22

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repeat_region /clone_lib="RPC1-11.2"
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repeat_region /note="AluSp repeat: matches 1..299 of consensus"
repeat_region 1931..1969
repeat_region /note="L2 repeat: matches 2653..2691 of consensus"
repeat_region 2097..2579
repeat_region /note="L2 repeat: matches 2244..2749 of consensus"
repeat_region 2652..3105
repeat_region /note="L2 repeat: matches 1154..1657 of consensus"
repeat_region 3143..3311
repeat_region /note="FAM repeat: matches 1..169 of consensus"
repeat_region 4123..4178
repeat_region /note="L2 repeat: matches 2686..2744 of consensus"
repeat_region 5710..5802
repeat_region /note="3 copies 31 mer 77% conserved"
repeat_region 6442..6736
repeat_region /note="AluY repeat: matches 1..295 of consensus"
repeat_region 6797..6887
repeat_region /note="L2 repeat: matches 2611..2710 of consensus"
repeat_region 8158..8475
repeat_region /note="AluJb repeat: matches 1..312 of consensus"
repeat_region 8562..8866
repeat_region /note="AluSq repeat: matches 1..306 of consensus"
repeat_region 8890..9040
repeat_region /note="MIR repeat: matches 20..180 of consensus"
repeat_region 9448..9784
repeat_region /note="L2 repeat: matches 1155..1516 of consensus"
repeat_region 9802..10111
repeat_region /note="AluX repeat: matches 1..310 of consensus"
repeat_region 11283..11446
repeat_region /note="MER20 repeat: matches 1..175 of consensus"
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repeat_region 13965..14267
repeat_region /note="AluY repeat: matches 1..309 of consensus"
repeat_region 15875..15916
repeat_region /note="7 copies 6 mer tggtg 81% conserved"
repeat_region 15876..15913
repeat_region /note="19 copies 2 mer gt 84% conserved"

BASE COUNT 7 a 2 c 6 g 7 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
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Db 1 TGACTGTGAACGTTATAGATGA 22

RESULT 15
ALJ58135 49523 bp DNA PRI 02-FEB-2001
LOCUS Human DNA sequence from clone RP11-342L7 on chromosome 6, complete
DEFINITION sequence.
ACCESSION ALJ58135
VERSION ALJ58135.19 GI:12666263
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49523)
Donnelly, S.
Direct Submission
Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 5, 2001 this sequence version replaced gi:12657153.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TrEMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-342L7 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

FEATURES

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/clone_lib="RPC1-11.2"
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1931..1969
/note="L2 repeat: matches 2653..2691 of consensus"
2097..2579
/note="L2 repeat: matches 2244..2749 of consensus"
2652..3105
/note="L2 repeat: matches 1154..1657 of consensus"
3143..3311
/note="FAM repeat: matches 1..169 of consensus"
4123..4178
/note="L2 repeat: matches 2686..2744 of consensus"
5710..5802
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6442..6736
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6797..6887
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8158..8475
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8562..8866
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8890..9040
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9448..9784
/note="L2 repeat: matches 1155..1516 of consensus"
9802..10111
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11283..11446
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13965..14267
/note="AluY repeat: matches 1..309 of consensus"
15875..15916
/note="7 copies 6 mer tggtg 81% conserved"
15876..15913
/note="19 copies 2 mer gt 84% conserved"

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/Note="19 copies 2 mer tg 92% conserved"
repeat_region 16900..16935
/Note="6 copies 6 mer tgtgtg 94% conserved"
repeat_region 17375..17451
/Note="L2 repeat: matches 2632..2710 of consensus"
repeat_region 17509..17674
/Note="Alusg/x repeat: matches 138..303 of consensus"
repeat_region 19709..20783
/Note="L2 repeat: matches 1509..2603 of consensus"
repeat_region 20892..20974
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repeat_region 21159..21200
/Note="21 copies 2 mer tg 88% conserved"
repeat_region 21408..21567
/Note="Alusg/x repeat: matches 150..312 of consensus"
repeat_region 23613..23660
/Note="24 copies 2 mer ct 83% conserved"
repeat_region 25953..26068
/Note="L2 repeat: matches 2579..2710 of consensus"
repeat_region 26244..26561
/Note="L2 repeat: matches 2159..2493 of consensus"
repeat_region 27715..28031
/Note="Alusg repeat: matches 1..313 of consensus"
repeat_region 28163..28258
/Note="16 copies 6 mer atgtat 71% conserved"
repeat_region 28186..28227
/Note="21 copies 2 mer tg 85% conserved"
repeat_region 28795..28921
/Note="L2 repeat: matches 2576..2699 of consensus"
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repeat_region 30241..30587
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repeat_region 30597..31061
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repeat_region 31062..31233
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repeat_region 32217..32252
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repeat_region 32219..32254
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repeat_region 32619..32694
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misc_feature 33954..34091
/Note="Sequence confirmed by AC067921 sequenced by WBR."
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repeat_region 35978..36189
/Note="L1PB3 repeat: matches 5937..6150 of consensus"
repeat_region 36261..36338
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repeat_region 36830..36891
/Note="MIR repeat: matches 59..121 of consensus"
repeat_region 38837..39104
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repeat_region 39152..39582
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repeat_region 40034..40329
/Note="L2 repeat: matches 2379..2667 of consensus"
repeat_region 40452..40678
/Note="MIR repeat: matches 12..260 of consensus"
repeat_region 42418..42477
/Note="10 copies 6 mer atttat 73% conserved"
repeat_region 44917..45015
/Note="MERSA repeat: matches 78..184 of consensus"
repeat_region 45285..45898
/Note="L2 repeat: matches 2124..2710 of consensus"
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/Note="AluJb repeat: matches 2..301 of consensus"
BASE COUNT 13888 a 9541 c 10167 g 15927 t
ORIGIN

```

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Query Match      80.0%; Score 17.6; DB 90; Length 49523;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbaggatg 21
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Db 17245 TGACTGTGAATGTTGAGATG 17265

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Search completed: October 9, 2001, 16:20:40
Job time: 2610 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17.8	80.9	463	107	AU083559	AU083559 AU083559
2	17.8	80.9	479	107	AU089685	AU089685 AU089685
3	17.6	80.0	527	149	BF487041	BF487041 AT21713.5
4	17.6	80.0	548	228	AQ397925	AQ397925 mgxb0008L
5	17.6	80.0	612	32	AV653619	AV653619 AV653619
6	17.7	77.3	63	243	AZ431742	AZ431742 IM0216018
7	17.7	77.3	118	256	B79766	B79766 CIT-NSP-205
8	17.7	77.3	290	124	BB068341	BB068341 BB068341
9	17.7	77.3	343	7	AA438163	AA438163 ve64f06.r
10	17.7	77.3	374	226	AQ245026	AQ245026 HS.2056_B
11	17.7	77.3	471	113	AW270792	AW270792 xp54b05.x
12	17.7	77.3	493	150	BF563081	BF563081 UI-R-B01-
13	17.7	77.3	514	117	AW526035	AW526035 UI-R-B01-
14	17.7	77.3	525	171	BF954072	BF954072 QV2-NN004
15	17.7	77.3	592	244	AZ460464	AZ460464 IM0265L18
16	17.7	77.3	614	244	AZ460101	AZ460101 IM0265L18
17	17.7	77.3	665	249	AZ759002	AZ759002 IM0551114
18	17.7	77.3	697	174	BG138405	BG138405 EST478847
19	17.7	77.3	972	222	CNS05PD9	AL347814 Tetraodon
20	17.7	77.3	1043	220	CNS05J4W	AL199769 Tetraodon
21	16.8	76.4	398	167	BE428418	BE428418 MTD006.G1
22	16.8	76.4	474	167	BE419241	BE419241 WWR021.G5
23	16.8	76.4	477	149	BF475131	BF475131 WHE2111_B
24	16.8	76.4	561	249	AZ755668	AZ755668 ev02q09.x
25	16.8	76.4	620	162	BE060267	BE060267 HVSME9001
26	16.8	76.4	667	149	BF484589	BF484589 WHE2317_D
27	16.8	76.4	930	146	BF257509	BF257509 HVSMEF001
28	16.6	75.5	360	156	C61384	C61384 C61384 Yuj1
29	16.6	75.5	360	156	D37148	D37148 CELK041CNF
30	16.6	75.5	397	122	AH930320	AH930320 EST340873
31	16.6	75.5	513	231	AQ607969	AQ607969 HS.2126_B
32	16.6	75.5	681	32	AV732648	AV732648 AV732648
33	16.2	73.6	424	139	BE723539	BE723539 193384_MA
34	16.2	73.6	533	143	BF039764	BF039764 BP250014B
35	16.2	73.6	546	237	AZ058706	AZ058706 RPCI-23-4
36	16.2	73.6	554	241	AZ280611	AZ280611 RPCI-23-1
37	16.2	73.6	585	244	AZ490370	AZ490370 IM0323K14
38	16.2	73.6	599	237	AZ068022	AZ068022 RPCI-23-4
39	16.2	73.6	711	250	AZ818181	AZ818181 2M0088L01
40	16.2	73.6	934	220	CNS027SC	AL185061 Tetraodon
41	16.2	72.7	130	3	AA217796	AA217796 mv54h02.r
42	16.2	72.7	202	4	AA236074	AA236074 ZS05304.r
43	16.2	72.7	236	127	BB183285	BB183285 BB183285
44	16.2	72.7	236	171	BF932252	BF932252 IL2-NT019
45	16.2	72.7	251	161	BB565758	BB565758 BB565758

ALIGNMENTS

RESULT 1						
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DEFINITION	AU083559	Rice green shoot	Oryza sativa	cdna clone	SI4862, mrna	
ACCESSION	AU083559					
VERSION	AU083559.1	GI:7274015				
KEYWORDS	EST.					
SOURCE	Oryza sativa.					
ORGANISM	Oryza sativa.					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
AUTHORS	1 (bases 1 to 463)					
TITLE	Sasaki, T. and Yamamoto, K.					
JOURNAL	Rice cdna from green shoot (2000)					

COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = 'RGP', SI4862_62.
FEATURES	Location/Qualifiers 1..463 /organism="Oryza sativa" /strain="Nipponbare" /db_xref="taxon:4530" /clone="SI4862" /clone_lib="Rice green shoot" /note="Green shoot (8 days old)" 2 others
BASE COUNT	151 a 74 c 109 g 127 t
ORIGIN	
Query Match	80.9%; Score 17.8; DB 107; Length 463;
Best Local Similarity	86.4%; Pred. No. 1.5e+02;
Matches	19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 tgactgtgaangttbgaatga 22
Db	151 TGAGTGTGAATGTTAGAGATGA 172
RESULT 2	
LOCUS	AU089685 479 bp mrna EST 27-APR-2000
DEFINITION	AU089685 Rice callus Oryza sativa subsp. japonica cdna clone C40060
ACCESSION	AU089685
VERSION	AU089685.1 GI:7652165
KEYWORDS	EST.
SOURCE	Oryza sativa subsp. japonica.
ORGANISM	Oryza sativa subsp. japonica Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 479)
AUTHORS	Sasaki, T. and Yamamoto, K.
TITLE	Rice cdna from callus (2000)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba Ibaraki, Japan 305 Tel: 0298-38-7441 Fax: 0298-38-7468 Email: tsasaki@abr.affrc.go.jp PROJECT = 'RGP', C40060_32.
FEATURES	Location/Qualifiers 1..479 /organism="Oryza sativa subsp. japonica" /strain="cultivar Nipponbare, sub_species Japonica" /db_xref="taxon:39947" /clone="C40060" /clone_lib="Rice callus" /note="Vector: pBluescript II SK+; Site_1: SalI; Site_2: NotI; cdna prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the SalI-NotI site of pBluescript II SK+ phagemid."
BASE COUNT	149 a 96 c 104 g 130 t
ORIGIN	

```

Query Match      80.9%; Score 17.8; DB 107; Length 479;
Best Local Similarity 86.4%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    ||| ||||| ||| ||||| |||
Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 3
BF487041/c
LOCUS
DEFINITION
  AT21713.5prime AT Drosophila melanogaster adult testes p0TB7
  Drosophila melanogaster cDNA clone AT21713 5 similar to CG11526;
  FBan0011526 last_updated:000321, mRNA sequence.
ACCESSION
  BF487041
VERSION
  BF487041.1 GI:11570342
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 527)
AUTHORS
  Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman
  , B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan
  , D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P.,
  Liao, G., Miranda, A., Misra, S., Mungall, C. J., Nunoo, J., Pacleb, J.,
  Park, S., Paragas, V., Phraenavong, S., Wan, K., Yu, C., Lewis, S. E.,
  Celnikier, S. and Rubin, G. M.
  Berkeley Drosophila Gene Collection Project
  Unpublished (2000)
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  hit genomic sequence AE003477
  Plate: AT:217 row: B column: 1
  High quality sequence stop: 420.
  Location/Qualifiers
    1..527
      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone="AT21713"
      /clone_lib="AT Drosophila melanogaster adult testes p0TB7"
      /dev_stage="0-3 day old Ore-R males"
      /lab_host="Plates AT:10-AT:120; DHS-alpha. Plates
      AT:121-AT:319; DHS-alpha Tona"
      /note="Organ: ADULT testes; Vector: p0TB7; Site:1: EcoRI;
      Site:2: XhoI; The mRNA for the testis library was made
      from testes and seminal vesicles hand dissected from 0-3
      day old Ore-R males. RNA kindly provided by the lab of
      Margaret Fuller. Sized fractionated cDNAs were directly
      ligated into p0TB7. Plasmid cDNA library."
BASE COUNT      140 a 144 c 136 g 107 t
ORIGIN

Query Match      80.0%; Score 17.6; DB 149; Length 527;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatg 21
    ||| ||||| ||| ||||| |||
Db 51 TGACTGTGAATTTGGAGATG 31

RESULT 4
BF487041/c
LOCUS
DEFINITION
  AT21713.5prime AT Drosophila melanogaster adult testes p0TB7
  Drosophila melanogaster cDNA clone AT21713 5 similar to CG11526;
  FBan0011526 last_updated:000321, mRNA sequence.
ACCESSION
  BF487041
VERSION
  BF487041.1 GI:11570342
KEYWORDS
  EST.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 527)
AUTHORS
  Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman
  , B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan
  , D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P.,
  Liao, G., Miranda, A., Misra, S., Mungall, C. J., Nunoo, J., Pacleb, J.,
  Park, S., Paragas, V., Phraenavong, S., Wan, K., Yu, C., Lewis, S. E.,
  Celnikier, S. and Rubin, G. M.
  Berkeley Drosophila Gene Collection Project
  Unpublished (2000)
  Contact: Stapleton, M.
  BDGP
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  hit genomic sequence AE003477
  Plate: AT:217 row: B column: 1
  High quality sequence stop: 420.
  Location/Qualifiers
    1..527
      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone="AT21713"
      /clone_lib="AT Drosophila melanogaster adult testes p0TB7"
      /dev_stage="0-3 day old Ore-R males"
      /lab_host="Plates AT:10-AT:120; DHS-alpha. Plates
      AT:121-AT:319; DHS-alpha Tona"
      /note="Organ: ADULT testes; Vector: p0TB7; Site:1: EcoRI;
      Site:2: XhoI; The mRNA for the testis library was made
      from testes and seminal vesicles hand dissected from 0-3
      day old Ore-R males. RNA kindly provided by the lab of
      Margaret Fuller. Sized fractionated cDNAs were directly
      ligated into p0TB7. Plasmid cDNA library."
BASE COUNT      140 a 144 c 136 g 107 t
ORIGIN

```

```

AQ397925/c
LOCUS
DEFINITION
  mgxb0008L06f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
  clone mgxb0008L06f, DNA sequence.
ACCESSION
  AQ397925
VERSION
  AQ397925.1 GI:4368952
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea.
  Magnaporthe grisea
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
  1 (bases 1 to 548)
  Yu, Y., Zhu, H., Boyd, C. A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R. A. and Dean, R. A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished (1998)
  Contact: Dean RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdeane@clemson.edu
  Seq primer: TAATACGACTCTACTATAGCG
  Class: BAC ends
  High quality sequence start: 56
  High quality sequence stop: 467.
  Location/Qualifiers
    1..548
      /organism="Magnaporthe grisea"
      /strain="70-15"
      /db_xref="taxon:148305"
      /clone="mgxb0008L06f"
      /clone_lib="CUGI Rice Blast BAC Library"
      /tissue_type="Protoplasts"
      /lab_host="E. coli DH10B"
      /note="Vector: pBACWICH; Site:1: HindIII; Site:2: HindIII;
      Rice blast is one of the most devastating fungal diseases
      of rice world wide. It is a filamentous ascomycete with
      a haploid genome (n=7) of approximately 40 Mbp. Rice
      blast is an important model fungal pathogen for studying
      numerous aspects of the fungal-host interaction. In
      order to facilitate genome wide analysis, a BAC library
      containing 9216 clones with an average insert size of 130
      kbp was constructed. This library represents greater
      than 25X genome coverage. High density colony filters
      are available upon request."
BASE COUNT      159 a 134 c 110 g 144 t
ORIGIN

Query Match      80.0%; Score 17.6; DB 228; Length 548;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaangttbgagatga 22
    ||| ||||| ||| ||||| |||
Db 301 GACTGTGAATTTTGAGATGA 281

RESULT 5
AV653619/c
LOCUS
DEFINITION
  AV653619 GLC Homo sapiens cDNA clone GLCDMG10 3', mRNA sequence.
ACCESSION
  AV653619
VERSION
  AV653619.1 GI:9874633
KEYWORDS
  EST.
SOURCE
  human.
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 612)

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MGI:491227
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 336.
Location/Qualifiers

FEATURES

source
1. .343
/organism="Mus musculus"
/strain="C57BL6 x DBA"
/db_xref="taxon:10090"
/clone_lib="IMAGE:822947"
/clone_lib="Beddington mouse embryonic region"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"

/note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Gastrulating embryos were collected at 7.5dpc from C57BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"

78 a 123 c 74 g 68 t

BASE COUNT

ORIGIN

Query Match 77.3%; Score 17; DB 7; Length 343;

Best Local Similarity 81.8%; Pred. No. 3.6e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

DB 82 TCACGGTGACGGTTGGAGATGA 61

RESULT 10

AQ245026

LOCUS

DEFINITION

HS.2056.B1.E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate-2056 Col-5 Row-J, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2056 row: J column: 5

Class: BAC ends

High quality sequence stop: 374.

Location/Qualifiers

1. .374

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="plate-2056 Col-5 Row-J"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelosAC11; BAC Clones in

BASE COUNT 91 a 73 c 92 g 117 t 1 others

ORIGIN

Query Match 77.3%; Score 17; DB 226; Length 374;

Best Local Similarity 81.8%; Pred. No. 3.7e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

DB 207 TCACGTGACGATTGAGATCA 228

RESULT 11

AW270792

LOCUS

DEFINITION

AW270792 471-bp mRNA EST 03-JAN-2000

XP54B05.X1 NCI_CGAP_HN12 Homo sapiens cDNA clone IMAGE:2744145 3', mRNA sequence.

ACCESSION AW270792

VERSION AW270792.1 GI:6657822

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 471)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: John F. Ensley, M.D., Silvio Gutkind Ph.D.,

Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyt not found

Seq primer: -40UP from Gibco

High quality sequence stop: 427.

Location/Qualifiers

1. .471

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2744145"

/clone_lib="NCI_CGAP_HN12"

/tissue_type="moderate to poorly differentiated invasive

carcinoma"

/lab_host="DH10B"

/note="Organ: tongue; Vector: pAMP10; cDNA made by

oligo-dt priming. Non-directionally cloned into the UDG

sites of pAMP10. Size-selected on agarose gel, average

insert size 500 bp. Primary library; non-amplified.

cDNA Library Preparation: David B. Krizman, Ph.D (NCI).

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383."

BASE COUNT 127 a 100 c 124 g 120 t

ORIGIN

Query Match 77.3%; Score 17; DB 113; Length 471;

Best Local Similarity 81.8%; Pred. No. 3.9e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22

||||| ||||| ||||| ||||| |||||

DB 183 TGACGGTGACGGTGGAGATGA 204

```

RESULT 12
BF563081 493 bp mRNA EST 12-DEC-2000
LOCUS UI-R-B01-aly-e-06-0-UI-R1 UI-R-B01 Rattus norvegicus cDNA clone
DEFINITION UI-R-B01-aly-e-06-0-UI 5', mRNA sequence.
ACCESSION BF563081
VERSION BF563081.1 GI:11672811
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 493)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (infoimage.llnl.gov). IMAGE ID= 1797843
Seq primer: M13 Forward.
FEATURES
source
Location/Qualifiers
1..493
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
BASE COUNT 112 a 122 c 144 g 115 t
ORIGIN
Query Match 77.3%; Score 17; DB 150; Length 493;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
||||| ||||| ||||| ||||| |||||
Db 469 TGACACTGAAGTTTCAGATGA 490

RESULT 13
AW526035/c 514 bp mRNA EST 06-MAR-2000
LOCUS UI-R-B01-aly-e-06-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone
DEFINITION UI-R-B01-aly-e-06-0-UI 3', mRNA sequence.
ACCESSION AW526035
VERSION AW526035.1 GI:7168420
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 493)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (infoimage.llnl.gov). IMAGE ID= 1797843
Seq primer: M13 Forward.
FEATURES
source
Location/Qualifiers
1..493
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)."
BASE COUNT 112 a 122 c 144 g 115 t
ORIGIN
Query Match 77.3%; Score 17; DB 150; Length 493;
Best Local Similarity 81.8%; Pred. No. 3.9e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
||||| ||||| ||||| ||||| |||||
Db 469 TGACACTGAAGTTTCAGATGA 490

```

```

SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 514)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized medulla library cDNA library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..514
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aly-e-06-0-UI"
/clone_lib="UI-R-B01"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-B01
TAG_TISSUE=medulla
TAG_SEQ=GAACCG"
BASE COUNT 116 a 146 c 125 g 127 t
ORIGIN
Query Match 77.3%; Score 17; DB 117; Length 514;
Best Local Similarity 81.8%; Pred. No. 4e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgatga 22
||||| ||||| ||||| ||||| |||||
Db 42 TGACACTGAAGTTTCAGATGA 21

RESULT 14
BF954072/c 525 bp mRNA EST 22-JAN-2001
LOCUS QV2-NN0045-131100-412-g11 NN0045 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF954072
ACCESSION BF954072
VERSION BF954072.1 GI:12371347
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)

REFERENCE
AUTHORS

Dias Neto E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-131100-412-g11&t3=2000-11-13&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 525.

FEATURES

source

Location/Qualifiers

1..525

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NN0045"

/dev_stage="Adult"

/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

162 a 119 c 94 g 150 t

BASE COUNT
ORIGIN

Query Match 77.3%; Score 17; DB 171; Length 525;

Best Local Similarity 81.8%; Pred. No. 4e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

||||| ||| ||| ||| ||| |||

Db 385 TGACTGTGAATAATGGAGAGGA 364

RESULT 15

AZ460464/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (2000)

Eukaryota: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 592)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.A.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dduenne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0265 row: L column: 18

Seq primer: CACACGAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 592.

FEATURES

source

Location/Qualifiers

1..592

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_lib="UUC1M0265L18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g114732114/gb1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

166 a 112 c 122 g 192 t

BASE COUNT
ORIGIN

Query Match 77.3%; Score 17; DB 244; Length 592;

Best Local Similarity 81.8%; Pred. No. 4.1e+02;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

||||| ||| ||| ||| ||| |||

Db 425 TGACAGTGAATGATGGAGATGA 404

Search completed: October 9, 2001, 18:20:27

Job time: 9797 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-8
Perfect score: 22
Sequence: 1 tgactgtgaangttbgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/NA1980.DAT.*
2: /SID88/gcgdata/geneseq/NA1981.DAT.*
3: /SID88/gcgdata/geneseq/NA1982.DAT.*
4: /SID88/gcgdata/geneseq/NA1983.DAT.*
5: /SID88/gcgdata/geneseq/NA1984.DAT.*
6: /SID88/gcgdata/geneseq/NA1985.DAT.*
7: /SID88/gcgdata/geneseq/NA1986.DAT.*
8: /SID88/gcgdata/geneseq/NA1987.DAT.*
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11: /SID88/gcgdata/geneseq/NA1990.DAT.*
12: /SID88/gcgdata/geneseq/NA1991.DAT.*
13: /SID88/gcgdata/geneseq/NA1992.DAT.*
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17: /SID88/gcgdata/geneseq/NA1996.DAT.*
18: /SID88/gcgdata/geneseq/NA1997.DAT.*
19: /SID88/gcgdata/geneseq/NA1998.DAT.*
20: /SID88/gcgdata/geneseq/NA1999.DAT.*
21: /SID88/gcgdata/geneseq/NA2000.DAT.*
22: /SID88/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.2	91.8	22	19 AAV32080	Nucleotide sequenc
2	20.2	91.8	22	19 AAV32079	Nucleotide sequenc
3	20.2	91.8	22	20 AAX36624	ISS-ODN DY1018 nuc
4	20.2	91.8	22	20 AAX36625	ISS-ODN mutant DY1
5	20.2	91.8	22	20 AAV80097	Immunomodulatory o
6	20.2	91.8	22	20 AAV80102	Immunomodulatory o
7	20.2	91.8	22	20 AAV80103	Immunomodulatory o
8	20.2	91.8	22	21 AAC64051	Immunostimulatory
9	20.2	91.8	22	21 AAA96253	Sequence of a stab
10	20.2	91.8	22	21 AAA90458	CpG adjuvant oligo
11	20.2	91.8	22	21 AAA14467	Immunostimulatory

12	20.2	91.8	22	21 AAA14468	Inactive immunosti
13	20.2	91.8	22	21 AAA38065	Immunostimulatory
14	20.2	91.8	22	21 AAA38071	Immunostimulatory
15	20.2	91.8	22	21 AAA38072	Immunostimulatory
16	20.2	91.8	22	21 AAZ55876	Immunomodulatory o
17	20.2	91.8	22	21 AAZ55880	Immunomodulatory o
18	20.2	91.8	22	22 AAF77040	Immunomodulatory D
19	20.2	91.8	22	22 AAF77046	Immunostimulatory
20	20.2	91.8	22	22 AAF77047	Immunostimulatory
21	20.2	91.8	22	22 AAF29800	Cholera toxin immu
22	20.2	91.8	22	22 AAC82107	Oligonucleotide OD
23	20.2	91.8	22	22 AA92377	CG motif and CFA c
24	20.2	90.9	22	21 AAZ55881	Immunomodulatory o
25	19.4	88.2	22	20 AAV55797	Immunostimulatory
26	19.4	88.2	22	20 AAV55788	Immunostimulatory
27	19.4	88.2	22	20 AAV80104	Oligo used in expe
28	19.4	88.2	22	21 AAC64052	Non-CpG control ph
29	19.4	88.2	22	21 AA96252	Sequence of a stab
30	18.6	84.5	22	20 AAV80105	Oligo used in expe
31	18.6	84.5	22	20 AAV80096	Immunomodulatory o
32	18.6	84.5	22	20 AAV80099	Immunomodulatory o
33	18.6	84.5	22	20 AAV80101	Immunomodulatory o
34	18.6	84.5	22	21 AAA96254	Sequence of a stab
35	18.6	84.5	22	21 AAA38066	Immunostimulatory
36	18.6	84.5	22	21 AAA38068	Immunostimulatory
37	18.6	84.5	22	21 AAA38070	Immunostimulatory
38	18.6	84.5	22	21 AAZ55877	Immunomodulatory o
39	18.6	84.5	22	22 AAF77041	Immunostimulatory
40	18.6	84.5	22	22 AAF77043	Immunostimulatory
41	18.6	84.5	22	22 AAF77045	Immunostimulatory
42	17.8	80.9	22	20 AAV55790	Immunostimulatory
43	17.8	80.9	22	20 AAV55791	Immunostimulatory
44	17.8	80.9	22	20 AAV80106	Oligo used in expe
45	17.8	80.9	22	22 AAA92378	CG motif and CFA c

ALIGNMENTS

RESULT	1
AAV32080	
ID	AAV32080 standard; DNA; 22 BP.
XX	
AC	AAV32080;
XX	
DT	09-SEP-1998 (first entry)
XX	
DE	Nucleotide sequence of DY1019.
XX	
KW	DY1019; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW	immunisation; anaphylaxis; IgE; retinopathies; ss.
XX	
OS	synthetic.
XX	
FH	Key
FT	modified_base 1..22
FT	/*tag= a
FT	/note= "phosphothioate backbone"
XX	
PN	WO9816247-A1.
XX	
PD	23-APR-1998.
XX	
PF	09-OCT-1997; 97WO-US19004.
XX	
PR	11-OCT-1996; 96US-0028118.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Carson DA, Raz E, Roman M;
XX	
DR	WPI; 1998-261028/23.
XX	

PT New immunomodulatory compositions - comprising an antigen conjugated
 PT to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1019, which is conjugated to
 CC beta-gal in the method of the invention to form PN/IMM, comprising an
 CC immunomodulatory molecule (IMM), which comprises an antigen conjugated
 CC to a polynucleotide (PN) that contains at least one immunostimulatory
 CC nucleotide sequence (ISS). The conjugate synergistically boost the
 CC magnitude of the host immune response against an antigen to a level
 CC greater than the host immune response to either the IMM, antigen or
 CC ISS-PN alone. These responses to ISS-PN/IMM conjugates are
 CC particularly acute during the important early phase of the host immune
 CC response to an antigen. The ISS-PN/IMM conjugates boost both humoral
 CC (antibody) and cellular (Th1 type) immune responses of the host. Thus,
 CC use of the method to boost the immune responsiveness of a host to
 CC subsequent challenge by a sensitising antigen without immunisation
 CC avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by
 CC suppressing IgE production in response to the antigen challenge. The
 CC conjugates can also be used to combat pathogenic infection and to
 CC stimulate therapeutic angiogenesis to treat conditions in which
 CC localised blood flow plays a significant etiological role, e.g.
 CC retinopathies.

XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaangttbgagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaagttggagatga 22

RESULT 2

ID AAV32079 standard; DNA; 22 BP.

AC AAV32079;

DT 09-SEP-1998 (first entry)

DE Nucleotide sequence of DY1018.

XX DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.

XX synthetic.

XX Key Location/Qualifiers

FT modified_base 1..22

FT /*tag= a

FT /note= "phosphothioate backbone"

XX WO9816247-A1.

XX 23-APR-1998.

XX 09-OCT-1997; 97WO-US19004.

XX 11-OCT-1996; 96US-0028118.

XX (REGC) UNIV CALIFORNIA.

XX Carson DA, Raz E, Roman M;

XX WPI; 1998-261028/23.

PT New immunomodulatory compositions - comprising an antigen conjugated
 PT to a polynucleotide that contains an immunostimulatory sequence

XX Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1018, which is conjugated to
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
 CC (IMM), which comprises an antigen conjugated to a polynucleotide
 CC (PN) that contains at least one immunostimulatory nucleotide sequence
 CC (ISS). The conjugate synergistically boost the magnitude of the host
 CC immune response against an antigen to a level greater than the host
 CC immune response to either the IMM, antigen or ISS-PN alone. These
 CC responses to ISS-PN/IMM conjugates are particularly acute during
 CC the important early phase of the host immune response to an antigen.
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular
 CC (Th1 type) immune responses of the host. Thus, use of the method to
 CC boost the immune responsiveness of a host to subsequent challenge by a
 CC sensitising antigen without immunisation avoids the risk of
 CC Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE
 CC production in response to the antigen challenge. The conjugates can
 CC also be used to combat pathogenic infection and to stimulate
 CC therapeutic angiogenesis to treat conditions in which localised blood
 CC flow plays a significant etiological role, e.g. retinopathies.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaangttbgagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaagttcgagatga 22

RESULT 3

AA336624

ID AAX36624 standard; DNA; 22 BP.

XX AAX36624;

XX 09-JUL-1999 (first entry)

XX ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hyperesoiniphilic syndrome;

XX cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC) UNIV CALIFORNIA.

XX Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation.

XX Example 2; Page 30; 69pp; English.

CC This is the ISS-ODN DY1018 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing

CC and to modulate the host's immune responsiveness to an antigen,
CC particularly where the subject suffers from asthma, nasal polyposis,
CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
CC eosinophilic fasciitis, idiopathic hypersensitivity syndrome, or
CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
CC antigen immunisation, the method is an antigen-independent method,
CC and avoids host production of both interleukin-4 (IL-4), which carries
CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;
XX

Query Match	91.8%	Score 20.2;	DB 20;	Length 22;
Best Local Similarity	90.9%	Pred. No. 0.42;		

Qy 1 cgactgtgaangttbgagatga 22
 |||||
Pb 1 cgactgtgaaagtctggagatga 22

RESULT 5
AAV80097
ID AAV80097 standard; DNA; 22 BP.

12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
AA
KW
KW
ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW
KW
human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW
B. pertussis; malaria; plasmodia Leishmania; Trypanosoma Schistosoma.

OS Synthetic.

PN W09855495-A2.

XX

PD 10-DEC-1998.

XX

PF 05-JUN-1998;

XX
DD
06-JUN-1997.

PR 00-JUN-1997;
XX

PA (DYNA-) DYNAM

XX
XX
XX

PI Dina D, Roma

XX

DR WPI; 1999-059

[illegible]

PT
BT

Oy 1 tgactgtgaangttbgagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 8
 AAC64051
 ID AAC64051 standard; DNA; 22 BP.
 XX
 AC AAC64051;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
 XX
 KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
 KW enhanced antigen presentation; antigen-presenting cell; APC;
 KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
 KW vaccine; ss.
 XX
 OS Synthetic.
 XX
 PN WO200062787-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US09664.
 XX
 PR 15-APR-1999; 99US-0292278.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Raz E, Martin-Orozco E;
 XX
 DR WPI; 2000-679548/66.
 XX
 PT Enhancing antigen-presentation capabilities of T-cells for cancer
 PT immunotherapy, by contacting cells with an immunostimulatory
 PT oligonucleotide
 XX
 PS Example 1; Page 18; 42pp; English.
 XX
 CC The invention relates to a method of inducing activation of T-cells
 CC to respond to an antigen, comprising contacting antigen-presenting cells
 CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
 CC thus treated have enhanced antigen presenting capabilities compared to
 CC antigen-activated APCs. APCs with enhanced antigen-presentation
 CC capabilities then present the antigen to T-cells. The method is useful
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell
 CC activation, and is therefore useful for treating tumours. Additionally,
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation
 CC of Fc-receptor expression, to present antigen through upregulation of
 CC major histocompatibility complex (MHC) Class I and II expression and
 CC CD4 expression, to produce co-stimulatory factors (B7 and CD40), to
 CC provide cell-to-cell adhesion through upregulation of intercellular
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
 CC cytokine production, all at levels greater than that achieved through
 CC contact of APC with antigen alone. The present sequence represents
 CC a phosphorothioate cpG ISS-ODN used in the exemplifications of the
 CC invention.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 9
 AAA96253
 ID AAA96253 standard; DNA; 22 BP.
 XX
 AC AAA96253;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Sequence of a stabilised oligonucleotide with antitumour activity.
 XX
 KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
 KW glioblastoma; medullablastoma; neuroblastoma; carcinoma; ss.
 XX
 OS Synthetic.
 XX
 PN WO2000056342-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-FR00676.
 XX
 PR 19-MAR-1999; 99FR-0003433.
 XX
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 PI Carpentier A;
 XX
 DR WPI; 2000-602192/57.
 XX
 PT Use of stabilized oligonucleotides as antitumor agents, particularly
 PT against nervous system tumors, have optimal activity and are not toxic
 PT
 XX
 PS Example 2; Page 16; 57pp; French.
 XX
 CC The present sequence represents a stabilised oligonucleotide which has
 CC antitumour activity. The oligonucleotide comprises an octamer motif
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
 CC immunostimulatory, and are not toxic. They may be adapted for use in
 CC animals or humans. The stabilised oligonucleotides are used for
 CC treating tumours, of any type and any degree of anaplasia, particularly
 CC human tumours in the peripheral or central nervous systems, specifically
 CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttcgagatga 22

RESULT 10
 AAA90458
 ID AAA90458 standard; DNA; 22 BP.
 XX
 AC AAA90458;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE CpG adjuvant oligonucleotide, SEQ ID NO:19.
 XX
 KW CpG oligonucleotide; CpG motif; adjuvant; microdroplet emulsion;
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;

KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.

XX Synthetic.

XX WO200050006-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-US03331.

XX 26-FEB-1999; 99US-0121858.

XX 29-JUL-1999; 99US-0146391.

XX 28-OCT-1999; 99US-0161997.

XX (CHIR) CHIRON CORP.

XX O'Hagan D, Ott GS, Donnelly J, Kazzaz J, Uguzzoli M, Singh M;

XX Barackman J;

XX WPI; 2000-597123/55.

XX Microemulsion having an adsorbent surface comprising a microdroplet
 PT emulsion consisting of a metabolizable oil and an emulsifying agent
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,
 PT and parasitic infection

XX Claim 17; Page 40; 95pp; English.

XX The invention relates to a microdroplet emulsion (microemulsion) with an
 CC adsorbent surface, and which comprises a metabolizable oil and an
 CC emulsifying agent (a detergent). It also relates to a composition
 CC comprising the microemulsion and a microparticle with an adsorbent
 CC surface, where the microparticle comprises a polymer selected from a
 CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a
 CC polycyanoacrylate, a polyorthoester, a polyhydride, and a
 CC polycyanoacrylate, and a second detergent. The surface of the
 CC microparticle efficiently adsorb biologically active macromolecules such
 CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,
 CC mediators of transcription or translation, metabolic intermediates and
 CC adjuvants. Additionally, a second biologically active molecule may be
 CC encapsulated within the microparticle. The microemulsion can be used in
 CC methods of immunising a host animal, particularly a human, against a
 CC viral, bacterial or parasitic infection, and in methods of increasing a
 CC Th1 immune response. The microemulsions (having the appropriate antigens
 CC adsorbed) may be particularly used as vaccines for hepatitis C virus
 CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human
 CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and
 CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and
 CC pertussis; Helicobacter pylori and Haemophilus influenzae; and
 CC malaria-causing parasites. Sequences AAA90447-A90467 represent Th1
 CC lymphocyte stimulating oligonucleotides containing at least one CpG motif
 CC which are claimed for use as adjuvants in the compositions of the
 CC invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 11

AAA14467

ID AAA14467 standard; DNA; 22 BP.

XX

AC AAA14467;
 XX 21-AUG-2000 (first entry)
 DT Immunostimulatory oligonucleotide (ISS-ODN) DY1018.
 XX Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
 KW secretory immunoglobulin A production; sigA; Th1 phenotype; ds.
 KW Synthetic.

OS WO200020039-A1.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-US21203.

XX 05-OCT-1998; 98US-0167039.

XX (REGC) UNIV CALIFORNIA.

XX Raz E, Horner AA, Carson DA;

XX WPI; 2000-303647/26.

XX Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
 PT an antigen in a mammalian host through production of secretory
 PT immunoglobulin A

XX Claim 8; Page 21; 64pp; English.

XX The invention relates to a method of inducing mucosal immunity to an
 CC antigen in a mammalian host, including the production of secretory
 CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal
 CC site of entry of most foreign antigens) is mediated by mucosa-associated
 CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
 CC cell sub-populations. The primary immune response which characterises
 CC the induction of mucosal immunity to an antigen is sIgA production by
 CC activated B-cells. The method comprises introducing an immunostimulatory
 CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
 CC ISS-ODN includes a core nucleotide sequence. The core nucleotide
 CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
 CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID Nos 1-3). A
 CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
 CC as an adjuvant with an antigen for stimulating mucosal immunity. The
 CC level of sIgA production induced in the host is at least 3 times the
 CC magnitude of sIgA production achievable in response to introduction of
 CC antigen alone into the mucosal tissue and is equivalent or greater than
 CC the magnitude of sIgA production achievable in response to introduction
 CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The
 CC host immune response is stimulated to antigen specific IgA production,
 CC biased towards the Th1 phenotype while antigen-induced IgE production is
 CC avoided. The adjuvant has little or no known toxicity in mammals and its
 CC efficacy is comparable to that of cholera toxin which is used as a
 CC mucosal adjuvant. The present sequence represents the immunostimulatory
 CC oligonucleotide DY1018.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.42;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22

Db 1 tgactgtgaacgttcgagatga 22

RESULT 12

AAA14468

ID AAA14468 standard; DNA; 22 BP.

XX

```

AC AA14468;
XX
XX
DT 21-AUG-2000 (first entry)
XX
XX
DE Inactive immunostimulatory oligonucleotide DY1019.
XX
XX
KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.
XX
XX
OS Synthetic.
XX
XX
PN WO200020039-A1.
XX
XX
PD 13-APR-2000.
XX
XX
PF 15-SEP-1999; 99WO-US21203.
XX
XX
PR 05-OCT-1998; 98US-0167039.
XX
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX
PI Raz E, Horner AA, Carson DA;
XX
XX
DR WPI; 2000-303647/26.
XX
XX
PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
PT an antigen in a mammalian host through production of secretory
PT immunoglobulin A.
XX
XX
PS Example 7; Page 63; 64pp; English.
XX
XX
CC The invention relates to a method of inducing mucosal immunity to an
CC antigen in a mammalian host, including the production of secretory
CC immunoglobulin A (sigA). Immune protection in the mucosa (the principal
CC site of entry of most foreign antigens) is mediated by mucosa-associated
CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
CC cell sub-populations. The primary immune response which characterises
CC the induction of mucosal immunity to an antigen is sigA production by
CC activated B-cells. The method comprises introducing an immunostimulatory
CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
CC ISS-ODN includes a core nucleotide sequence. The core nucleotide
CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A
CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
CC as an adjuvant with an antigen for stimulating mucosal immunity. The
CC level of sigA production induced in the host is at least 3 times the
CC magnitude of sigA production achievable in response to introduction of
CC antigen alone into the mucosal tissue and is equivalent or greater than
CC the magnitude of sigA production achievable in response to introduction
CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The
CC host immune response is stimulated to antigen specific IgA production,
CC biased towards the Th1 phenotype while antigen-induced IgE production is
CC avoided. The adjuvant has little or no known toxicity in mammals and its
CC efficacy is comparable to that of cholera toxin which is used as a
CC mucosal adjuvant. The present sequence represents an inactive ISS-ODN,
CC DY1019, used in an exemplification of the invention.
XX
XX
SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagttbgagatga 22
||||||| |||:|||||
Db 1 tgactgtgaagttbgagatga 22

RESULT 13
AAA38065
ID AAA38065 standard; DNA; 22 BP.
XX

```

```

AC AAA38065;
XX
XX
DT 24-AUG-2000 (first entry)
XX
XX
DE Immunostimulatory sequence (ISS) #1.
XX
XX
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200021556-A1.
XX
XX
PD 20-APR-2000.
XX
XX
PF 08-OCT-1999; 99WO-US23677.
XX
XX
PR 09-OCT-1998; 98US-0103733.
XX
XX
PR 07-OCT-1999; 99US-0415186.
XX
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX
PI Tighe H, Raz E, Schwartz D, Takabayashi K;
XX
XX
DR WPI; 2000-317846/27.
XX
XX
PT Anti-HIV composition comprises immunostimulatory polynucleotides and
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT response against HIV in an HIV infected individual.
XX
XX
PS Claim 3; Page 16; 65pp; English.
XX
XX
CC The present invention relates to an immunostimulatory composition
CC comprising a human immunodeficiency virus (HIV) antigen, and an
CC immunostimulatory polynucleotide comprising an immunostimulatory sequence
CC (ISS). This sequence represents an ISS that can be used in the
CC composition. An immunostimulatory polynucleotide, or is proximately
CC conjugated to an immunomodulatory polynucleotide, is used for modulating or
CC associated to it and not conjugated, is used against gp120 in an individual
CC stimulating a specific immune response against gp120 in an individual
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC is also used for suppressing or delaying development of HIV infection in
CC an individual infected with HIV or an individual at risk of infection
CC with HIV, respectively. It is also used for treating an individual
CC infected with HIV in need of immune modulation.
XX
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagttbgagatga 22
||||||| |||:|||||
Db 1 tgactgtgaagttbgagatga 22

RESULT 14
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ID AAA38071 standard; DNA; 22 BP.
XX
XX
AC AAA38071;
XX
XX
DT 24-AUG-2000 (first entry)
XX
XX
DE Immunostimulatory sequence (ISS) #7.
XX
XX
KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX

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OS Synthetic.
XX Key Location/Qualifiers
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FT /*mod_base= OTHER
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FT /*note= "5-Bromocytosine"
XX
XX WO200021556-A1.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23677.
XX
XX 09-OCT-1998; 98US-0103733.
XX
XX 07-OCT-1999; 99US-0415186.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Tighe H, Raz E, Schwartz D, Takabayashi K;
XX WPI; 2000-317846/27.
XX
XX Anti-HIV composition comprises immunostimulatory polynucleotides and
XX HIV glycoprotein gp120 useful for modulating, stimulating an immune
XX response against HIV in an HIV infected individual.
XX
XX Disclosure; Page 17; 65pp; English.
XX
XX The present invention relates to an immunostimulatory composition
XX comprising a human immunodeficiency virus (HIV) antigen, and an
XX immunomodulatory polynucleotide comprising an immunostimulatory sequence
XX (ISS). This sequence represents an ISS that can be used in the
XX composition. An immunostimulatory polynucleotide, or is proximately
XX conjugated to an immunomodulatory polynucleotide, or is proximately
XX associated to it and not conjugated, is used for modulating or
XX stimulating a specific immune response against gp120 in an individual by
XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
XX is also used for suppressing or delaying development of HIV infection in
XX an individual infected with HIV or an individual at risk of infection
XX with HIV, respectively. It is also used for treating an individual
XX infected with HIV in need of immune modulation.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
DB 1 tgactgtgaacgttcgagatga 22

RESULT 15
AAA38072
ID AAA38072 standard; DNA; 22 BP.
XX
XX AAA38072;
XX
XX 24-AUG-2000 (first entry)
XX
XX Immunostimulatory sequence (ISS) #7.
XX
XX Immunostimulatory sequence; ISS; Immunomodulator; glycoprotein 120;
XX gp120; human immunodeficiency virus; HIV; immune response; infection;
XX development; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
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FT /*mod_base= OTHER
FT /*note= "5-Bromocytosine"
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FT /*mod_base= OTHER
FT /*note= "5-Bromocytosine"
XX
XX WO200021556-A1.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23677.
XX
XX 09-OCT-1998; 98US-0103733.
XX
XX 07-OCT-1999; 99US-0415186.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Tighe H, Raz E, Schwartz D, Takabayashi K;
XX WPI; 2000-317846/27.
XX
XX Anti-HIV composition comprises immunostimulatory polynucleotides and
XX HIV glycoprotein gp120 useful for modulating, stimulating an immune
XX response against HIV in an HIV infected individual.
XX
XX Disclosure; Page 17; 65pp; English.
XX
XX The present invention relates to an immunostimulatory composition
XX comprising a human immunodeficiency virus (HIV) antigen, and an
XX immunomodulatory polynucleotide comprising an immunostimulatory sequence
XX (ISS). This sequence represents an ISS that can be used in the
XX composition. An immunostimulatory polynucleotide, or is proximately
XX conjugated to an immunomodulatory polynucleotide, or is proximately
XX associated to it and not conjugated, is used for modulating or
XX stimulating a specific immune response against gp120 in an individual by
XX producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
XX is also used for suppressing or delaying development of HIV infection in
XX an individual infected with HIV or an individual at risk of infection
XX with HIV, respectively. It is also used for treating an individual
XX infected with HIV in need of immune modulation.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 91.8%; Score 20.2; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.42;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
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DB 1 tgactgtgaacgttcgagatga 22

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Job time: 2981 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:47 ; Search time 10334.3 Seconds
(without alignments)
31.457 Million cell updates/sec

Title: US-09-713-136-8

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Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues 28310096

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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5	20.2	91.8	22	1	PCT-US01-03029-2
6	20.2	91.8	22	1	PCT-US01-06034-1
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8	20.2	91.8	22	1	PCT-US01-10118-1
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13	20.2	91.8	22	1	PCT-US99-21203-19
14	20.2	91.8	22	1	PCT-US99-21203-20
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17	20.2	91.8	22	15	US-09-167-039-19
18	20.2	91.8	22	15	US-09-167-039-20
19	20.2	91.8	22	16	US-09-235-742-19
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22	20.2	91.8	22	16	US-09-296-477-15
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37	20.2	91.8	22	25	US-09-642-492-7
38	20.2	91.8	22	28	US-09-700-354-1
39	20.2	91.8	22	28	US-09-700-354-2
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ALIGNMENTS

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; Sequence 32, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 06510/201WO1
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR FILING DATE: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-32

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Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 1 tgactgtgaacgttcgagatga 22

RESULT 2
PCT-US00-35064-1
; Sequence 1, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; FILE REFERENCE: 06510/201WO1
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR FILING DATE: 60/171,830
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid molecule
PCT-US00-35064-1

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttbgagatga 22
||||||| |||:|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 3
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; Sequence 2, Application PC/TUS0035064
; GENERAL INFORMATION:

; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; FILE REFERENCE: 06510/201WO1
; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
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; OTHER INFORMATION: mutant
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Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 1 tgactgtgaacgttcgagatga 22

RESULT 4
PCT-US01-03029-1
; Sequence 1, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166WO1
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR FILING DATE: 60/179,353
; PRIOR FILING DATE: 2000-01-31
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; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
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Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tgactgtgaangttbgagatga 22
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Db 1 tgactgtgaacgttcgagatga 22

RESULT 5
PCT-US01-03029-2
; Sequence 2, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi

```

; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 06510/166WO1
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
   ||||| |||:|||||
Db 1 tgactgtgaagttcgagatga 22

RESULT 6
PCT-US01-06034-1
; Sequence 1, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; OTHER INFORMATION: oligonucleotide primer
PCT-US01-06034-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
   ||||| |||:|||||
Db 1 tgactgtgaagttcgagatga 22

RESULT 7
PCT-US01-06034-4
; Sequence 4, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-4

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
   ||||| |||:|||||
Db 1 tgactgtgaagttcgagatga 22

RESULT 8
PCT-US01-10118-1
; Sequence 1, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-1

Query Match          91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgaatga 22
   ||||| |||:|||||
Db 1 tgactgtgaagttcgagatga 22

RESULT 9
PCT-US01-10118-3
; Sequence 3, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; FILE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188WO1
; CURRENT APPLICATION NUMBER: PCT/US01/10118

```

; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
PCT-US01-10118-3

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| |||:|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 10
PCT-US01-11290-1
; Sequence 1, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
PCT-US01-11290-1

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| |||:|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 11
PCT-US01-11290-2
; Sequence 2, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; FILE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control nucleic acid sequence
PCT-US01-11290-2

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| |||:|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 12
PCT-US01-14508-1
; Sequence 1, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Loiz, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168WO1
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-1

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| |||:|||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
PCT-US99-21203-19
; Sequence 19, Application PC/TUS9921203
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski L.L.P.
; STREET: 865 S. Figueroa Street, 29th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: US
; ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/21203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-892-9200
TELEFAX: 213-680-4518
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
PCT-US99-21203-19

Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACCTTCGAGATGA 22

RESULT 14
PCT-US99-21203-20
Sequence 20, Application PC/TUS9921203
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
MUCOSAL IMMUNITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 865 S. Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/21203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,120
FILING DATE: 05 September 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-892-9200
TELEFAX: 213-680-4518
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
PCT-US99-21203-20
Query Match 91.8%; Score 20.2; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAAGTTCGAGATGA 22
RESULT 15
US-08-927-120-19
Sequence 19, Application US/08927120
GENERAL INFORMATION:
APPLICANT: Raz, Eyal
TITLE OF INVENTION: IMMUNIZATION-FREE METHODS
FOR STIMULATING IMMUNE RESPONSIVENESS AND REDUCING
INFLAMMATION IN A HOST
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,120
FILING DATE: 22-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/054001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: non-coding oligonucleotides
US-08-927-120-19

Query Match 91.8%; Score 20.2; DB 13; Length 22;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 TGACTGTGAACCTTCGAGATGA 22

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us-09-713-136-8.rnp

Page 6

Search completed: October 9, 2001, 21:12:47
Job time: 20072 sec

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; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 3
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.91;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 4
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
US-09-802-359-7
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 5
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match          91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.91;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttcgagatga 22

RESULT 6
US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7
```


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```
Query Match      91.8%; Score 20.2; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.91;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 7
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802.518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 8
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

US-09-802-376-8
; Sequence 8, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8

Query Match      90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
    |||||
Db 1 tgactgtgaangttcgagatga 22
    |||||

RESULT 10
US-09-770-943-1
; Sequence 1, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-1

Query Match      88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaangttbgagatga 22
```

```
Db 1 tgactgtgaaggttagagatga 22
|||||
RESULT 11
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2
Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22
|||||

RESULT 12
US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10
Query Match 88.2%; Score 19.4; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaacgttagagatga 22
|||||

RESULT 13
US-09-802-518-10
; Sequence 10, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-10
Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22
|||||

RESULT 14
US-09-802-359-9
; Sequence 9, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-9
Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22
|||||

RESULT 15
US-09-802-376-9
; Sequence 9, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
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; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-9

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbtagatga 22
||| ||||| ||| |||||
Db 1 tgactgtgaaggttagatga 22

Search completed: October 9, 2001, 21:36:22
Job time: 21242 sec


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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match      88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 4
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      80.9%; Score 17.8; DB 4; Length 22;
Best Local Similarity 86.4%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaangttbgagatga 22
   ||||| ||||| |||||
Db 1 tgactgtgaacgttagagatga 22

RESULT 6
US-08-070-301-2
; Sequence 2, Application US/08070301
; Patent No. 5871995
; GENERAL INFORMATION:
; APPLICANT: IIDA, Toshio
; APPLICANT: KANINUMA, Toshihiko
; APPLICANT: FUSE, Yuka
; APPLICANT: TAJIMA, Masahiro
; APPLICANT: YANAGI, Mitsuo
; APPLICANT: OKAMOTO, Hiroshi
; APPLICANT: KISHIMOTO, Jiro
; APPLICANT: IFUKU, Ohji
; APPLICANT: KATO, Ichiro
; TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
; TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
; STREET: 1233 20th Street, N.W.
; CITY: Washington
```

```
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,301
; FILING DATE: 24-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-209687
; FILING DATE: 15-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-181933
; FILING DATE: 31-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-76331
; FILING DATE: 26-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-106412
; FILING DATE: 24-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-205475
; FILING DATE: 02-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-450-22830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-040
; TELEFAX: (202) 835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Horse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..3070
; US-08-070-301-2

Query Match 75.5%; Score 16.6; DB 2; Length 6638;
Best Local Similarity 85.0%; Pred. No. 14;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatg 21
||||| | | | |
Db 2380 GACTGTGATGTTGGAGATG 2399

RESULT 7
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; PATENT NO. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US/08/070,301
; PRIOR FILING DATE: 1991-05-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SEQ ID NO: 2
; LENGTH: 6638
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Horse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..3070
; US-08-070-301-2
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; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-7

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| | | | |
Db 1 tgactgtgaggctcagagatga 22

RESULT 8
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; PATENT NO. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-092-314-8

Query Match 73.6%; Score 16.2; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.4;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| | | | |
Db 1 tgactgtgaggctcagagatga 22

RESULT 9
US-08-975-703-5
; Sequence 5, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
```

```
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,703
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2691
US-08-975-703-5

Query Match 72.7%; Score 16; DB 3; Length 2694;
Best Local Similarity 81.0%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGAGAATGTTTATGATGA 1805

RESULT 10
US-09-515-884-5
Sequence 5, Application US/09515884
Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
Teng, David H.-F.
Tavtigian, Sean V.
TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Flagg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
```

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,703
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2318-0174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2691
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-515-884-5

Query Match 72.7%; Score 16; DB 4; Length 2694;
Best Local Similarity 81.0%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22
||||| ||| ||| ||| |||
Db 1785 GACTGAGAATGTTTATGATGA 1805

RESULT 11
US-08-391-615-7
Sequence 7, Application US/08391615
Patent No. 5550054
GENERAL INFORMATION:
APPLICANT: Witte, Owen
APPLICANT: Tsukada, Satoshi
APPLICANT: Saffran, Douglas
APPLICANT: Rawlings, David
TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,615
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,449
FILING DATE: 21-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
```

us-09-713-136-8.rni

Wed Oct 10 05:59:28 2001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-391-615-7

Query Match 70.0%; Score 15.4; DB 1; Length 1418;
Best Local Similarity 77.3%; Pred. No. 41;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| ||||| || : ||||| ||
Db 218 TGACTTTGAACGTTGGGAGA 239

RESULT 12
US-09-019-931-2
Sequence 2, Application US/09019931
Patent No. 6194148
GENERAL INFORMATION:
APPLICANT: Hori, Kunio, Takahashi, Takeo, Okada, Takao
TITLE OF INVENTION: A Method For Detecting A Hybridized
MOLECULE TYPE: Nucleic Acid Molecule
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frischauf, Holtz, Goodman, Langer & Chick
STREET: 767 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017-2023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ inch, 1.44 mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,931
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-025291
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 980048/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 319-4900
TELEFAX: (212) 319-5101
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
IMMEDIATE SOURCE:
LIBRARY: PGEX-PH
US-09-019-931-2

Query Match 70.0%; Score 15.4; DB 4; Length 1830;
Best Local Similarity 77.3%; Pred. No. 43;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| ||||| || : ||||| ||
Db 881 TGACTTTGAACGTTGGGAGA 902

RESULT 13
US-08-391-615-1
Sequence 1, Application US/08391615
Patent No. 5550054
GENERAL INFORMATION:
APPLICANT: Witte, Owen
APPLICANT: Tsukada, Satoshi
APPLICANT: Saffran, Douglas
APPLICANT: Rawlings, David
TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,615
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/006,449
FILING DATE: 21-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 137..2116
US-08-391-615-1

Query Match 70.0%; Score 15.4; DB 1; Length 2505;
Best Local Similarity 77.3%; Pred. No. 45;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagatga 22
||||| ||||| || : ||||| ||
Db 262 TGACTTTGAACGTTGGGAGA 283

RESULT 14
US-08-975-316-61
Sequence 61, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka

APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-61

Query Match 69.1%; Score 15.2; DB 2; Length 913;
Best Local Similarity 81.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 gactgtgaangttbgagatga 22
||||||| || |||||
Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 15
US-08-933-750C-66/c
Sequence 66, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Ngil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933.750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ballings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT03
CLONE: 641127
US-08-933-750C-66

Query Match 68.2%; Score 15; DB 2; Length 1892;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaangttbgagat 20
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Db 1278 TGAATGTGAAGGTCGAGCT 1259

Search completed: October 9, 2001, 15:42:10
Job time: 300 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:20:40 ; Search time 2150.93 Seconds
(without alignments)
158.206 Million cell updates/sec

Title: US-09-713-136-9

Perfect score: 22
Sequence: 1 tgactgtgaagggttagagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
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- 7: gb_om:*
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- 9: gb_pat1:*
- 10: gb_pat2:*
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- 12: gb_p11:*
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58: gb_v1:*

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60: gb_htg1:*

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65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

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78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_rol:*

95: gb_rol2:*

96: gb_in4:*

97: gb_pr10:*

98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	22	9	AX036944
2	20	90.9	22	10	AX083682
3	20	90.9	183869	73	AC068700
4	19.4	88.2	22	10	AX083681
5	18.8	85.5	22	9	AX036945
6	18.8	85.5	22	9	AX036952
7	18.8	85.5	22	9	AX046993
8	18.8	85.5	22	10	AX083675
					AX036944 Sequence
					AX083682 Sequence
					AC068700 Homo sapi
					AX083681 Sequence
					AX036945 Sequence
					AX036952 Sequence
					AX046993 Sequence
					AX083675 Sequence

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9      18.8  85.5 171790 62 AC011106 Homo sapi
10     18.8  85.5 173506 64 AC016323
11     18.8  85.5 195308 74 AC073525
12     18.8  85.5 201579 73 AC068773
13     18.4  83.6 50487 73 AC068211
14     18.4  83.6 121682 78 AL139127
15     18.4  83.6 125661 89 AL138773
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18     17.8  80.9 7031 94 AF320616
19     17.8  80.9 100000 85 AB020870
20     17.8  80.9 100000 85 AB020870
21     17.8  80.9 100000 85 AB020871
22     17.8  80.9 150803 74 AC073490
23     17.8  80.9 165337 70 AC027442
24     17.8  80.9 167237 86 AC007938
25     17.8  80.9 170056 77 AC087643
26     17.8  80.9 172974 68 AC024605
27     17.8  80.9 174829 76 AC079611
28     17.8  80.9 180223 73 AC068979
29     17.8  80.9 181371 65 AC018893
30     17.8  80.9 191442 63 AC015551
31     17.8  80.9 194485 76 AC084030
32     17.8  80.9 200203 72 AC053510
33     17.8  80.9 201214 75 AC074012
34     17.8  80.9 209777 69 AC024934
35     17.8  80.9 215434 65 AC019214
36     17.4  79.1 38247 15 SPCCL259
37     17.4  79.1 103009 34 AC087261
38     17.4  79.1 103009 88 AC087225
39     17.4  79.1 113803 85 AC004460
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41     17.4  79.1 158738 63 AC015500
42     17.4  79.1 159798 83 AP003383
43     17.4  79.1 163565 81 AC009585
44     17.4  79.1 171900 71 AC027735
45     17.4  79.1 177387 76 AC079680 Mus muscu

Query Match      100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGACTGTGAAGGTTAGAGATGA 22

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ALIGNMENTS

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RESULT 1
LOCUS AX036944 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 1 from Patent FR2790955.
ACCESSION AX036944
VERSION AX036944.1 GI:11226372
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
TITLE Patent: FR 2790955-A 1 22-SEP-2000;
JOURNAL ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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        1..22
        /organism="synthetic construct"
        /db_xref="taxon:32630"
        /note=" oligodesoxynucleotide"
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ORIGIN

Query Match      100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
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Db 1 TGACTGTGAAGGTTAGAGATGA 22

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RESULT 2
LOCUS AX083682 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0112223.
ACCESSION AX083682
VERSION AX083682.1 GI:13185414
KEYWORDS synthetic construct.
          synthetic construct
          artificial sequence.
ORGANISM 1 (bases 1 to 22)
REFERENCE van Nest,G.
          Methods of modulating an immune response using immunostimulatory s
          equences and compositions for use therein
          Patent: WO 0112223-A 8 22-FEB-2001;
          Dynavax Technologies Corporation (US)
FEATURES
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        /organism="synthetic construct"
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    modified_base 11
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        /note="5-bromocytosine"
BASE COUNT 6 a 1 c 7 g 6 t 2 others
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Query Match      90.9%; Score 20; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
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Db 1 TGACTGTGAAGGTTAGAGATGA 22

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RESULT 3
LOCUS AC068700/c 183869 bp DNA HTG 25-JUN-2000
DEFINITION Homo sapiens chromosome 8 clone RP11-594N15 map 8, WORKING DRAFT
          SEQUENCE, 17 unordered pieces.
ACCESSION AC068700
VERSION AC068700.2 GI:8705190
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 183869)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-594N15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 183869)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
          Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
          Boguslavsky,L., Bouckgalter,B., Brown,A., Burket,G.,
          Campopiano,A., Castle,A., Choepei,Y., Colangelo,M., Collins,S.,
          Collymore,A., Cooke,P., DeAtrellano,K., Dewar,K., Diaz,J.S.,
          Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
          Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
          Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
          Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
          Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
          Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
          McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
          Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
          Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
          O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
          Pisani,C., Pollara,V., Raymond,C., Riley,K., Rogov,P., Rothman,D.,

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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TGACTGTGAANGTTCGAGATGA 22

RESULT 5
LOCUS AX036945 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
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BASE COUNT      6 a      3 c      7 g      6 t
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Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagatga 22
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Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 6
LOCUS AX036952 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier A.
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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BASE COUNT      7 a      2 c      6 g      7 t
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Query Match      85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagatga 22
||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 7
LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moss, R.B.
JOURNAL HIV Immunogenic compositions and methods
Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES
source
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  /db_xref="taxon:32630"
  /note="phosphorothioate-modified synthetic
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BASE COUNT      6 a      3 c      7 g      6 t
ORIGIN

Query Match      85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagatga 22
||||| ||||| ||||| |||||
Db 1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 8
LOCUS AX083675 22 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 22)
AUTHORS van Nest, G.
JOURNAL Methods of modulating an immune response using immunostimulatory s
sequences and compositions for use therein
Patent: WO 0112223-A 1 22-FEB-2001;
Dynavax Technologies Corporation (US)
FEATURES
source
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BASE COUNT      6 a      3 c      7 g      6 t
ORIGIN

Query Match      85.5%; Score 18.8; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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LOCUS		AC011106	171790 bp DNA HTG 30-NOV-1999
DEFINITION		Homo sapiens chromosome 3 clone RP11-400P3 map 3, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	
ACCESSION		AC011106	
VERSION		AC011106.2	GI:6479142
KEYWORDS		HTG; HTGS_PHASE1.	
SOURCE		human.	
ORGANISM		Homo sapiens	
Eukaryota;		Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia;		Eutheria;	Primates; Catarrhini; Hominidae; Homo.
REFERENCE		1 (bases 1 to 171790)	
AUTHORS		Birren,B., Linton,L., Nusbaum,C. and Lander,E.	
TITLE		Homo sapiens chromosome 3, clone RP11-400P3	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 171790)	
AUTHORS		Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collumore,A., Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Lander,E., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.	
DIRECT SUBMISSION			
Submitted (01-OCT-1999)		Whitehead Institute/MIT Center for Genome Research,	320 Charles Street, Cambridge, MA 02141, USA
On Nov 30, 1999		this sequence version replaced gi:6006223.	All repeats were identified using RepeatMasker:
Sait, A.P.A. & Green, P.		(1996-1997)	http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center:		Genome Center	
Center:		Whitehead Institute/ MIT Center for Genome Research	
Center code:		WIBR	
Web site:		http://www-seq.wi.mit.edu	
Contact:		sequence_submission@genome.wi.mit.edu	
Project Information			
Center project name:		L1839	
Center clone name:		400_P_3	
NOTE:		This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.	
1		1154:	contig of 1154 bp in length
		gap of unknown length	
1155		2246:	contig of 1092 bp in length
		gap of unknown length	
2247		3610:	contig of 1364 bp in length
		gap of unknown length	
3611		4929:	contig of 1319 bp in length
		gap of unknown length	
4930		6513:	contig of 1584 bp in length
		gap of unknown length	
6514		7865:	contig of 1352 bp in length
		gap of unknown length	
* * *			
7866		9274:	contig of 1409 bp in length
*		gap of unknown length	
9275		10813:	contig of 1539 bp in length
*		gap of unknown length	
10814		12951:	contig of 2138 bp in length
*		gap of unknown length	
12952		14173:	contig of 1222 bp in length
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14174		16264:	contig of 2091 bp in length
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16265		17933:	contig of 1669 bp in length
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17934		19427:	contig of 1494 bp in length
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19428		20694:	contig of 1267 bp in length
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20695		23140:	contig of 2446 bp in length
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23141		25542:	contig of 2402 bp in length
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25543		29256:	contig of 3714 bp in length
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31895		35730:	contig of 3836 bp in length
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35731		37730:	contig of 2000 bp in length
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37731		40878:	contig of 3148 bp in length
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40879		43394:	contig of 2516 bp in length
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43395		46817:	contig of 3423 bp in length
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46818		50213:	contig of 3396 bp in length
*		gap of unknown length	
50214		53478:	contig of 3265 bp in length
*		gap of unknown length	
53479		58333:	contig of 4855 bp in length
*		gap of unknown length	
58334		61663:	contig of 3330 bp in length
*		gap of unknown length	
61664		64521:	contig of 2858 bp in length
*		gap of unknown length	
64522		69899:	contig of 5378 bp in length
*		gap of unknown length	
69900		75112:	contig of 5213 bp in length
*		gap of unknown length	
75113		79169:	contig of 4057 bp in length
*		gap of unknown length	
79170		84604:	contig of 5435 bp in length
*		gap of unknown length	
84605		88809:	contig of 4205 bp in length
*		gap of unknown length	
88810		92798:	contig of 3989 bp in length
*		gap of unknown length	
92799		100287:	contig of 7489 bp in length
*		gap of unknown length	
100288			

* as soon as it is available and the accession number will
* be preserved.

* 92251: contig of 92251 bp in length
* 92251: gap of unknown length
* 92352
* 115219: contig of 22868 bp in length
* 115220
* 115319: gap of unknown length
* 115320
* 130980: contig of 15661 bp in length
* 130981
* 131080: gap of unknown length
* 131081
* 140758: contig of 9678 bp in length
* 140759
* 140858: gap of unknown length
* 140859
* 143950: contig of 3092 bp in length
* 143951
* 144050: gap of unknown length
* 144051
* 146265: contig of 2215 bp in length
* 146266
* 146365: gap of unknown length
* 146366
* 149065: contig of 2700 bp in length
* 149066
* 149165: gap of unknown length
* 149166
* 150835: contig of 1670 bp in length
* 150836
* 150935: gap of unknown length
* 150936
* 152644: contig of 1709 bp in length
* 152645
* 152744: gap of unknown length
* 152745
* 154629: contig of 1885 bp in length
* 154630
* 154729: gap of unknown length
* 154730
* 156167: contig of 1438 bp in length
* 156168
* 156267: gap of unknown length
* 156268
* 157702: contig of 1435 bp in length
* 157703
* 157702: gap of unknown length
* 157703
* 158950: contig of 1148 bp in length
* 158951
* 159050: gap of unknown length
* 159051
* 160223: contig of 1173 bp in length
* 160224
* 160323: gap of unknown length
* 160324
* 161608: contig of 1285 bp in length
* 161609
* 161709: gap of unknown length
* 161709
* 163277: contig of 1569 bp in length
* 163278
* 163377: gap of unknown length
* 163378
* 164699: contig of 1322 bp in length
* 164700
* 164799: gap of unknown length
* 164800
* 166225: contig of 1426 bp in length
* 166226
* 166325: gap of unknown length
* 166326
* 168051: contig of 1726 bp in length
* 168052
* 168131: gap of unknown length
* 168132
* 169384: contig of 1213 bp in length
* 169385
* 169464: gap of unknown length
* 169465
* 171125: contig of 1661 bp in length
* 171126
* 171225: gap of unknown length
* 171226
* 172510: contig of 1285 bp in length
* 172511
* 172610: gap of unknown length
* 172611
* 173929: contig of 1319 bp in length
* 173930
* 174029: gap of unknown length
* 174030
* 175488: contig of 1459 bp in length
* 175489
* 175589: gap of unknown length
* 175589
* 177362: contig of 1774 bp in length
* 177363
* 177462: gap of unknown length
* 177463
* 178962: contig of 1500 bp in length
* 178963
* 179062: gap of unknown length
* 179063
* 180184: contig of 1122 bp in length
* 180185
* 180284: gap of unknown length
* 180285
* 181420: contig of 1136 bp in length
* 181421
* 181540: gap of unknown length
* 181541
* 182873: contig of 1353 bp in length
* 182874
* 182973: gap of unknown length
* 182974
* 184094: contig of 1121 bp in length
* 184095
* 184194: gap of unknown length
* 184195
* 185336: contig of 1142 bp in length
* 185337
* 185436: gap of unknown length
* 185437
* 186747: contig of 1311 bp in length
* 186748
* 186848: gap of unknown length
* 186849
* 187917: contig of 1070 bp in length
* 187918
* 188017: gap of unknown length
* 188018
* 189057: contig of 1080 bp in length
* 189058
* 189197: gap of unknown length
* 189198
* 190398: contig of 1201 bp in length
* 190399
* 190498: gap of unknown length
* 190499
* 191607: contig of 1109 bp in length

* 191608 191707: gap of unknown length
* 191708 192719: contig of 1012 bp in length
* 192720 192819: gap of unknown length
* 192820 193858: contig of 1039 bp in length
* 193859 193958: gap of unknown length
* 193959 195308: contig of 1350 bp in length.
* Location/Qualifiers
* 1..195308
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="12"
* /clone="RP11-81K13"
BASE COUNT 60902 a 35603 c 36045 g 58883 t 3875 others
ORIGIN

Query Match 85.5%; Score 18.8; DB 74; Length 195308;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggtagagatga 22
|||||
Db 182471 TGATTCTGAAGGTGAGAGATGA 182492

RESULT 12
AC068773/c
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-875H7, WORKING DRAFT SEQUENCE,
19 unordered pieces.
AC068773
AC068773.12 GI:10645231
VERSION
KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 201579)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barberia,J.,
Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisege,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshtari,N.,
Slisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,

Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczka, R., Wood, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 201579)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 5, 2000 this sequence version replaced gi:9665007.

Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: HBHM
Center clone name: RP11-875H7

Summary Statistics
Sequencing vector: M13: L08821
Chemistry: Dye-terminator Big Dye: 7% of reads
Chemistry: Dye-terminator Big Dye: 8% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 179484 bases at least Q40
Consensus quality: 189049 bases at least Q30
Consensus quality: 194048 bases at least Q20
Estimated insert size: 197176, sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 3.7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 26889: contig of 26889 bp in length
* 26990: gap of unknown length
* 26990: contig of 21923 bp in length
* 48912: gap of unknown length
* 48913: contig of 22847 bp in length
* 71859: gap of unknown length
* 71959: contig of 19513 bp in length
* 71960: gap of unknown length
* 91473: contig of 19055 bp in length
* 91573: contig of 14127 bp in length
* 110828: contig of 14127 bp in length
* 124834: gap of unknown length
* 124954: contig of 17275 bp in length
* 124955: gap of unknown length
* 142229: contig of 16058 bp in length
* 142330: gap of unknown length
* 158387: contig of 462 bp in length
* 158388: gap of unknown length
* 164949: contig of 462 bp in length
* 165049: gap of unknown length
* 165050: contig of 5773 bp in length
* 170823: gap of unknown length
* 170923: contig of 3945 bp in length
* 174867: gap of unknown length
* 174868: contig of 4800 bp in length
* 179768: gap of unknown length
* 179768: gap of unknown length
* 184387: contig of 4519 bp in length
* 184387: gap of unknown length
* 184387: contig of 4799 bp in length
* 189285: gap of unknown length
* 189286: gap of unknown length
* 189386: contig of 4168 bp in length
* 193553: gap of unknown length
* 193554: gap of unknown length

* 193654 195798: contig of 2145 bp in length
* 195799 195898: gap of unknown length
* 195899 197854: contig of 1956 bp in length
* 197855 197954: gap of unknown length
* 197955 200320: contig of 2366 bp in length
* 200321 200420: gap of unknown length
* 200421 201579: contig of 1159 bp in length.

Location/Qualifiers
1..201579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-875H7"

BASE COUNT 55675 a 43175 c 42625 g 58257 t 1847 others
ORIGIN

Query Match 85.5%; Score 18.8; DB 73; Length 201579;
Best Local Similarity 90.9%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tgactgtgaaggttagagatga 22
|||||
Db 52875 TGATTGTGAAGGTGAGAGATGA 52854

RESULT 13
AC068211/c
AC068211/c
LOCUS
DEFINITION
Homo sapiens chromosome 4 clone RP11-510P6 map 4, LOW-PASS SEQUENCE
SAMPLING.
AC068211 50487 bp DNA HTG 15-JUN-2000
AC068211.2 GI:8567828
HTG: HTGS_PHASE0.
human.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50487)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-510P6
Unpublished
2 (bases 1 to 50487)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bida, F.,
Boguslavsky, L., Bouckhaghter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehotzky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Meng, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, F.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 15, 2000 this sequence version replaced gi:7671271.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

TITLE
JOURNAL
COMMENT

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TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project information
 Center project name: L10078
 Center clone name: 510_P_6

 * NOTE: This record contains 64 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.
 *
 * 1 692: contig of 692 bp in length
 * 693 792: gap of 100 bp
 * 793 1480: contig of 688 bp in length
 * 1481 1580: gap of 100 bp
 * 1581 2274: contig of 694 bp in length
 * 2275 2374: gap of 100 bp
 * 2375 3068: contig of 694 bp in length
 * 3069 3168: gap of 100 bp
 * 3169 3868: contig of 700 bp in length
 * 3869 3968: gap of 100 bp
 * 3969 4677: contig of 709 bp in length
 * 4678 4777: gap of 100 bp
 * 4778 5497: contig of 720 bp in length
 * 5498 5597: gap of 100 bp
 * 5598 6280: contig of 683 bp in length
 * 6281 6380: gap of 100 bp
 * 6381 7062: contig of 682 bp in length
 * 7063 7162: gap of 100 bp
 * 7163 7858: contig of 696 bp in length
 * 7859 7958: gap of 100 bp
 * 7959 8643: contig of 685 bp in length
 * 8644 8743: gap of 100 bp
 * 8744 9462: contig of 719 bp in length
 * 9463 9562: gap of 100 bp
 * 9563 10243: contig of 681 bp in length
 * 10244 10343: gap of 100 bp
 * 10344 11021: contig of 678 bp in length
 * 11022 11121: gap of 100 bp
 * 11122 11832: contig of 711 bp in length
 * 11833 11932: gap of 100 bp
 * 11933 12635: contig of 703 bp in length
 * 12636 12735: gap of 100 bp
 * 12736 13454: contig of 719 bp in length
 * 13455 13554: gap of 100 bp
 * 13555 14247: contig of 693 bp in length
 * 14248 14347: gap of 100 bp
 * 14348 15042: contig of 695 bp in length
 * 15043 15142: gap of 100 bp
 * 15143 15823: contig of 681 bp in length
 * 15824 15923: gap of 100 bp
 * 15924 16617: contig of 694 bp in length
 * 16618 16717: gap of 100 bp
 * 16718 17386: contig of 669 bp in length
 * 17387 17486: gap of 100 bp
 * 17487 18178: contig of 692 bp in length
 * 18179 18278: gap of 100 bp
 * 18279 18979: contig of 701 bp in length
 * 18980 19079: gap of 100 bp
 * 19080 19780: contig of 701 bp in length
 * 19781 19880: gap of 100 bp
 * 19881 20555: contig of 675 bp in length
 * 20556 20655: gap of 100 bp
 * 20656 21327: contig of 672 bp in length
 * 21328 21427: gap of 100 bp
 * 21428 22111: contig of 684 bp in length

22112 22211: gap of 100 bp
 22212 22882: contig of 671 bp in length
 22883 22982: gap of 100 bp
 22983 23676: contig of 694 bp in length
 23677 23776: gap of 100 bp
 23777 24484: contig of 708 bp in length
 24485 24584: gap of 100 bp
 24585 25284: contig of 700 bp in length
 25285 25384: gap of 100 bp
 25385 26079: contig of 695 bp in length
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 27775 28463: contig of 689 bp in length
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 28564 29246: contig of 683 bp in length
 29247 29346: gap of 100 bp
 29347 30031: contig of 685 bp in length
 30032 30131: gap of 100 bp
 30132 30816: contig of 685 bp in length
 30817 30916: gap of 100 bp
 30917 31620: contig of 704 bp in length
 31621 31720: gap of 100 bp
 31721 32386: contig of 666 bp in length
 32387 32486: gap of 100 bp
 32487 33154: contig of 668 bp in length
 33155 33254: gap of 100 bp
 33255 33931: contig of 677 bp in length
 33932 34031: gap of 100 bp
 34032 34720: contig of 689 bp in length
 34721 34820: gap of 100 bp
 34821 35504: contig of 684 bp in length
 35505 35604: gap of 100 bp
 35605 36290: contig of 686 bp in length
 36291 36390: gap of 100 bp
 36391 37111: contig of 721 bp in length
 37112 37211: gap of 100 bp
 37212 37876: contig of 665 bp in length
 37877 37976: gap of 100 bp
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 38676 38775: gap of 100 bp
 38776 39440: contig of 665 bp in length
 39441 39540: gap of 100 bp
 39541 40234: contig of 694 bp in length
 40235 40334: gap of 100 bp
 40335 41019: contig of 685 bp in length
 41020 41119: gap of 100 bp
 41120 41804: contig of 685 bp in length
 41805 41904: gap of 100 bp
 41905 42596: contig of 692 bp in length
 42597 42696: gap of 100 bp
 42697 43397: contig of 701 bp in length
 43398 43497: gap of 100 bp
 43498 44201: contig of 704 bp in length
 44202 44301: gap of 100 bp
 44302 44971: contig of 670 bp in length
 44972 45071: gap of 100 bp
 45072 45747: contig of 676 bp in length
 45748 45847: gap of 100 bp
 45848 46525: contig of 678 bp in length
 46526 46625: gap of 100 bp
 46626 47313: contig of 688 bp in length
 47314 47413: gap of 100 bp
 47414 48102: contig of 689 bp in length
 48103 48202: gap of 100 bp
 48203 48893: contig of 691 bp in length
 48894 48993: gap of 100 bp
 48994 49683: contig of 690 bp in length
 49684 49783: gap of 100 bp
 49784 50487: contig of 704 bp in length.

Location/Qualifiers

FEATURES

```

source
1. 50487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-510P6"
/clone_lib="RPC1-11 Human Male BAC"
BASE COUNT 9358 a 12945 c 11645 g 9887 t 6652 others
ORIGIN

Query Match 83.6% Score 18.4; DB 73; Length 50487;
Best Local Similarity 95.0%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 gactgtgaaggttagagatga 22
|||||
Db 46016 ACTGTGAAGGTAGAGATGA 45997

RESULT 14
AL139127 121682 bp DNA HTG 20-JAN-2001
LOCUS
DEFINITION Homo sapiens chromosome 10 clone RP5-964H6 map p14-15.3, ***
SEQUENCING IN PROGRESS ***, 5 unordered pieces.
ACCESSION AL139127
VERSION AL139127.3 GI:9931359
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 121682)
Sims, S.
Direct Submission
Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerquest@sanger.ac.uk
On Aug 28, 2000 this sequence version replaced gi:9863522.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dj964H6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 119498 bases at least Q40
Consensus quality: 120247 bases at least Q30
Consensus quality: 120704 bases at least Q20
Insert size: 121282; sum-of-contigs
Insert size: 131684; 5.8% error; agarose-fp
Quality coverage: 4.1ix in Q20 bases; sum-of-contigs Quality
coverage: 3.35x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 59702: contig of 59702 bp in length
* 59703 59802: gap of 100 bp
* 59803 66307: contig of 6505 bp in length
* 66308 66407: gap of 100 bp
* 66408 112097: contig of 45690 bp in length
* 112098 112197: gap of 100 bp
* 112198 117976: contig of 5779 bp in length
* 117977 118076: gap of 100 bp

FEATURES
* 118077 121682: contig of 3606 bp in length.
Location/Qualifiers
1. 121682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="p14-15.3"
/clone="RP5-964H6"
/clone_lib="RPC1-5"
1. 59702
/clone="assembly_fragment:01296"
vector_end:SP6
vector_side:left"
59803. 66307
/clone="assembly_fragment:01300"
fragment_chain:1"
66408. 112097
/clone="assembly_fragment:00869"
fragment_chain:1"
112198. 117976
/clone="assembly_fragment:00252"
fragment_chain:1"
118077. 121682
/clone="assembly_fragment:00060"
fragment_chain:1"
BASE COUNT 37596 a 22666 c 22252 g 38767 t 401 others
ORIGIN

Query Match 83.6% Score 18.4; DB 78; Length 121682;
Best Local Similarity 95.0%; Pred. No. 81;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gactgtgaaggttagagatg 21
|||||
Db 79149 GAATGTGAAGGTAGAGATG 79168

RESULT 15
AL138773 125661 bp DNA PRI 26-SEP-2000
LOCUS
DEFINITION Human DNA sequence from clone RP4-660B20 on chromosome 10 Contains
STSS, GSSs and a CpG island, complete sequence.
ACCESSION AL138773
VERSION AL138773.4 GI:7801531
KEYWORDS HTG; CpG island.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 125661)
Chapman, J.
Direct Submission
Submitted (08-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerquest@sanger.ac.uk
On May 14, 2000 this sequence version replaced gi:7799640.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at

```

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>
 RP4-660B20 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>
 VECTOR: pCYPAC2

This sequence is the entire Insert of clone RP4-660B20.

FEATURES

source

Location/Qualifiers
 1..125661
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP4-660B20"
 /clone_lib="RPCI-4"

repeat_region
 1..888
 /note="Cheshire repeat: matches 843..1750 of consensus"
 repeat_region
 893..1043
 /note="L1M48 repeat: matches 6130..6280 of consensus"
 repeat_region
 1276..1381
 /note="Cheshire repeat: matches 717..822 of consensus"
 repeat_region
 1381..1449
 /note="L1R16A repeat: matches 260..328 of consensus"
 repeat_region
 1753..2052
 /note="L1MB8 repeat: matches 5870..6171 of consensus"
 repeat_region
 2208..2409
 /note="L1M4C repeat: matches 1528..1718 of consensus"
 repeat_region
 2413..2593
 /note="L1MC/D repeat: matches 3511..3697 of consensus"
 repeat_region
 2594..3771
 /note="L1PA3 repeat: matches 4125..5302 of consensus"
 repeat_region
 3770..4606
 /note="L1PA3 repeat: matches 5310..6146 of consensus"
 repeat_region
 4627..5363
 /note="L1MC/D repeat: matches 3684..4447 of consensus"
 repeat_region
 5479..5530
 /note="26 copies 2 mer ca 71% conserved"
 repeat_region
 5482..5529
 /note="12 copies 4 mer acac 75% conserved"
 repeat_region
 5542..5809
 /note="L1MC/D repeat: matches 4533..4783 of consensus"
 repeat_region
 5875..6636
 /note="L1MC/D repeat: matches 4769..5403 of consensus"
 repeat_region
 7633..7942
 /note="L1ME3A repeat: matches 5840..6142 of consensus"
 repeat_region
 7987..8160
 /note="MER5A repeat: matches 9..184 of consensus"
 repeat_region
 8343..8701
 /note="L1T1A2 repeat: matches 1..369 of consensus"
 misc_feature
 8451..8918
 /note="match: GSS: Em:AQ737749"
 repeat_region
 8848..8960
 /note="12 repeat: matches 2575..2689 of consensus"
 repeat_region
 9291..9592
 /note="AluX repeat: matches 1..304 of consensus"
 repeat_region
 9639..9880
 /note="121 copies 2 mer aa 57% conserved"
 repeat_region
 9678..9803
 /note="6 copies 21 mer 83% conserved"
 repeat_region
 9888..10250
 /note="THE1B repeat: matches 1..364 of consensus"
 repeat_region
 11020..11299
 /note="AluX repeat: matches 1..284 of consensus"
 repeat_region
 11743..11828
 /note="MIR repeat: matches 128..240 of consensus"
 repeat_region
 12587..12914
 /note="MER1B repeat: matches 1..337 of consensus"
 repeat_region
 14357..14647
 /note="AluX repeat: matches 9..304 of consensus"
 repeat_region
 14648..14673
 /note="13 copies 2 mer ga 92% conserved"

repeat_region
 15356..15643
 /note="144 copies 2 mer at 59% conserved"
 repeat_region
 15365..15644
 /note="70 copies 4 mer tata 58% conserved"
 misc_feature
 complement(15685..15951)
 /note="match: GSS: Em:AQ312235"
 repeat_region
 15719..16026
 /note="AluSg repeat: matches 1..308 of consensus"
 repeat_region
 16421..16536
 /note="L1MA6 repeat: matches 5903..6012 of consensus"
 repeat_region
 16553..16859
 /note="Tigger2a repeat: matches 2..299 of consensus"
 repeat_region
 17186..17221
 /note="18 copies 2 mer tt 80% conserved"
 repeat_region
 17366..17466
 /note="L1MA6 repeat: matches 5903..5997 of consensus"
 repeat_region
 18160..18458
 /note="AluX repeat: matches 1..312 of consensus"
 repeat_region
 18947..19238
 /note="AluSc repeat: matches 1..304 of consensus"
 repeat_region
 19328..19571
 /note="MIR repeat: matches 2..257 of consensus"
 misc_feature
 20189..20715
 /note="match: GSS: Em:AQ286231"
 repeat_region
 20305..21057
 /note="L1MB7 repeat: matches 5320..6171 of consensus"
 repeat_region
 21058..21340
 /note="Alu2b repeat: matches 1..286 of consensus"
 repeat_region
 21341..21408
 /note="L1MB7 repeat: matches 5255..5320 of consensus"
 repeat_region
 21498..21732
 /note="L1MB7 repeat: matches 4849..5084 of consensus"
 repeat_region
 21777..21950
 /note="L1M4C repeat: matches 1955..1651 of consensus"
 repeat_region
 21976..22031
 /note="14 copies 4 mer tata 75% conserved"
 repeat_region
 21981..22018
 /note="19 copies 2 mer at 86% conserved"
 repeat_region
 22032..22343
 /note="AluY repeat: matches 1..311 of consensus"
 repeat_region
 23476..23864
 /note="L1T1B repeat: matches 1..387 of consensus"
 repeat_region
 25026..25333
 /note="AluSg repeat: matches 1..311 of consensus"
 repeat_region
 25379..25692
 /note="AluX repeat: matches 1..312 of consensus"
 repeat_region
 25706..25833
 /note="L1M4C repeat: matches 198..321 of consensus"
 repeat_region
 25834..26206
 /note="NSTA repeat: matches 5..424 of consensus"
 repeat_region
 26207..27128
 /note="L1M4C repeat: matches 321..1280 of consensus"
 repeat_region
 27201..27463
 /note="L1M4C repeat: matches 1368..1622 of consensus"
 repeat_region
 27464..27827
 /note="THE1B repeat: matches 1..364 of consensus"
 repeat_region
 27828..28192
 /note="L1M4C repeat: matches 1622..2015 of consensus"
 misc_feature
 28136..28640
 /note="match: GSS: Em:AQ572610"
 repeat_region
 28631..29947
 /note="L1MEC repeat: matches 2338..3341 of consensus"
 repeat_region
 29953..30242
 /note="AluX repeat: matches 1..302 of consensus"
 repeat_region
 30464..30705
 /note="12 repeat: matches 2514..2746 of consensus"
 repeat_region
 31139..31184
 /note="L1PA15-16 repeat: matches 42..86 of consensus"
 repeat_region
 31403..31700
 /note="AluSg repeat: matches 1..298 of consensus"
 repeat_region
 33240..33303
 /note="32 copies 2 mer aa 68% conserved"
 misc_feature
 complement(34175..34584)

```
misc_feature      /note="match: GSS: Em:AQ076707"  
complement(34241..34577)  
repeat_region    /note="match: GSS: Em:AQ076705"  
34366..34571  
misc_feature      /note="L1M1 repeat: matches 6087..6304 of consensus"  
complement(35050..35753)  
repeat_region    /note="match: GSS: Em:AQ508227"  
35339..35396  
misc_feature      /note="AluYb8 repeat: matches 243..304 of consensus"  
repeat_region    /note="L1M1 repeat: matches 300..422 of consensus"  
35376..35492  
misc_feature      /note="MSTB repeat: matches 35725..35995"  
complement(35725..35995)  
repeat_region    /note="match: STS: Em:L30522"  
35874..35971  
misc_feature      /note="49 copies 2 mer ct 73% conserved"  
repeat_region    35885..35972  
misc_feature      /note="22 copies 4 mer tcta 79% conserved"  
repeat_region    36012..36375  
misc_feature      /note="MLT1A1 repeat: matches 2..365 of consensus"  
repeat_region    36437..36480  
/note="11 copies 4 mer tcca 86% conserved"
```

Query Match 83.6%; Score 18.4; DB 89; Length 125661;
Best Local Similarity 95.0%; Pred No. 81;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gactgtgaaggttagagatg 21
|||
DB 114151 GAATGTGACGTTAGAGATG 114170

Search completed: October 9, 2001, 16:21:09
Job time: 2639 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:27 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-9
Perfect score: 22
Sequence: 1 tgactgtgaaggttagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues 20456230
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_estl1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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9: gb_est9:*
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116: gb_est38:*

```

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188: gb_est108:*
189: gb_est109:*

```

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194: em_gss_hum1:*
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196: em_gss_hum3:*
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217: em_gss_vrt3:*
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253: em_gss_rod6:*
254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = "RGP",
S14862_62.

FEATURES Location/Qualifiers
source
1. .463
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="S14862"
/clone_lib="Rice green shoot"
/note="green shoot (8 days old)" 2 others
BASE COUNT 151 a 74 c 109 g 127 t

Query Match 85.5%; Score 18.8; DB 107; Length 463;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagatga 22
|||||
Db 151 TGAGTGTGAATGTTAGAGATGA 172

RESULT 2
LOCUS AU089685 479 bp mRNA EST 27-APR-2000
DEFINITION AU089685 Rice callus Oryza sativa subsp. japonica cDNA clone C40060
ACCESSION AU089685
VERSION AU089685.1 GI:7652165
KEYWORDS EST.
SOURCE Oryza sativa subsp. japonica.
ORGANISM Oryza sativa subsp. japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 479)
AUTHORS Sasaki, T. and Yamamoto, K.
TITLE Rice cDNA from callus (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = "RGP",
C40060_32.

FEATURES Location/Qualifiers
source
1. .479
/organism="Oryza sativa subsp. japonica"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:39947"
/clone="C40060"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site1: SalI; Site2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid."
BASE COUNT 149 a 96 c 104 g 130 t

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	463	107	AU083559
2	18.8	85.5	479	107	AU089685
3	17.8	80.9	267	139	BE752532
4	17.8	80.9	398	167	BE428418
5	17.8	80.9	474	167	BE419241
6	17.8	80.9	477	149	BF475131
7	17.8	80.9	541	114	AW305665
8	17.8	80.9	558	114	AW282093
9	17.8	80.9	561	249	AV755668
10	17.8	80.9	612	32	AV653619
11	17.8	80.9	620	162	BE060267
12	17.8	80.9	622	245	AZ503307
13	17.8	80.9	667	149	BF484589
14	17.8	80.9	930	146	BF257509
15	17.8	80.9	1616	81	BF631455
16	17.4	79.1	468	244	AZ447787
17	17.4	79.1	468	243	AZ431843
18	17.4	79.1	497	151	BF651333
19	17.4	79.1	627	243	AZ391922
20	17.4	79.1	711	106	AL586641
21	17.2	78.2	361	32	AV695932
22	17.2	78.2	361	32	AV697012
23	17.2	78.2	364	32	AV697012
24	17.2	78.2	367	152	BG373458
25	17.2	78.2	374	148	BF395765
26	17.2	78.2	380	163	BE116790
27	17.2	78.2	402	163	BE104970
28	17.2	78.2	405	239	AZ179136
29	17.2	78.2	411	32	AV684231
30	17.2	78.2	424	139	BE723539
31	17.2	78.2	452	238	AZ105474
32	17.2	78.2	456	240	AZ227719
33	17.2	78.2	471	21	A1555197
34	17.2	78.2	471	113	AW270792
35	17.2	78.2	510	228	AQ435695
36	17.2	78.2	513	148	BF388422
37	17.2	78.2	519	168	BF681745
38	17.2	78.2	521	230	AQ567409
39	17.2	78.2	533	143	BF039764
40	17.2	78.2	547	140	BE803661
41	17.2	78.2	573	242	AZ385615
42	17.2	78.2	588	232	AQ680793
43	17.2	78.2	616	240	AZ229260
44	17.2	78.2	624	21	A1514086
45	17.2	78.2	665	249	AZ759002

ALIGNMENTS

RESULT 1
LOCUS AU083559 463 bp mRNA EST 21-MAR-2000
DEFINITION AU083559 Rice green shoot Oryza sativa cDNA clone S14862, mRNA
ACCESSION AU083559
VERSION AU083559.1 GI:7274015
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 463)
AUTHORS Sasaki, T. and Yamamoto, K.
TITLE Rice cDNA from green shoot (2000)
JOURNAL Unpublished (2000)

```

Query Match      85.5%; Score 18.8; DB 107; Length 479;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagatga 22
    ||| ||||| ||||| |||||
Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 3
BE752532      267 bp mRNA EST 15-SEP-2000
LOCUS 204944 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE752532
ACCESSION BE752532
VERSION BE752532.1 GI:10166524
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 267)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrnerkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 53 row: M column: 1
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source
1..267
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 86 a 56 c 63 g 62 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 139; Length 267;
Best Local Similarity 90.5%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaaggttagatga 22
    ||| ||||| ||||| |||||
Db 223 GCCTGTGAAGGTTAAGATGA 243

RESULT 4
BE428418      398 bp mRNA EST 26-JUL-2000
LOCUS MTD006.G10F990616 ITEC MTD Durum Wheat Root Library Triticum
DEFINITION turgidum subsp. durum cDNA clone MTD006.G10, mRNA sequence.

Query Match      80.9%; Score 17.8; DB 167; Length 398;
Best Local Similarity 90.3%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaaggttagatga 22
    ||| ||||| ||||| |||||
Db 321 GACGGTGAAAGTTAGAGATGA 341

RESULT 5
BE419241      474 bp mRNA EST 24-JUL-2000
LOCUS WMR021.G5R000101 ITEC WMR Wheat Root Library Triticum aestivum cDNA
DEFINITION clone WMR021.G5, mRNA sequence.
ACCESSION BE419241
VERSION BE419241.1 GI:9417087
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 474)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
TITLE International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
JOURNAL Unpublished (2000)

ACCESSION BE428418.1 GI:9426261
VERSION BE428418.1
KEYWORDS EST.
SOURCE durum wheat.
ORGANISM Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 398)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
TITLE International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
JOURNAL Unpublished (2000)

FEATURES
source
1..398
/organism="Triticum turgidum subsp. durum"
/cultivar="Sillana"
/db_xref="taxon:4567"
/clone_lib="ITEC MTD Durum Wheat Root Library"
/tissue_type="root"
/dev_stage="3-day-old seedling, water-stressed"
/notes="Vector: pSPORT1; T7 primers used. See pSPORT1
polylinker site. 0.3-2.0 kbp average insert size."
BASE COUNT 99 a 77 c 104 g 118 t
ORIGIN

```

COMMENT

Contact: Schuch W
zeneca wheat improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
Email: wolfgang.schuch@zeneca.com
International Triticeae EST Cooperative (ITPC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers

FEATURES

source

1...474

/organism="Triticum aestivum"

/cultivar="Novosibirskaya 67"

/db_xref="taxon:4565"

/clone="WNR021.G5"

/clone_lib="ITPC WMR Wheat Root Library"

/tissue_type="root"

/note="M13 Reverse sequencing primer used for 5' end of

clone."

BASE COUNT 119 a 87 c 127 g 141 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 167; Length 474;
Best Local Similarity 90.5%; Pred. NO. 3.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaagggttagagatga 22

||||| ||||| ||||| ||||| |||||

Db 350 GACGGTGAAGTTAGAGATGA 370

RESULT 6

BF475131

LOCUS 477 bp mRNA EST 04-DEC-2000

DEFINITION WHE2111_B12_D23ZS wheat salt-stressed crown cDNA library Triticum aestivum cDNA clone WHE2111_B12_D23, mRNA sequence.

ACCESSION BF475131

VERSION BF475131.1 GI:11544313

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.

1 (bases 1 to 477)

REFERENCE Akhunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J., Dvorak, J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Lazo, G.R., Miller, R., Otto, C., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C. and Zhang, D.

The structure and function of the expressed

genomes - Salt-stressed crown cDNA library

Unpublished (2000)

JOURNAL

COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: andersn@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1...477

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE2111_B12_D23"

/clone_lib="Wheat salt-stressed crown cDNA library"

/tissue_type="Crown"

/dev_stage="Adult plant"

/lab_host="E. coli SOLR"

/note="Vector: Lambda Uni-2AP XR, excised phagemid;

FEATURES

source

1...541

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone_lib="zebrafish adult brain"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

Site_1: ECORI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA and poly(A) RNA were prepared from crown tissue, equal portions of RNA were pooled from the two treatments, a cDNA library was made, and the cDNA clones were in vivo excised to give phaluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OB Anderson lab (all other authors)."

BASE COUNT 132 a 84 c 120 g 140 t 1 others

ORIGIN

Query Match 80.9%; Score 17.8; DB 149; Length 477;
Best Local Similarity 90.5%; Pred. NO. 3.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaagggttagagatga 22

||||| ||||| ||||| ||||| |||||

Db 197 GACGGTGAAGTTAGAGATGA 217

RESULT 7

AW305665

LOCUS 541 bp mRNA EST 20-JAN-2000

DEFINITION f162b09.y1 zebrafish adult brain Danio rerio cDNA 5' similar to TR:075223 O75223 WUGSC:H_DJ077023.1 PROTEIN.; contains Alu repetitive element;; mRNA sequence.

ACCESSION AW305665

VERSION AW305665.1 GI:6718018

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.

1 (bases 1 to 541)

REFERENCE Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: f162b09.x1

JOURNAL

COMMENT

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: John Ngai, cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

Seq primer: T3 ET from Amersham

High quality sequence stop: 458.

Location/Qualifiers

1...541

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone_lib="zebrafish adult brain"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

```

/lab_host="E. coli DH10B"
/notes="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZIPLOX. Mass
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library."
BASE COUNT      145 a   123 c   161 g   112 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 114; Length 541;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaggttagagatga 22
||| ||||| ||||| |||||
Db 434 GAGTGTGACAGATTAGAGATGA 454

RESULT 8
AW282093/c      558 bp      mRNA      EST      04-JAN-2000
LOCUS
DEFINITION      f162809.x1 zebrafish adult brain Danio rerio cDNA 3' similar to
TR:075223 O75223 WUGSC:H_DJ077023.1 PROTEIN. ; mRNA sequence.
ACCESSION      AW282093
VERSION
KEYWORDS
SOURCE
ORGANISM      Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE
AUTHORS      Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
TITLE      WashU Zebrafish EST Project 1998
JOURNAL
COMMENT      Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Ngai. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatabank, Berlin, Germany (web address:
www.fzpd.de)
Seq primer: T7 ET from Amersham
High quality sequence stop: 406.
FEATURES
source
Location/Qualifiers
1..558
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/notes="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZIPLOX. Mass
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library."
BASE COUNT      111 a   165 c   123 g   158 t
ORIGIN

/lab_host="E. coli DH10B"
/notes="vector: pGEM-T Easy; Human genomic DNA was
partially digested with Sau3AI, ligated to ds linkers,
and enriched for binding to human PAX3d+ protein using a
whole genome PCR-based strategy. DNA fragments containing
putative PAX3d+ binding sites were amplified by PCR and
cloned into pGEM-T Easy (Promega). The ligation products
were transformed into DH10B electrocompetent cells (Life
Technologies)."
BASE COUNT      126 a   149 c   152 g   134 t
ORIGIN

Query Match      80.9%; Score 17.8; DB 249; Length 561;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatg 21
||||| ||||| ||| |||||
Db 461 TGACTGTGACAGTCAGAGATG 441

RESULT 10
AV653619
LOCUS
DEFINITION      AV653619 GLC Homo sapiens cDNA clone GLC2MG10 3', mRNA sequence.

```

```

ACCESSION      AV653619      1  GI:9874633
VERSION        AV653619.1
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 612)
              Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.
              Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Qu,J.,
              Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
              G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
              Homo sapiens cDNA clone
              Unpublished (2000)
              Contact: Zequang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex.45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.
FEATURES       Location/Qualifiers
               1..612
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="GICDMG10"
                /clone_lib="GLC"
                /tissue_type="corresponding non cancerous liver tissue"
                /dev_stage="Adult"
                /lab_host="SOLR"
                /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                XhoI"
BASE COUNT    155 a 121 c 152 g 183 t 1 others
ORIGIN
Query Match      80.9%; Score 17.8; DB 32; Length 612;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaagggttagagatg 21
    ||||| |||| |||||
Db 10 TGACTGTGACAGTTGGAGATG 30

RESULT 11
BE060267      620 bp      mRNA      EST      27-FEB-2001
LOCUS         HVSMEG0011M13f Hordeum vulgare pre-anthesis spike EST library
DEFINITION    HVCDA0008 (white to yellow anther) Hordeum vulgare cDNA clone
              HVSMEG0011M13f, mRNA sequence.
ACCESSION     BE060267
VERSION       BE060267.2  GI:13154164
KEYWORDS      EST.
SOURCE        Hordeum vulgare
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
              ; Triticeae; Hordeum.
              1 (bases 1 to 620)
REFERENCE     Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
AUTHORS       Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
              T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
              Wood,T.
              Development of a genetically and physically anchored EST resource
              for barley genomics
              Unpublished (2000)
              On Jun 9, 2000 this sequence version replaced gi:8404917.
              Contact: Wing RA
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 471.
Location/Qualifiers
1..620
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEG0011M13f"
HVCDA0008 (white to yellow anther)
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/note="Vector: lambda2AP; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT    165 a 115 c 155 g 185 t
ORIGIN
Query Match      80.9%; Score 17.8; DB 162; Length 620;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 gactgtgaagggttagagatga 22
    ||||| ||||| |||||
Db 302 GACGTCGAAAGTTAGAGATGA 322

RESULT 12
AZ503307/c    622 bp      DNA      GSS      05-OCT-2000
LOCUS         1M0343F02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    Clone UUGC1M0343F02 F, DNA sequence.
ACCESSION     AZ503307
VERSION       AZ503307.1  GI:10684623
KEYWORDS      GSS.
SOURCE        house mouse.
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 622)
REFERENCE     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS       Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0343 row: F column: 02
              Seq primer: CGTTGTAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 622.
              Location/Qualifiers
              1..622
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0343F02"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 177 a 144 c 140 g 161 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 245; Length 622;
Best Local Similarity 90.5%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaaggttagagatga 22
||||| ||||||| |||||

Db 34 GACTGTGTTAGGTAGATCA 14

RESULT 13
BF484589 667 bp mRNA EST 06-DEC-2000
LOCUS
DEFINITION WHE2317_D03_G0525 wheat pre-anthesis spike cDNA library Triticum aestivum
ACCESSION BF484589
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 667)
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han P.S., Haia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@nwp.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers

FEATURES
source 1..667
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2317_D03_G05"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="vector: Lambda Uni-2AP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; plants were grown in the greenhouse. Whole spike with awns trimmed, white, green

and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the T3 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 172 a 125 c 170 g 199 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 149; Length 667;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaaggttagagatga 22
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Db 333 GACGGTGAAGTTAGAGATGA 353

RESULT 14
BF257509 930 bp mRNA EST 23-FEB-2001
LOCUS
DEFINITION HVSMEF0013B18f Hordeum vulgare seedling root EST library HVCNDA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone
ACCESSION BF257509
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE 1 (bases 1 to 930)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
TITLE Development of a genetically and physically anchored EST resource for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCCTAAAGG
High quality sequence start: 48
High quality sequence stop: 764.
Location/Qualifiers

FEATURES
source 1..930
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEF0013B18f"
/clone_lib="Hordeum vulgare seedling root EST library HVCNDA0007 (etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 241 a 195 c 251 g 242 t
ORIGIN

Query Match 80.9%; Score 17.8; DB 146; Length 930;
Best Local Similarity 90.5%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaaggttagagatga 22
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Wed Oct 10 05:59:37 2001

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Db 539 GACGGTGAAGCTTAGAGATGA 559
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XX
AC BF631455;
XX
SV BF631455.1
XX
DT 21-DEC-2000 (Rel. 66, Created)
DT 21-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE HVSMEB0016A02f Hordeum vulgare seedling shoot EST library HVCDNA0002
DE (Dehydration stress) Hordeum vulgare cDNA clone HVSMEB0016A02f, mRNA
DE sequence.
XX
KW EST.
XX
OS Hordeum vulgare (barley)
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
XX
RN [1]
RP 1-1616
RA Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yu Y.,
RA Anderson H., Dale J., Henry D., Kernodle S., Palmer M., Rambo T.,
RA Saski C., Schwartzbeck J., Simmons J., Choi D.W., Main D., Wood T.;
RT "Development of a genetically and physically anchored EST resource for
RT barley genomics";
RL Unpublished.
XX
CC Contact: Wing RA
CC Clemson University Genomics Institute
CC Clemson University
CC 100 Jordan Hall, Clemson, SC 29634, USA
CC Tel: 864 656 7288
CC Fax: 864 656 4293
CC Email: rwing@clemson.edu
CC Seq primer: AATTACCTCCTACTAAGGG
CC High quality sequence start: 6
CC High quality sequence stop: 146.
XX
FH Key
FH Location/Qualifiers
FT source
FT 1. 1616
FT /db_xref="taxon:4513"
FT /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
FT /organism="Hordeum vulgare"
FT /cultivar="Morex"
FT /clone="HVSMEB0016A02f"
FT /clone_lib="Hordeum vulgare seedling shoot EST library
FT HVCDNA0002 (dehydration stress)"
FT /tissue_type="Seedling shoot"
FT /lab_host="TJC121"
XX
SQ Sequence 1616 BP; 471 A; 350 C; 385 G; 341 T; 69 other;
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Best Local Similarity 86.4%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Oy 1 tgactgtgaaggtagagatga 22
   ||| ||||| ||||| |||||
Db 1405 TTACGGTGANGTTAGAGATGA 1426
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Search completed: October 9, 2001, 18:20:29
Job time: 9799 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-9
Perfect score: 22
Sequence: 1 tgcgtgtagatgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601.*

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15: /SID58/gcgdata/geneseq/geneseq/NA1994.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV55788	Immunostimulatory
2	22	100.0	22	AAV80104	Oligo used in expe
3	22	100.0	22	AAC64052	Non-Cpg control ph
4	22	100.0	22	AAV96252	Sequence of a stab
5	20.4	92.7	22	AAV32080	Nucleotide sequenc
6	20.4	92.7	22	AAV36625	ISS-ODN mutant DY1
7	20.4	92.7	22	AAV55791	Immunostimulatory
8	20.4	92.7	22	AAV55797	Immunostimulatory
9	20.4	92.7	22	AAV80110	Oligo used in expe
10	20.4	92.7	22	AAV14468	Inactive Immunost
11	20.4	92.7	22	AAV55878	Non-immunomodulat

12	20	90.9	22	AAV55881	Immunomodulatory o
13	19.6	89.1	22	AAV77046	Immunostimulatory
14	19.6	89.1	22	AAV77047	Immunostimulatory
15	19.4	88.2	22	AAV55880	Immunomodulatory o
16	18.8	85.5	22	AAV32079	Nucleotide sequenc
17	18.8	85.5	22	AAV36624	ISS-ODN DY1018 nuc
18	18.8	85.5	22	AAV55790	Immunostimulatory
19	18.8	85.5	22	AAV55794	Immunostimulatory
20	18.8	85.5	22	AAV80106	Oligo used in expe
21	18.8	85.5	22	AAV80097	Immunomodulatory o
22	18.8	85.5	22	AAV80102	Immunomodulatory o
23	18.8	85.5	22	AAV80103	Immunomodulatory o
24	18.8	85.5	22	AAV64051	Immunostimulatory
25	18.8	85.5	22	AAV96253	Sequence of a stab
26	18.8	85.5	22	AAV96260	Sequence of a stab
27	18.8	85.5	22	AAV90458	Cpg adjuvant oligo
28	18.8	85.5	22	AAV90459	Cpg adjuvant oligo
29	18.8	85.5	22	AAV14467	Immunostimulatory
30	18.8	85.5	22	AAV14469	Mutant immunostimu
31	18.8	85.5	22	AAV38065	Immunostimulatory
32	18.8	85.5	22	AAV38071	Immunostimulatory
33	18.8	85.5	22	AAV38072	Immunostimulatory
34	18.8	85.5	22	AAV55876	Immunomodulatory o
35	18.8	85.5	22	AAV77040	Immunomodulatory D
36	18.8	85.5	22	AAV29800	Cholera toxin immu
37	18.8	85.5	22	AAV31345	Immune response en
38	18.8	85.5	22	AAV82107	Oligonucleotide OD
39	18.8	85.5	22	AAV92377	CG motif and CFA c
40	18.8	85.5	22	AAV92378	CG motif and CFA c
41	18	81.8	22	AAV77045	Immunostimulatory
42	17.8	80.9	22	AAV55877	Immunomodulatory o
43	17.2	78.2	22	AAV80105	Oligo used in expe
44	17.2	78.2	22	AAV80107	Oligo used in expe
45	17.2	78.2	22	AAV92379	CG motif and CFA c

ALIGNMENTS

RESULT 1

AAV55788
ID AAV55788 standard; DNA; 22 BP.
XX AAV55788;
AC AAV55788;
XX 29-MAR-1999 (first entry)
DT 29-MAR-1999 (first entry)
XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.
XX Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW Immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
XX Synthetic.
OS Synthetic.
XX WO9855609-A1.
XX 10-DEC-1998.
XX 05-JUN-1998; 98WO-US11391.
XX 06-JUN-1997; 97US-0048793.
PR (REGC) UNIV CALIFORNIA.
XX Ray E. Roman M;
XX WPI; 1999-080827/07.
XX New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease

XX PS Example 1; Fig 1; 50pp; English.

XX CC This sequence represents an example of a immunostimulatory sequence

CC CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN

CC CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-2-Py-Py or

CC CC 5'-Pu-Pu-Y-2-Py-polyPy for inhibiting immunostimulation caused by

CC CC ISS-ODNs that contain a hexamer region consisting of at least one CpG

CC CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;

CC CC Y = any natural or synthetic nucleotide other than C; Z = any natural or

CC CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.

CC CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs

CC CC when this is present in (i) a recombinant expression vector (being used

CC CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly

CC CC one in a host and associated with an autoimmune disease). Particularly

CC CC the inhibitors prolong gene expression from the vector and reduce

CC CC inflammation caused by microbial infection. They also modulate activity

CC CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune

CC CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes

CC CC or monocytes by reducing the Th1-type response and stimulating the

CC CC Th2-type response to an antigen (including antigen-stimulated

CC CC immunoglobulin G1 production). Prolonged expression from the gene therapy

CC CC vector avoids the need for repeated treatments and re-engineering of the

CC CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over

CC CC the effect of ISS-ODN-based adjuvants and can be used even where the

CC CC existence, identity and location of the ISS-ODNs are unknown. The

CC CC inhibitors are effective at very low doses.

XX CC

SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22

RESULT 2
 AAV80104
 ID AAV80104 standard; DNA; 22 BP.
 AC AAV80104;
 XX
 XX 12-MAR-1999 (first entry)
 DT
 XX
 DE Oligo used in experiments for stimulation of cytokine production.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; trypanosoma; schistosoma.
 XX
 OS Synthetic.
 XX
 XX WO9855495-A2.
 PN
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 XX 06-JUN-1997; 97US-0048793.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA
 PI Dina D, Roman M, Schwartz D;
 XX
 XX WPI; 1999-059898/05.
 DR
 XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and
 contain an immune-stimulating octanucleotide sequence; for treating

PT cancer, allergic and infectious diseases

XX

PS Example 1; Page 29; 63pp; English.

XX

CC The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG, GAGTTCC, and GAGTTCCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent

CC oligonucleotides that were tested for immunostimulatory activity. These

CC were used in experiments for the stimulation of cytokine production and

CC were found to lack immunostimulatory activity. The invention provides

CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX

SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22

RESULT 3
 AAC64052
 ID AAC64052 standard; DNA; 22 BP.
 XX
 AC AAC64052;
 XX
 XX 15-FEB-2001 (first entry)
 DT
 XX
 DE Non-CpG control phosphorothioate oligodeoxynucleotide.
 XX
 KW Non-CpG control oligodeoxynucleotide; phosphorothioate;
 KW immunostimulatory; CpG ISS ODN; enhanced antigen presentation;
 KW antigen-presenting cell; APC; T-cell activation; tumour cell;
 KW tumour antigen; cancer immunotherapy; vaccine; ss.
 XX
 OS Synthetic.
 XX
 XX WO200062787-A1.
 PN
 XX
 PD 26-OCT-2000.
 XX
 XX 11-APR-2000; 2000WO-US09664.
 PF
 XX
 PR 15-APR-1999; 99US-0292278.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 PI Raz E, Martin-Orozco E;
 XX
 XX WPI; 2000-679548/66.
 DR
 XX
 XX Enhancing antigen-presentation capabilities of T-cells for cancer
 PT immunotherapy, by contacting cells with an immunostimulatory
 PT oligonucleotide -
 XX
 XX Example 1; Page 18; 42pp; English.
 PS
 XX The invention relates to a method of inducing activation of T-cells
 CC to respond to an antigen, comprising contacting antigen-presenting cells

CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
 CC thus treated have enhanced antigen presenting capabilities compared to
 CC antigen-activated APCs. APCs with enhanced antigen-presentation
 CC capabilities then present the antigen to T-cells. The method is useful
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell
 CC activation, and is therefore useful for treating tumours. Additionally,
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation
 CC of Fc-receptor expression, to present antigen through upregulation of
 CC major histocompatibility complex (MHC) Class I and II expression and
 CC CD1d expression, to produce co-stimulatory factors (B7 and CD40), to
 CC provide cell-to-cell adhesion through upregulation of intercellular
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
 CC cytokine production, all at levels greater than that achieved through
 CC contact of APC with antigen alone. The present sequence represents
 CC a phosphorothioate non-CpG oligodeoxynucleotide used as a control
 CC with ISS-ODN AAC64051 in the exemplifications of the invention.
 XX
 SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
 |||||
 Db 1 tgactgtgaagggttagagatga 22

RESULT 4
 AAA96252
 ID AAA96252 standard; DNA; 22 BP.
 AC AAA96252;
 XX
 DT 08-FEB-2001 (first entry)
 DE
 XX Sequence of a stabilised oligonucleotide with antitumour activity.
 XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
 KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
 XX
 OS Synthetic.
 XX
 PN WO200056342-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-FR00676.
 XX
 PR 19-MAR-1999; 99FR-0003433.
 XX
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 XX (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 PI Carpentier A;
 XX
 DR WPI; 2000-602192/57.
 XX

PT Use of stabilized oligonucleotides as antitumor agents, particularly
 PT against nervous system tumors, have optimal activity and are not toxic
 PT
 PS Example 2; Page 16; 57pp; French.

XX The present sequence represents a stabilised oligonucleotide which has
 CC antitumour activity. The oligonucleotide comprises an octamer motif
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
 CC immunostimulatory, and are not toxic. They may be adapted for use in
 CC animals or humans. The stabilised oligonucleotides are used for

CC treating tumours, of any type and any degree of anaplasia, particularly
 CC human tumours in the peripheral or central nervous systems, specifically
 CC glioblastomas, medullablastomas, neuroblastomas, melanomas or carcinomas.
 XX
 SQ Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
 |||||
 Db 1 tgactgtgaagggttagagatga 22

RESULT 5
 AAV32080
 ID AAV32080 standard; DNA; 22 BP.
 XX
 AC AAV32080;
 XX
 DT 09-SEP-1998 (first entry)
 XX
 DE Nucleotide sequence of DY1019.
 XX
 KW DY1019; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.
 XX
 OS synthetic.

FH Key Location/Qualifiers
 FT modified_base 1..22
 FT /*tag= a
 FT /note= "phosphothioate backbone"
 XX
 PN WO9816247-A1.
 XX
 PD 23-APR-1998.
 XX
 PF 09-OCT-1997; 97WO-US19004.
 XX
 PR 11-OCT-1996; 96US-0028118.
 XX

PA (REGC) UNIV CALIFORNIA.
 XX
 PI Carson DA, Raz E, Roman M;
 XX
 DR WPI; 1998-261028/23.

XX New immunomodulatory compositions - comprising an antigen conjugated
 PT to a polynucleotide that contains an immunostimulatory sequence
 PT
 PS Example 1; Page 36; 69pp; English.

XX This is the nucleotide sequence of DY1019, which is conjugated to
 CC beta-gal in the method of the invention to form PN/IMM, comprising an
 CC immunomodulatory molecule (IMM), which comprises an antigen conjugated
 CC to a polynucleotide (PN) that contains at least one immunostimulatory
 CC nucleotide sequence (ISS). The conjugate synergistically boost the
 CC magnitude of the host immune response against an antigen to a level
 CC greater than the host immune response to either the IMM, antigen or
 CC ISS-PN alone. These responses to ISS-PN/IMM conjugates are
 CC particularly acute during the important early phase of the host immune
 CC response to an antigen. The ISS-PN/IMM conjugates boost both humoral
 CC (antibody) and cellular (Th1 type) immune responses of the host. Thus,
 CC use of the method to boost the immune responsiveness of a host to
 CC subsequent challenge by a sensitising antigen without immunisation
 CC avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by
 CC suppressing IgE production in response to the antigen challenge. The
 CC conjugates can also be used to combat pathogenic infection and to
 CC stimulate therapeutic angiogenesis to treat conditions in which
 CC localised blood flow plays a significant etiological role, e.g.

CC retinopathies.
 XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;
 SQ Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match
 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22
 |||||

RESULT 7
 AAV55791
 ID AAV55791 standard; DNA; 22 BP.
 XX
 AC AAV55791;
 XX
 DT 29-MAR-1999 (first entry)
 XX
 DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1041.
 XX
 KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
 KW immunostimulatory activity; gene therapy; genetic immunisation;
 KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
 XX
 OS Synthetic.
 XX
 PN W09855609-A1.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11391.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Ray E; Roman M;
 XX
 DR WPI; 1999-080827/07.
 XX
 PT New oligonucleotide that inhibits action of immunostimulatory
 PT sequence oligonucleotides - particularly those present in gene
 PT therapy vectors or microbial pathogens, used to prolong gene therapy
 PT expression and to treat e.g. infections or autoimmune disease
 XX
 PS Example 1; Fig 1; 50pp; English.
 XX
 SS This sequence represents an example of an immunostimulatory sequence
 CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
 CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or
 CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by
 CC ISS-ODNs that contain a hexamer region consisting of at least one Cpg
 CC motif flanked by two 5'-Pu and two 3'-py. Pu = purine; py = pyrimidine;
 CC Y = any natural or synthetic nucleotide other than C; Z = any natural or
 CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.
 CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
 CC when this is present in (i) a recombinant expression vector (being used
 CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
 CC one in a host and associated with an autoimmune disease). Particularly
 CC the inhibitors prolong gene expression from the vector and reduce
 CC inflammation caused by microbial infection. They also modulate activity
 CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
 CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
 CC or monocytes by reducing the Th1-type response and stimulating the
 CC Th2-type response to an antigen (including antigen-stimulated
 CC immunoglobulin G1 production). Prolonged expression from the gene therapy
 CC vector avoids the need for repeated treatments and re-engineering of the
 CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
 CC the effect of ISS-ODN-based adjuvants and can be used even where the
 CC existence, identity and location of the ISS-ODNs are unknown. The
 CC inhibitors are effective at very low doses.
 XX
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

CC
 XX
 SQ Query Match.
 92.7%; Score 20.4; DB 20; Length 22;

CC
 XX
 SQ retinopathies.
 XX Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;
 SQ Best Local Similarity 92.7%; Score 20.4; DB 19; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match
 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22
 |||||

RESULT 6
 AAX36625
 ID AAX36625 standard; DNA; 22 BP.
 XX
 AC AAX36625;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE ISS-ODN mutant DY1019 nucleotide sequence.
 XX
 KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;
 KW allergic rhinitis; atopic dermatitis; asthma; nasal polyposis;
 KW eosinophilic fasciitis; therapy; ss.
 XX
 OS Synthetic.
 XX
 PN W09911275-A2.
 XX
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18382.
 XX
 PR 05-SEP-1997; 97US-0927120.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Ray E;
 XX
 DR WPI; 1999-312404/26.
 XX
 PT Reducing antigen-stimulated granulocyte-mediated inflammation
 XX
 PS Example 2; Page 30; 69pp; English.
 XX
 SS This is the ISS-ODN mutant DY1019 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.
 XX
 SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
 |||||
 DB 1 tgactgtgaagcttagagatga 22

RESULT 8

AAV55797
 ID AAV55797 standard; DNA; 22 BP.

XX
 AC AAV55797;

XX
 DT 29-MAR-1999 (first entry)

XX
 DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DV1061.

XX
 KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;

KW Immunostimulatory activity; gene therapy; genetic immunisation;

KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.

XX
 OS Synthetic.

XX
 PN WO9855609-A1.

XX
 PD 10-DEC-1998.

XX
 PF 05-JUN-1998; 98WO-US11391.

XX
 PR 06-JUN-1997; 97US-0048793.

XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Ray E, Roman M;

XX
 DR WPI; 1999-080827/07.

XX
 PT New oligonucleotide that inhibits action of immunostimulatory

PT sequence oligonucleotides - particularly those present in gene

PT therapy vectors or microbial pathogens, used to prolong gene therapy

PT expression and to treat e.g. infections or autoimmune disease

XX
 PS Example 1; Fig 3; 50pp; English.

XX
 CC This sequence represents an example of a immunostimulatory sequence

CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN

CC sequences have a hexamer region of sequence 5'-pu-pu-y-2-py-py or

CC 5'-pu-pu-y-2-py-polypr for inhibiting immunostimulation caused by

CC ISS-ODNs that contain a hexamer region consisting of at least one Cpg

CC motif flanked by two 5'-pu and two 3'-py. Pu = purine; Py = pyrimidine;

CC y = any natural or synthetic nucleotide other than C; z = any natural or

CC synthetic nucleotide, but if y is not G or inosine (I), then z is G or I.

CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs

CC when this is present in (i) a recombinant expression vector (being used

CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly

CC one in a host and associated with an autoimmune disease). Particularly

CC the inhibitors prolong gene expression from the vector and reduce

CC inflammation caused by microbial infection. They also modulate activity

CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune

CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes

CC or monocytes by reducing the Th1-type response and stimulating the

CC Th2-type response to an antigen (including antigen-stimulated

CC immunoglobulin G1 production). Prolonged expression from the gene therapy

CC vector avoids the need for repeated treatments and re-engineering of the

CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over

CC the effect of ISS-ODN-based adjuvants and can be used even where the

CC existence, identity and location of the ISS-ODNs are unknown. The

CC inhibitors are effective at very low doses.

XX
 SQ Sequence 22 BP; 7 A; 1 C; 7 G; 7 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
 |||||
 DB 1 tgactgtgaatgttagagatga 22

RESULT 9

AAV80110

ID AAV80110 standard; DNA; 22 BP.

XX
 AC AAV80110;

XX
 DT 12-MAR-1999 (first entry)

XX
 DE Oligo used in experiments for stimulation of cytokine production.

XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;

KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;

KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;

KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX
 OS Synthetic.

XX
 PN WO9855495-A2.

XX
 PD 10-DEC-1998.

XX
 PF 05-JUN-1998; 98WO-US11578.

XX
 PR 06-JUN-1997; 97US-0048793.

XX
 PA (DYNA-) DYNAX TECHNOLOGIES CORP.

XX
 PI Dina D, Roman M, Schwartz D;

XX
 DR WPI; 1999-059898/05.

XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and

PT contain an immune-stimulating octanucleotide sequence; for treating

PT cancer, allergic and infectious diseases

XX
 PS Example 2; Page 30; 63pp; English.

XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise

CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS

CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,

CC GAGGTTC, and GAGGTTCG. The immunomodulatory sequences are used to treat

CC patients needing immune regulation, such as those suffering from cancer,

CC an allergic disease and asthma. They are also used to prevent infectious

CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency

CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and

CC Bordetella pertussis, malarial plasmodia, Leishmania, trypanosoma and

CC Schistosoma. The immunomodulatory sequences are used to screen for human

CC immunostimulatory activity by incubating macrophage cells and the

CC oligonucleotide; and determining the relative amount of Th1-biased

CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent

CC oligonucleotides that were tested for immunostimulatory activity. These

CC were used in experiments for the stimulation of cytokine production and

CC were found to lack immunostimulatory activity. The invention provides

CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 Other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.8;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22

Db 1 tgactgtgaagcttagagatga 22

RESULT 10
AAA14468
ID AAA14468 standard; DNA; 22 BP.
XX
AC AAA14468;
XX
DT 21-AUG-2000 (first entry)
XX
DE Inactive immunostimulatory oligonucleotide DY1019.
XX
KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.
XX
OS Synthetic.
XX
PN WO200020039-A1.
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US21203.
XX
PR 05-OCT-1998; 98US-0167039.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Raz E, Horner AA, Carson DA;
XX
DR WPI; 2000-303647/26.
XX
PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
PT an antigen in a mammalian host through production of secretory
PT immunoglobulin A -
XX
PS Example 7; Page 63; 64pp; English.

The invention relates to a method of inducing mucosal immunity to an antigen in a mammalian host, including the production of secretory immunoglobulin A (sigA). Immune protection in the mucosa (the principal site of entry of most foreign antigens) is mediated by mucosa-associated lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory cell sub-populations. The primary immune response which characterizes the induction of mucosal immunity to an antigen is sigA production by activated B-cells. The method comprises introducing an immunostimulatory oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the ISS-ODN includes a core nucleotide sequence. The core nucleotide sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID NOS 1-3). A specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used as an adjuvant with an antigen for stimulating mucosal immunity. The level of sigA production induced in the host is at least 3 times the magnitude of sigA production achievable in response to introduction of antigen alone into the mucosal tissue and is equivalent or greater than the magnitude of sigA production achievable in response to introduction of the antigen and cholera toxin adjuvant into the mucosal tissue. The host immune response is stimulated to antigen specific IgA production, biased towards the Th1 phenotype while antigen-induced IgE production is avoided. The adjuvant has little or no known toxicity in mammals and its efficacy is comparable to that of cholera toxin which is used as a mucosal adjuvant. The present sequence represents an inactive ISS-ODN, DY1019, used in an exemplification of the invention.

Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.8;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaagcttagagatga 22

Db 1 tgactgtgaagcttagagatga 22

RESULT 11
AAZ55878
ID AAZ55878 standard; DNA; 22 BP.
XX
AC AAZ55878;
XX
DT 10-APR-2000 (first entry)
XX
DE Non-immunomodulatory oligonucleotide SEQ ID NO: 3.
XX
KW Non-immunomodulatory; immunostimulatory sequence; adjuvant;
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
KW asthma; immunocontraception; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /*tag= a
FT /note= "Phosphorothioate linkages"
XX
PN WO9962923-A2.
XX
PD 09-DEC-1999.
XX
PF 04-JUN-1999; 99WO-US12538.
XX
PR 05-JUN-1998; 98US-0088310.
PR 01-JUN-1999; 99US-0324191.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D;
XX
DR WPI; 2000-105687/09.
XX
PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
PT response, e.g. to tumor antigens -
XX
PS Example 1; Page 35; 54pp; English.
XX
CC Sequences AAZ55878-255879 represent oligonucleotides which do not
CC contain an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT,
CC AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTCC and GACGTTCC),
CC and which did not exhibit immunomodulatory activity in an
CC exemplification of the present invention. The invention relates to
CC oligonucleotides comprising one or more ISSs, where the ISS comprises at
CC least one modified cytosine with an electron-withdrawing moiety at
CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
CC contain ISSs comprising at least one bromocytosine, whereas sequence
CC AAZ55876 contains an unmodified ISS. The immunomodulatory
CC oligonucleotides have an adjuvant-like effect: when formulated with an
CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
CC and induce a Th1-type immune response (activation of cytotoxic T cells),
CC while simultaneously downregulating the Th2-type response. The Th1
CC response is particularly effective for control of viruses and
CC intracellular parasites. The immunomodulatory oligonucleotides are used,
CC particularly when formulated with an antigen or a facilitator, for
CC modulating immune responses. Such compositions may be used in tumour
CC therapy, in treatment of allergy (including asthma), for inducing a
CC vigorous cellular response (against a virus, bacterium, fungus or
CC protozoan), and also in contraceptive vaccines based on sperm antigens.
XX
SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.8;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22

RESULT 12
 AA255881
 ID AA255881 standard; DNA; 22 BP.
 AC AA255881;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Immunomodulatory oligonucleotide SEQ ID NO: 6.
 XX
 KW Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunosuppression; 5-bromocytosine; ss.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FH modified_base 1..22
 FT /tag= a
 FT /note= "Phosphorothioate linkages"
 FT misc_feature 9..16
 FT /tag= b
 FT /note= "Immunostimulatory sequence (ISS)"
 FT modified_base 11
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 FT modified_base 15
 FT /tag= d
 FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 XX
 PN WO962923-A2.
 XX
 PD 09-DEC-1999.
 XX
 XX 04-JUN-1999; 99WO-US12538.
 XX
 XX 05-JUN-1998; 98US-0088310.
 PR 01-JUN-1999; 99US-0324191.
 XX
 XX (DYNA-) DYNAX TECHNOLOGIES CORP.
 PA
 XX
 XX Schwartz D;
 PI
 XX
 DR WPI; 2000-105687/09.
 XX
 XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
 PT response, e.g. to tumor antigens
 PT
 XX
 XX Claim 31; Page 35; 54pp; English.
 PS
 XX

Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
 CC AACGTC, AACGTC, AGCGTC, AGCGTC, AGCGTC, GACGTC, GACGTC, GCGGTT,
 CC AACGTC and GACGTC). The invention relates to oligonucleotides
 CC comprising one or more ISSs, where the ISS comprises at least
 CC one modified cytosine with an electron-withdrawing moiety at
 CC position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886
 CC contain ISSs comprising at least one bromocytosine, whereas sequence
 CC AA255876 contains an unmodified ISS. The immunomodulatory
 CC oligonucleotides have an adjuvant-like effect; when formulated with an
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),
 CC while simultaneously downregulating the Th2-type response. The Th1

CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX
 SQ Sequence 22 BP; 6 A; 1 C; 7 G; 6 T; 2 other;

Query Match 90.9%; Score 20; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22
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 Db 1 tgactgtgaaggttagagatga 22

RESULT 13
 AAF77046
 ID AAF77046 standard; DNA; 22 BP.
 XX
 AC AAF77046;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Immunostimulatory DNA #6.
 XX
 KW Modulate; immune; antigen; immunostimulatory; ds.
 XX
 OS Synthetic.
 XX
 PN WO200112223-A2.
 XX
 PD 22-FEB-2001.
 XX
 XX 18-AUG-2000; 2000WO-US22835.
 XX
 XX 19-AUG-1999; 99US-0149768.
 PR
 XX (DYNA-) DYNAX TECHNOLOGIES CORP.
 PA
 XX
 XX Van Nest G;
 PI
 XX
 XX WPI; 2001-211136/21.
 DR
 XX
 XX Modulating immune response to a second antigen in humans involves
 PT administering an immunostimulatory polynucleotide comprising an
 PT immunostimulatory sequence and a first antigen
 PT
 XX Disclosure; Page 15; 63pp; English.
 PS
 XX The present invention relates to modulating an immune response to
 CC a second antigen in an individual, involving
 CC administering to the individual an immunomodulatory polynucleotide
 CC comprising an immunostimulatory sequence (ISS) and a first antigen.
 XX
 XX Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;

Query Match 89.1%; Score 19.6; DB 22; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.9;
 Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaggttagagatga 22
 |||||
 Db 1 tgactgtgaaggttagagatga 22

RESULT 14
 AAF77047

```

ID AAF77047 standard; DNA; 22 BP.
XX AAF77047;
XX
XX
DT 15-MAY-2001 (first entry)
XX
DE Immunostimulatory DNA #7.
XX
KW Modulate; immune; antigen; immunostimulatory; ds.
XX
OS Synthetic.
XX
PN WO200112223-A2.
XX
XX
PD 22-FEB-2001.
XX
XX
PF 18-AUG-2000; 2000WO-US22835.
XX
XX
PR 19-AUG-1999; 99US-0149768.
XX
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX
PI Van Nest G;
XX
XX
DR WPI; 2001-211136/21.
XX
XX
PT Modulating immune response to a second antigen in humans involves
PT administering an immunostimulatory polynucleotide comprising an
PT immunostimulatory sequence and a first antigen.
XX
XX
PS Disclosure; Page 15; 63pp; English.
XX
XX
CC The present invention relates to modulating an immune response to
CC a second antigen in an individual, involving
CC administering to the individual an immunomodulatory polynucleotide
CC comprising an immunostimulatory sequence (ISS) and a first antigen.
XX
XX
SQ Sequence 22 BP; 6 A; 1 C; 7 G; 6 T; 2 other;

Query Match 89.1%; Score 19.6; DB 22; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.9;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaabgttagagatga 22

RESULT 15
AAZ55880
ID AAZ55880 standard; DNA; 22 BP.
XX
XX
AC AAZ55880;
XX
XX
DT 10-APR-2000 (first entry)
XX
XX
DE Immunomodulatory oligonucleotide SEQ ID NO: 5.
XX
XX
KW Immunomodulation; immunostimulatory sequence; adjuvant;
KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
KW asthma; immunosuppression; 5-bromocytosine; ss.
XX
XX
OS Mus musculus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /*tag a
FT /*note "Phosphorothioate linkages"
FT misc_feature 9..16
FT /*tag b
FT /*note "Immunostimulatory sequence (ISS)"

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FT modified_base 11
FT /*tag c
FT /*mod_base OTHER
FT /*note "5-bromocytosine"
XX
PN WO9962923-A2.
XX
PD 09-DEC-1999.
XX
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PF 04-JUN-1999; 99WO-US12538.
XX
XX
PR 05-JUN-1998; 98US-0088310.
PR 01-JUN-1999; 99US-0324191.
XX
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX
PI Schwartz D;
XX
XX
DR WPI; 2000-105687/09.
XX
XX
PT Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
PT response, e.g. to tumor antigens.
XX
XX
PS Claim 30; Page 35; 54pp; English.
XX
XX
CC Sequences AAZ55876-255877 and AAZ55880-255886 represent immunomodulatory
CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
CC AACGTC, AAGGTT, AGCGTC, AGCGTC, AGCGTC, GACGTC, GACGTC, GACGTC,
CC AACGTC and GACGTC). The invention relates to oligonucleotides
CC comprising one or more ISSs, where the ISS comprises at least
CC one modified cytosine with an electron-withdrawing moiety at
CC position C-5 or C-6 of the base. Sequences AAZ55877 and AAZ55880-255886
CC contain ISSs comprising at least one bromocytosine, whereas sequence
CC AAZ55876 contains an unmodified ISS. The immunomodulatory
CC oligonucleotides have an adjuvant-like effect: when formulated with an
CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
CC and induce a Th1-type immune response (activation of cytotoxic T cells),
CC while simultaneously downregulating the Th2-type response. The Th1
CC response is particularly effective for control of viruses and
CC intracellular parasites. The immunomodulatory oligonucleotides are used,
CC particularly when formulated with an antigen or a facilitator, for
CC modulating immune responses. Such compositions may be used in tumour
CC therapy, in treatment of allergy (including asthma), for inducing a
CC vigorous cellular response (against a virus, bacterium, fungus or
CC protozoan), and also in contraceptive vaccines based on sperm antigens.
XX
XX
SQ Sequence 22 BP; 6 A; 2 C; 7 G; 6 T; 1 other;

Query Match 88.2%; Score 19.4; DB 21; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaangttcagatga 22

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16: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*

17: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*

18: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*

19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*

20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*

21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*

22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*

23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*

24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*

25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*

26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*

27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*

28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*

29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*

30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*

31: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*

32: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*

33: /cgn2_6/ptodata/1/pna/US6001_COMB.seq:*

34: /cgn2_6/ptodata/1/pna/US6002_COMB.seq:*

35: /cgn2_6/ptodata/1/pna/US6003_COMB.seq:*

36: /cgn2_6/ptodata/1/pna/US6004_COMB.seq:*

37: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:*

38: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:*

39: /cgn2_6/ptodata/1/pna/US6007_COMB.seq:*

40: /cgn2_6/ptodata/1/pna/US6008_COMB.seq:*

41: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:*

42: /cgn2_6/ptodata/1/pna/US6010_COMB.seq:*

43: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	1	PCT-US01-03029-3
2	22	100.0	22	1	PCT-US01-11290-4
3	22	100.0	22	1	PCT-US01-14508-12
4	22	100.0	22	16	US-09-296-477-3
5	22	100.0	22	18	US-09-470-382-70
6	22	100.0	22	28	US-09-713-136-9
7	22	100.0	22	30	US-09-774-403-3
8	22	100.0	22	31	US-09-828-505-4
9	20.4	92.7	22	1	PCT-US00-35064-2
10	20.4	92.7	22	1	PCT-US01-03029-2
11	20.4	92.7	22	1	PCT-US01-06034-4
12	20.4	92.7	22	1	PCT-US01-06034-5
13	20.4	92.7	22	1	PCT-US01-06034-6
14	20.4	92.7	22	1	PCT-US01-06034-8
15	20.4	92.7	22	1	PCT-US01-11290-2
16	20.4	92.7	22	1	PCT-US01-14508-10
17	20.4	92.7	22	1	PCT-US01-14508-11
18	20.4	92.7	22	1	PCT-US99-21203-20
19	20.4	92.7	22	13	US-08-927-120-20
20	20.4	92.7	22	15	US-09-167-039-20
21	20.4	92.7	22	16	US-09-235-742-20
22	20.4	92.7	22	16	US-09-296-477-13
23	20.4	92.7	22	17	US-09-308-036A-2
24	20.4	92.7	22	17	US-09-324-191A-3
25	20.4	92.7	22	22	US-09-570-325-20
26	20.4	92.7	22	28	US-09-700-354-2
27	20.4	92.7	22	29	US-09-746-130-2
28	20.4	92.7	22	30	US-09-774-403-2
29	20.4	92.7	22	30	US-09-791-500-4
30	20.4	92.7	22	30	US-09-791-500-5
31	20.4	92.7	22	30	US-09-791-500-6
32	20.4	92.7	22	30	US-09-791-500-8
33	20.4	92.7	22	31	US-09-828-505-2
34	20	90.9	22	16	US-09-296-477-16
35	20	90.9	22	17	US-09-324-191A-6
36	20	90.9	22	25	US-09-642-492-8
37	19.6	89.1	22	18	US-09-415-186-7
38	19.6	89.1	22	18	US-09-415-186-8
39	19.4	88.2	22	16	US-09-296-477-15
40	19.4	88.2	22	17	US-09-324-191A-5
41	19.4	88.2	22	25	US-09-642-492-7
42	19.4	88.2	22	28	US-09-713-136-7
43	19.4	88.2	22	28	US-09-713-136-8
44	18.8	85.5	22	1	PCT-US00-18229-32
45	18.8	85.5	22	1	PCT-US00-18229-33


```

? GENERAL INFORMATION:
? APPLICANT: Raz, Eyal
? APPLICANT: Lois, Augusto F.
? APPLICANT: Takabayashi, Kenji
? TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
? TITLE OF INVENTION: Methods of Use Thereof
? FILE REFERENCE: 06510/168WO1
? CURRENT APPLICATION NUMBER: PCT/US01/14508
? CURRENT FILING DATE: 2000-05-04
? PRIOR APPLICATION NUMBER: 60/362,321
? PRIOR FILING DATE: 2001-01-17
? PRIOR APPLICATION NUMBER: 60/202,274
? PRIOR FILING DATE: 2000-05-05
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 12
? LENGTH: 22
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: M-ODN
PCT-US01-14508-12
Query Match 100.0% Score 22: DB 1: Length 22:

```

	mismatches	44;	conservative	mismatches	insc15	comp
Oy	1	tgaactgtgaagggtagagatga	22			
Dd	1	tgaactgtgaagggtagagatga	22			
RESULT	4					

```

? sequence 37. Application: 05/052504778
?
? GENERAL INFORMATION:
?
? APPLICANT: RAZ, E.
? APPLICANT: SCHWARTZ, D.
? APPLICANT: ROMAN, M.
? APPLICANT: DINA, D.
?
? TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
? COMPOSITIONS THEREOF AND METHODS OF USE
?
? TITLE OF INVENTION: THEREOF
?
? FILE REFERENCE: 377882000420
?
? CURRENT APPLICATION NUMBER: US/09/296,477A
?
? CURRENT FILING DATE: 1999-04-22
?
? EARLIER APPLICATION NUMBER: 09/092,329
?
? EARLIER FILING DATE: 1998-06-05
?
? EARLIER APPLICATION NUMBER: 60/048,793
?
? EARLIER FILING DATE: 1997-06-06
?
? NUMBER OF SEQ ID NOS: 21
?
? SOFTWARE: FastSeq for Windows Version 3.0
?
? SEQ ID NO 3
?
? LENGTH: 22
?
? TYPE: DNA
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: Synthetic construct

```

Query Match	100.0%;	Score 22;	DB 16;	Length 22;
Best Local Similarity	100.0%;	Pred. NO. 1.7;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	tgactgtgaagggttagagatga	22	
	.			
Db	1	tgactgtgaagggttagagatga	22	

```

RESULT 5
US-09-470-382-70
; Sequence 70, Application US/09470382
; GENERAL INFORMATION:
; APPLICANT: Eyal R. Raz
; APPLICANT: M. Teresa Magone
; TITLE OF INVENTION: METHOD FOR AMELIORATING AN ALLERGIC
; TITLE OF INVENTION: REACTION
; FILE REFERENCE: 30448.73US01
; CURRENT APPLICATION NUMBER: US/09/470.382
; CURRENT FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-470-382-70

Query Match      100.0%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 6
US-09-713-136-9
; Sequence 9, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: An Immunomodulatory Compositions Containing
; TITLE OF INVENTION: Sequence Linked To Antigen And Methods
; TITLE OF INVENTION: Of Use Thereof
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713.136
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165.467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-9

Query Match      100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 7
US-09-774-403-3
; Sequence 3, Application US/09774403
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth

```

```

; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: 6510-166US1
; CURRENT APPLICATION NUMBER: US/09/774.403
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
US-09-774-403-3

```

```

Query Match      100.0%; Score 22; DB 30; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

```

```

RESULT 8
US-09-828-505-4
; Sequence 4, Application US/09828505
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; TITLE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203
; CURRENT APPLICATION NUMBER: US/09/828.505
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control nucleic acid sequence
US-09-828-505-4

```

```

Query Match      100.0%; Score 22; DB 31; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 tgactgtgaagggttagagatga 22
   |||||
Db 1 tgactgtgaagggttagagatga 22

```

```

RESULT 9
PCT-US00-35064-2
; Sequence 2, Application PC/TUS0035064
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Preventing an Anaphylactic
; TITLE OF INVENTION: Reaction
; FILE REFERENCE: 06510/201WO1

```

; CURRENT APPLICATION NUMBER: PCT/US00/35064
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/171,830
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant
PCT-US00-35064-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||||| ||||| ||||| |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 10
PCT-US01-03029-2
; Sequence 2, Application PC/TUS0103029
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; FILE REFERENCE: 06510/166W01
; CURRENT APPLICATION NUMBER: PCT/US01/03029
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control sequence
PCT-US01-03029-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||||| ||||| ||||| |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 11
PCT-US01-06034-4
; Sequence 4, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-4

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||||| ||||| ||||| |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 12
PCT-US01-06034-5
; Sequence 5, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-5

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||||| ||||| ||||| |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 13
PCT-US01-06034-6
; Sequence 6, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmillewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;

Search completed: October 9, 2001, 21:12:48
Job time: 20073 sec

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 14

PCT-US01-06034-8
; Sequence 8, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-8

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 15

PCT-US01-11290-2
; Sequence 2, Application PC/TUS0111290
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; TITLE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203WO
; CURRENT APPLICATION NUMBER: PCT/US01/11290
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control nucleic acid sequence
PCT-US01-11290-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22
|||||
Db 1 tgactgtgaaggttagagatga 22


```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-10

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 3
US-09-802-359-9
; Sequence 9, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-9

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 4
US-09-802-376-9
; Sequence 9, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-9
```

```
Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 5
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2
```

```
Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
   |||||
DB 1 tgactgtgaagggttagagatga 22

RESULT 6
US-09-770-943-4
; Sequence 4, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-4
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Query Match      92.7%; Score 20.4; DB 6; Length 22;
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Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaagcttagagatga 22

RESULT 7
US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10

Query Match 92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaagcttagagatga 22

RESULT 8
US-09-802-518-8
; Sequence 8, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 95.5%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaagcttagagatga 22

RESULT 9
US-09-802-359-8
; Sequence 8, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaangttngagatga 22

RESULT 10
US-09-802-376-8
; Sequence 8, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-8

Query Match 90.9%; Score 20; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||| ||||| ||||| ||||| |||||

Db 1 tgactgtgaangttngagatga 22

RESULT 11
US-09-802-518-7
; Sequence 7, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 37788201100
; CURRENT APPLICATION NUMBER: US/09/802,518
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine)G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-518-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaangttcgagatga 22

RESULT 12
US-09-802-359-7
; Sequence 7, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-359-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaangttcgagatga 22

RESULT 13

US-09-802-376-7
; Sequence 7, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing (5-bromocytosine) G
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = 5-bromocytosine
US-09-802-376-7

Query Match 88.2%; Score 19.4; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaangttcgagatga 22

RESULT 14
US-09-770-943-3
; Sequence 3, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-3

Query Match 85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggttagagatga 22

Db 1 tgactgtgaaccttagagatga 22

RESULT 15

US-09-770-943-7


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; Sequence 7, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-7
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```
Query Match      85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggtagagatga 22
   ||||| |||| |||||
Db 1 tgactgtgaggtagagatga 22
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Search completed: October 9, 2001, 21:36:23
Job time: 21243 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:10 ; Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

Title: US-09-713-136-9

Perfect score: 22
Sequence: 1 tgactgtgaaggtagagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	4	US-09-092-314-1
2	20.4	92.7	22	4	US-09-092-314-2
3	20.4	92.7	22	4	US-09-092-314-4
4	20.4	92.7	22	4	US-09-092-314-10
5	18.8	85.5	22	4	US-09-092-314-3
6	18.8	85.5	22	4	US-09-092-314-7
7	18.8	85.5	22	4	US-09-092-314-8
8	16.2	73.6	913	2	US-08-975-316-61
9	15.6	70.9	22	4	US-09-092-314-5
10	15.6	70.9	6909	2	US-08-804-196-1
11	15.6	70.9	6909	2	US-08-658-340-1
12	15.6	70.9	6909	2	US-08-746-111-26
13	15.2	69.1	1892	3	US-08-933-750C-66
14	15.2	69.1	1892	3	US-09-234-613-66
15	15.2	69.1	3655	3	US-08-878-474-6
16	15.2	69.1	4440	3	US-07-792-600-1
17	15.2	69.1	4440	3	US-09-157-021-1
18	15.2	69.1	4440	3	US-09-156-842-1
19	15.2	69.1	5433	3	US-09-157-021-35
20	15.2	69.1	5433	3	US-09-156-842-35
21	15.2	69.1	6638	2	US-08-070-301-2
22	15	68.2	6623	2	US-08-687-080-68
23	14.8	67.3	882	1	US-08-622-354-4
24	14.8	67.3	1129	3	US-08-755-587-30
25	14.6	66.4	419	4	US-08-998-416-118
26	14.6	66.4	864	1	US-08-173-510B-94
27	14.6	66.4	864	1	US-08-173-510B-96

Sequence 92, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 96, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 3, Appl
Patent No. 5340934
Sequence 4, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 25, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 1, Appl

28 14.6 66.4 864 1 US-08-458-218-92
29 14.6 66.4 864 1 US-08-458-218-94
30 14.6 66.4 864 2 US-08-450-497-94
31 14.6 66.4 864 2 US-08-450-497-96
32 14.6 66.4 1272 4 US-09-053-702-1
33 14.6 66.4 2694 3 US-08-975-703-5
34 14.6 66.4 2694 4 US-09-515-884-5
35 14.6 66.4 3846 2 US-08-691-814B-3
36 14.6 66.4 5687 2 US-08-380-403A-3
37 14.6 66.4 5687 2 US-08-895-628-3
38 14.6 65.5 1357 6 5340934-7
39 14.4 65.5 2658 2 US-08-910-927B-4
40 14.4 65.5 2658 4 US-09-270-270-4
41 14.2 64.5 756 2 US-08-530-165-1
42 14.2 64.5 1261 3 US-08-961-083-25
43 14.2 64.5 1314 1 US-07-662-005A-15
44 14.2 64.5 2572 3 US-08-976-255-1
45 14.2 64.5 2675 1 US-08-232-079-1

ALIGNMENTS

RESULT 1
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaggtagagatga 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgactgtgaaggtagagatga 22

RESULT 2
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
      ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 3
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
      ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

US-09-092-314-10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

Query Match          92.7%  Score 20.4;  DB 4;  Length 22;
Best Local Similarity 95.5%  Pred. No. 0.1;
Matches 21;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
      ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 5
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match          85.5%  Score 18.8;  DB 4;  Length 22;
Best Local Similarity 90.9%  Pred. No. 0.62;
Matches 20;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy  1  tgactgtgaaggttagagatga 22
      ||||| ||||| ||||| |||||
Db  1  tgactgtgaacgttagagatga 22

RESULT 6
US-09-092-314-7
; Sequence 7, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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;
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-7

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||| |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 7
US-09-092-314-8
; Sequence 8, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-8

Query Match 85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
||||| ||| |||||
Db 1 tgactgtgaagggttagagatga 22

RESULT 8
US-08-975-316-61
; Sequence 61, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316

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; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-975-316-61

Query Match 73.6%; Score 16.2; DB 2; Length 913;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 gactgtgaagggttagagatga 22
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Db 513 GACTGTGAATTTTACAGATGA 533

RESULT 9
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-5

Query Match 70.9%; Score 15.6; DB 4; Length 22;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 tgactgtgaagggttagagatga 22
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Db 1 tgactgtgttccttagagatga 22

RESULT 10
US-08-804-196-1/c
; Sequence 1, Application US/08804196
; Patent No. 5874256
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter

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; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Akzo No. 5874256el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; US-08-804-196-1

Query Match 70.9%; Score 15.6; DB 2; Length 6909;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
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Db 793 TGACTGTGTACATTAGGATGA 772

RESULT 11
US-08-658-340-1/c
; Sequence 1, Application US/08/658340
; Patent No. 5910576
; Patent No. 5910576 5861489
; GENERAL INFORMATION:
; APPLICANT: Bertina, Rogier
; APPLICANT: Reitsma, Pieter
; TITLE OF INVENTION: A method for diagnosing an increased
; TITLE OF INVENTION: risk for thrombosis or a genetic defect causing
; TITLE OF INVENTION: thrombosis and kit for use with the same.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Akzo No. 5910576 5861489el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,340
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/454,353
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 948-7400
; TELEFAX: (301) 948-9751
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; US-08-658-340-1

Query Match 70.9%; Score 15.6; DB 2; Length 6909;
Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
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Db 793 TGACTGTGTACATTAGGATGA 772

RESULT 12
US-08-746-111-26/c
; Sequence 26, Application US/08746111
; Patent No. 6066778
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Cui, Jisong
; TITLE OF INVENTION: Compositions And Methods For Screening
; TITLE OF INVENTION: Compounds For Anticoagulant Activity
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,111
; FILING DATE: 06-NOV-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-746-111-26

Query Match 70.9%; Score 15.6; DB 3; Length 6909;
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Best Local Similarity 81.8%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagatga 22
||||||| | ||| |||||
Db 793 TGAATGTGATAGGATGA 772

RESULT 13

US-08-933-750C-66/c
; Sequence 66, Application US/08933750C
; Patent No. 5932442

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127

US-08-933-750C-66

Query Match 69.1%; Score 15.2; DB 2; Length 1892;

Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagat 20
||| ||||| ||||| |||
Db 1278 TGAATGTGAAGGTTCCAGCT 1259

RESULT 14

US-09-234-613-66/c

; Sequence 66, Application US/09234613
; Patent No. 6132973

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1892 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 641127

US-09-234-613-66

Query Match 69.1%; Score 15.2; DB 3; Length 1892;

Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaggttagagat 20
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Db 1278 TGAATGTGAAGGTTCCAGCT 1259

RESULT 15

US-08-878-474-6

; Sequence 6, Application US/08878474
; Patent No. 6133232

GENERAL INFORMATION:

; APPLICANT: De Robertis, Edward M.
; APPLICANT: Bouwmeester, Tewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,474
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,150
FILING DATE: 20-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3655 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-878-474-6

Query Match 69.18; Score 15.2; DB 3; Length 3655;
Best Local Similarity 85.08; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 actgtgaaggttagagatga 22
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Db 1467 ACAGTCAAGGTTAGTGATGA 1486

Search completed: October 9, 2001, 15:42:11
Job time: 301 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:21:09 ; Search time 2150.93 Seconds
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Title: US-09-713-136-10
Perfect score: 22
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues 2688314
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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94: gb_ro1.*
95: gb_ro2.*
96: gb_in4.*
97: gb_pr10.*
98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	22	9 AX036944	AX036944 Sequence
2	18.8	85.5	22	9 AX036945	AX036945 Sequence
3	18.8	85.5	22	9 AX036952	AX036952 Sequence
4	18.8	85.5	22	9 AX046993	AX046993 Sequence
5	18.8	85.5	22	10 AX083675	AX083675 Sequence
6	18.8	85.5	89163	91 HS1009H6	AL035682 Human DNA
7	18.4	83.6	22	10 AX083682	AX083682 Sequence
8	18	81.8	73938	71 AC044861	AC044861 Mus muscu


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9      18      81.8 121332 68 AC0233361
c 10      18      81.8 146306 78 AF248716 Mus muscu
c 11      18      81.8 180558 86 AC006482
c 12      18      81.8 194026 77 AC004313
c 13      18      81.8 292420 66 AC020873
c 14      17.8 80.9 22 10 AX083681
c 15      17.8 80.9 103108 87 AC083681
c 16      17.8 80.9 118091 81 AL450407
c 17      17.8 80.9 133310 80 AL360012
c 18      17.8 80.9 149557 61 AC009111
c 19      17.8 80.9 157875 60 AC007833
c 20      17.8 80.9 167237 86 AC007938
c 21      17.8 80.9 196697 80 AL390062
c 22      17.8 80.9 201214 75 AC074012
c 23      17.8 80.9 214186 75 AC078933
c 24      17.8 80.9 309430 62 AC012209
c 25      17.4 79.1 113803 85 AC004460
c 26      17.4 79.1 151928 63 AC015688
c 27      17.4 79.1 165655 70 AC027605
c 28      17.4 79.1 165747 71 AC027807
c 29      17.4 79.1 183976 74 AC073419
c 30      17.4 79.1 187647 74 AC073220
c 31      17.4 79.1 196084 74 AC073145
c 32      17.4 79.1 221335 71 AC027654
c 33      17.4 79.1 227675 94 AF162137S2
c 34      17.2 78.2 22 9 AX036946
c 35      17.2 78.2 22 10 AX083676
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c 39      17.2 78.2 1587 59 HSHSUDNA
c 40      17.2 78.2 2079 5 AF025951
c 41      17.2 78.2 2495 88 AF052109
c 42      17.2 78.2 2740 94 AF220033
c 43      17.2 78.2 6652 59 HSF488A
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ALIGNMENTS

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RESULT 1
LOCUS AX036944 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 1 from Patent FR2790955.
ACCESSION AX036944
VERSION AX036944.1 GI:11226372
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 1 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
Source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
BASE COUNT 7 a 1 c 8 g 6 t
ORIGIN
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tgactgtgaaccttagagatga 22
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Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
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1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 4
LOCUS AX046993 22 bp DNA PAT 15-DEC-2000
DEFINITION Sequence 2 from Patent WO006778.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE
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tgactgtgaaccttagagatga 22
|||||
1 TGACTGTGAAGGTTAGAGATGA 22

Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
|||||
1 TGACTGTGAAGGTTAGAGATGA 22

RESULT 2
LOCUS AX036945 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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/organism="synthetic construct"
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/note="oligodesoxynucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
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tgactgtgaaccttagagatga 22
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1 TGACTGTGAACGTTTCGAGATGA 22

Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
|||||
1 TGACTGTGAACGTTTCGAGATGA 22

RESULT 3
LOCUS AX036952 22 bp DNA PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2790955.
ACCESSION AX036952
VERSION AX036952.1 GI:11226380
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 9 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligodesoxynucleotide"
BASE COUNT 7 a 2 c 6 g 7 t
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|||||
1 TGACTGTGAACGTTTCGAGATGA 22

Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
|||||
1 TGACTGTGAACGTTTCGAGATGA 22

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ORGANISM      synthetic construct
REFERENCE      artificial sequence.
AUTHORS        1 (bases 1 to 22)
TITLE          Hiv immunogenic compositions and methods
JOURNAL        Patent: WO 0067787-A 2 16-NOV-2000;
                THE IMMUNE RESPONSE CORPORATION (US)
FEATURES       Location/Qualifiers
source         1..22
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="phosphorothioate-modified synthetic
               oligodeoxynucleotide"
BASE COUNT     6 a 3 c 7 g 6 t
ORIGIN
Query Match    85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagatga 22
    ||||| ||||| |||||
Db 1 TGACTGTGAACGTCGAGATGA 22

RESULT 5
AX083675      22 bp DNA PAT 28-FEB-2001
LOCUS         Sequence 1 from Patent WO0112223.
ACCESSION     AX083675
VERSION       AX083675.1 GI:13185407
KEYWORDS      synthetic construct.
SOURCE        synthetic construct.
ORGANISM      artificial sequence.
REFERENCE      van Nest, G.
AUTHORS        Methods of modulating an immune response using immunostimulatory s
TITLE          sequences and compositions for use therein
JOURNAL        Patent: WO 0112223-A 1 22-FEB-2001;
                Dynavax Technologies Corporation (US)
FEATURES       Location/Qualifiers
source         1..22
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="Synthetic construct"
BASE COUNT     6 a 3 c 7 g 6 t
ORIGIN
Query Match    85.5%; Score 18.8; DB 10; Length 22;
Best Local Similarity 90.9%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagatga 22
    ||||| ||||| |||||
Db 1 TGACTGTGAACGTCGAGATGA 22

RESULT 6
HS1009H6      89163 bp DNA PRI 10-MAR-2001
LOCUS         Human DNA sequence from clone RP5-1009H6 on chromosome 20 Contains
DEFINITION     parts of isoforms B and C of the NFATC2 (nuclear factor of
                activated T-cells, cytoplasmic 2) gene, ESTs, STSS and GSSs,
                complete sequence.
ACCESSION     AL035682
VERSION       AL035682.16 GI:5596686
KEYWORDS      HTG; NFATC2; nuclear factor.
SOURCE        human.
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 89163)

Laird, G.

Direct Submission

Submitted (07-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Jul 27, 1999 this sequence version replaced gi:5360968.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>

This sequence is the entire insert of clone RP5-1009H6. The true right end of clone RP5-906P16 is at 83953 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1009H6 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

Location/Qualifiers

1..89163

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="20"

/clone="RP5-1009H6"

/clone_lib="RPCI-5"

106..496

/note="MSTB repeat: matches 27..422 of consensus"

646..1236

/note="L2 repeat: matches 1760..2416 of consensus"

1256..1338

/note="L2 repeat: matches 2623..2700 of consensus"

1341..1706

/note="MSTC repeat: matches 53..404 of consensus"

1709..2197

/note="MLTID repeat: matches 3..484 of consensus"

3304..3695

/note="L2 repeat: matches 2309..2749 of consensus"

3733..4191

/note="L2 repeat: matches 1715..2226 of consensus"

5322..5376

/note="MIR repeat: matches 113..170 of consensus"

5429..5458

/note="15 copies 2 mer tt 86% conserved"

6497..6590

/note="MIR repeat: matches 78..190 of consensus"

complement(7436..7917)

/note="match: GSS: Em:A0429939"

complement(7444..7910)

/note="match: GSS: Em:A0429921"

7612..7982

/note="match: STS: Em:H80534"

complement(11131..74423)

/gene="NFATC2"

complement(join(11131..11186,51802..52491,54923..55049,55441..55496,74283..74423))


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                /mod_base=OTHER
modified_base 15
                /note="5-bromocytosine"
                /mod_base=OTHER
BASE COUNT    6 a 1 c 7 g 6 t 2 others
ORIGIN

Query Match      83.6%; Score 18.4; DB 10; Length 22;
Best Local Similarity 86.4%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccccttagatga 22
    |||||
Db 1 TGACTGTGAANGTNGACATGA 22

RESULT 8
AC044861/c      73938 bp      DNA      HTG      12-APR-2000
LOCUS           Mus musculus chromosome 11 clone RP23-91F19 map 11, LOW-PASS
DEFINITION      SEQUENCE SAMPLING.
AC044861
VERSION         AC044861.1 Gi:7543828
KEYWORDS        HTG; HTGS_PHASE0.
SOURCE          house mouse.
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS         Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE           Mus musculus chromosome 11, clone RP23-91F19
JOURNAL          Unpublished
REFERENCE
AUTHORS         2 (bases 1 to 73938)
                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
                Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                Bockaplano,A., Castelle,A., Choepel,Y., Colangelo,M., Collins,S.,
                Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
                Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
                Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
                Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
                Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
                McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
                Meldrim,J., Meneus,D., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
                Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
                O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
                Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
                Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
                Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigglio,J.,
                Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9468
Center clone name: 91_F19
-----
* NOTE: This record contains 87 individual

```

```

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 722: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1578: contig of 756 bp in length
* 1579 1678: gap of 100 bp
* 1679 2428: contig of 750 bp in length
* 2429 2528: gap of 100 bp
* 2529 3278: contig of 750 bp in length
* 3279 3378: gap of 100 bp
* 3379 4122: contig of 744 bp in length
* 4123 4222: gap of 100 bp
* 4223 4974: contig of 752 bp in length
* 4975 5074: gap of 100 bp
* 5075 5823: contig of 749 bp in length
* 5824 5923: gap of 100 bp
* 5924 6665: contig of 742 bp in length
* 6666 6765: gap of 100 bp
* 6766 7518: contig of 753 bp in length
* 7519 7618: gap of 100 bp
* 7619 8367: contig of 749 bp in length
* 8368 8467: gap of 100 bp
* 8468 9225: contig of 758 bp in length
* 9226 9325: gap of 100 bp
* 9326 10060: contig of 735 bp in length
* 10061 10160: gap of 100 bp
* 10161 10917: contig of 757 bp in length
* 10918 11017: gap of 100 bp
* 11018 11778: contig of 761 bp in length
* 11779 11878: gap of 100 bp
* 11879 12642: contig of 764 bp in length
* 12643 12742: gap of 100 bp
* 12743 13482: contig of 740 bp in length
* 13483 13582: gap of 100 bp
* 13583 14333: contig of 751 bp in length
* 14334 14433: gap of 100 bp
* 14434 15195: contig of 762 bp in length
* 15196 15295: gap of 100 bp
* 15296 16055: contig of 760 bp in length
* 16056 16155: gap of 100 bp
* 16156 16902: contig of 747 bp in length
* 16903 17002: gap of 100 bp
* 17003 17756: contig of 754 bp in length
* 17757 17856: gap of 100 bp
* 17857 18603: contig of 747 bp in length
* 18604 18703: gap of 100 bp
* 18704 19434: contig of 731 bp in length
* 19435 19534: gap of 100 bp
* 19535 20284: contig of 750 bp in length
* 20285 20384: gap of 100 bp
* 20385 21130: contig of 746 bp in length
* 21131 21230: gap of 100 bp
* 21231 21964: contig of 734 bp in length
* 21965 22064: gap of 100 bp
* 22065 22797: contig of 733 bp in length
* 22798 22897: gap of 100 bp
* 22898 23653: contig of 756 bp in length
* 23654 23753: gap of 100 bp
* 23754 24496: contig of 743 bp in length
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* 24597 25348: contig of 752 bp in length
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* 25449 26198: contig of 750 bp in length
* 26199 26298: gap of 100 bp
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* 27050 27149: gap of 100 bp
 * 27150 27897: contig of 748 bp in length
 * 27898 27997: gap of 100 bp
 * 27998 28750: contig of 753 bp in length
 * 28751 28850: gap of 100 bp
 * 28851 29599: contig of 749 bp in length
 * 29600 29699: gap of 100 bp
 * 29700 30458: contig of 759 bp in length
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 * 32163 32262: gap of 100 bp
 * 32263 32999: contig of 737 bp in length
 * 33000 33099: gap of 100 bp
 * 33100 33861: contig of 762 bp in length
 * 33862 33961: gap of 100 bp
 * 33962 34717: contig of 756 bp in length
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 * 34818 35567: contig of 750 bp in length
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 * 38205 38968: contig of 764 bp in length
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 * 40767 41517: contig of 751 bp in length
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 * 41618 42365: contig of 748 bp in length
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 * 43306 44062: contig of 757 bp in length
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 * 44163 44924: contig of 762 bp in length
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 * 45025 45772: contig of 748 bp in length
 * 45773 45872: gap of 100 bp
 * 45873 46627: contig of 755 bp in length
 * 46628 46727: gap of 100 bp
 * 46728 47472: contig of 745 bp in length
 * 47473 47572: gap of 100 bp
 * 47573 48320: contig of 748 bp in length
 * 48321 48420: gap of 100 bp
 * 48421 49179: contig of 759 bp in length
 * 49180 49279: gap of 100 bp
 * 49280 50029: contig of 750 bp in length
 * 50030 50129: gap of 100 bp
 * 50130 50890: contig of 761 bp in length
 * 50891 50990: gap of 100 bp
 * 50991 51736: contig of 746 bp in length
 * 51737 51836: gap of 100 bp
 * 51837 52584: contig of 748 bp in length
 * 52585 52684: gap of 100 bp
 * 52685 53460: contig of 776 bp in length
 * 53461 53560: gap of 100 bp
 * 53561 54310: contig of 750 bp in length
 * 54311 54410: gap of 100 bp
 * 54411 55140: contig of 730 bp in length
 * 55141 55240: gap of 100 bp
 * 55241 55995: contig of 755 bp in length
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 * 56096 56852: contig of 757 bp in length
 * 56853 56952: gap of 100 bp
 * 56953 57705: contig of 753 bp in length
 * 57706 57805: gap of 100 bp

* 57806 58547: contig of 742 bp in length
 * 58548 58647: gap of 100 bp

Query Match 81.8% Score 18; DB 71; Length 73938;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatg 21
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 DB 44413 CTGTGAACCTTAGAGATG 44396

RESULT 9
 AC023361 121332 bp DNA HTG 04-NOV-2000
 Locus Mus musculus clone RP23-316K16, *** SEQUENCING IN PROGRESS ***, 47
 DEFINITION unordered pieces.
 AC023361
 AC023361.4 GI:11079344
 VERSION HTG: HTGS_PHASE1.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 121332)
 Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
 Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
 Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
 Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
 Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
 Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
 Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Jia, Y., Kelly, J., Kelly, S.,
 Hosak, H., Hou, X., Huber, J., Jackson, L., Lozano, R.J., Martin, R.,
 Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozano, R.J., Martin, R.,
 Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
 Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogih, M., Parish, S.,
 Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
 Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
 Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstein, G.,
 Worley, K. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 121332)
 Worley, K.C.

Direct Submission
 Submitted (14-FEB-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 3, 2000 this sequence version replaced gi:7025658.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: MAAE
 Center clone name: RP23-316K16
 ----- Summary Statistics
 Sequencing vector: M13: L08821
 Chemistry: Dye-terminator Big Dye: 74% of reads
 Chemistry: Dye-terminator Big Dye: 26% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 79638 bases at least Q40
 Consensus quality: 100663 bases at least Q30
 Consensus quality: 110213 bases at least Q20
 Estimated insert size: 101687; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-gel estimation
 Quality coverage: 1.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 47 contigs. The true order of the pieces

* Is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 8407: contig of 8407 bp in length
 * 8408 8507: gap of unknown length
 * 8508 14631: contig of 6124 bp in length
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 * 14732 18775: contig of 4044 bp in length
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 * 18876 23354: contig of 4479 bp in length
 * 23355 23454: gap of unknown length
 * 23455 29014: contig of 5560 bp in length
 * 29015 29114: gap of unknown length
 * 29115 33875: contig of 4761 bp in length
 * 33876 33976: gap of unknown length
 * 33977 39221: contig of 5346 bp in length
 * 39222 42432: gap of unknown length
 * 42433 42532: contig of 3011 bp in length
 * 42533 45875: gap of unknown length
 * 45876 45975: contig of 3343 bp in length
 * 45976 49070: gap of unknown length
 * 49071 52556: contig of 3095 bp in length
 * 52557 52656: gap of unknown length
 * 52657 55765: contig of 3109 bp in length
 * 55766 55865: gap of unknown length
 * 55866 59213: contig of 3347 bp in length
 * 59214 59313: gap of unknown length
 * 59313 60922: contig of 1610 bp in length
 * 60923 61022: gap of unknown length
 * 61023 63102: contig of 2080 bp in length
 * 63103 63202: gap of unknown length
 * 63203 64446: contig of 1244 bp in length
 * 64447 64546: gap of unknown length
 * 64547 66365: contig of 1819 bp in length
 * 66366 66465: gap of unknown length
 * 66466 69328: contig of 2863 bp in length
 * 69329 69428: gap of unknown length
 * 69429 71591: contig of 2163 bp in length
 * 71592 71691: gap of unknown length
 * 71692 73841: contig of 2150 bp in length
 * 73842 73941: gap of unknown length
 * 73942 77152: contig of 3211 bp in length
 * 77153 77252: gap of unknown length
 * 77253 79347: contig of 2095 bp in length
 * 79348 79447: gap of unknown length
 * 79448 81197: contig of 1650 bp in length
 * 81198 83008: gap of unknown length
 * 83009 83108: gap of unknown length
 * 83109 85686: contig of 2578 bp in length
 * 85687 85786: gap of unknown length
 * 85787 87348: contig of 1562 bp in length
 * 87349 87448: gap of unknown length
 * 87449 88709: contig of 1261 bp in length
 * 88710 88809: gap of unknown length
 * 88810 90252: contig of 1443 bp in length
 * 90253 90352: gap of unknown length
 * 90353 92076: contig of 1724 bp in length
 * 92077 92176: gap of unknown length
 * 92177 93952: contig of 1776 bp in length
 * 93953 94052: gap of unknown length
 * 94053 95890: contig of 1838 bp in length
 * 95891 95990: gap of unknown length
 * 95991 97702: contig of 1712 bp in length
 * 97703 97802: gap of unknown length
 * 97803 99154: contig of 1352 bp in length
 * 99155 99254: gap of unknown length
 * 99255 100824: contig of 1570 bp in length

* 100825 100924: gap of unknown length
 * 100925 102458: contig of 1534 bp in length
 * 102459 102558: gap of unknown length
 * 102559 104019: contig of 1461 bp in length
 * 104020 104119: gap of unknown length
 * 104120 105953: contig of 1834 bp in length
 * 105954 106053: gap of unknown length
 * 106054 108172: contig of 2119 bp in length
 * 108173 108272: gap of unknown length
 * 108273 109818: contig of 1546 bp in length
 * 109819 109919: gap of unknown length
 * 109920 111179: contig of 1261 bp in length
 * 111180 111279: gap of unknown length
 * 111280 112976: contig of 1697 bp in length
 * 112977 113076: gap of unknown length
 * 113077 114376: contig of 1300 bp in length
 * 114377 114476: gap of unknown length
 * 114477 115792: contig of 1316 bp in length
 * 115793 115892: gap of unknown length
 * 115893 117014: contig of 1122 bp in length
 * 117015 117114: gap of unknown length
 * 117115 118392: contig of 1278 bp in length
 * 118393 118492: gap of unknown length
 * 118493 119759: contig of 1267 bp in length
 * 119760 119859: gap of unknown length
 * 119860 121332: contig of 1473 bp in length.

FEATURES

Source
 1. 121332
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="RP23-316K16"
 BASE COUNT 30929 a 27070 c 27181 g 31494 t 4658 others
 ORIGIN

Query Match 81.8% Score 18; DB 68; Length 121332;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ctgtgaaccttagagatg 21
 |||||

Db 21742 CTGTGACCTTAGAGATG 21759

RESULT 10
 AF248716/c
 LOCUS AF248716 146306 bp DNA HTG 12-APR-2000
 DEFINITION Mus musculus chromosome 11 clone CT7-327023, *** SEQUENCING IN
 PROGRESS ***, in ordered pieces.
 ACCESSION AF248716
 VERSION AF248716.1 GI:7542829
 KEYWORDS HTG; HTGS, PHASE2.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 146306)
 Loois, G.G., Locksley, R.M., Blankespoor, C.M., Wang, Z.E., Miller, W.,
 Rubin, E.M. and Frazer, K.A.
 Identification of a coordinate regulator of interleukins 4, 13, and
 5 by cross-species sequence comparisons
 Science 288 (5463), 136-140 (2000)
 JOURNAL MEDLINE 20217223
 PUBMED 10753117
 REFERENCE 2 (bases 1 to 146306)
 Dean, W.B., Lewis, K.D., Blankespoor, C.M., Nyugen, A., Loois, G.G.,
 Rubin, E.M. and Frazer, K.A.
 Direct Submission
 Submitted (23-MAR-2000) Genome Sciences Department, Lawrence
 Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA
 94720, USA
 TITLE
 JOURNAL
 COMMENT
 Note: This is a 'working draft' sequence. It consists of 8 contigs.
 The order of contigs is believed to be correct. Gaps between the


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repeat_region 4071..4567 /rpt_family="MaLR"
repeat_region 4589..4609 /rpt_family="AT_rich"
repeat_region 4623..4769 /rpt_family="MIR"
repeat_region 6394..6531 /rpt_family="MIR"
repeat_region 7056..9142 /rpt_family="L1"
repeat_region 9146..9316 /rpt_family="Alu"
repeat_region 9352..12747 /rpt_family="L1"
repeat_region 12748..13058 /rpt_family="Alu"
repeat_region 13059..14199 /rpt_family="L1"
repeat_region 14200..14518 /rpt_family="Alu"
repeat_region 14519..14893 /rpt_family="L1"
repeat_region 15129..15514 /rpt_family="MaLR"
repeat_region 15516..15636 /rpt_family="L2"
repeat_region 15637..16028 /rpt_family="MaLR"
repeat_region 16029..16213 /rpt_family="L2"
repeat_region 16266..16699 /rpt_family="L2"
repeat_region 17832..17892 /rpt_family="MERL_type"
repeat_region 17893..18176 /rpt_family="Alu"
repeat_region 18177..18350 /rpt_family="MERL_type"
repeat_region 18351..19056 /rpt_family="L1"
repeat_region 19076..19354 /rpt_family="L1"
repeat_region 19422..20569 /rpt_family="L1"
repeat_region 20570..20651 /rpt_family="MERL_type"
repeat_region 20652..20933 /rpt_family="Alu"
repeat_region 20934..20957 /rpt_family="(TAAA)n"
repeat_region 20958..21119 /rpt_family="MERL_type"
repeat_region 21120..21423 /rpt_family="Alu"
repeat_region 21424..22042 /rpt_family="MERL_type"
repeat_region 22043..22354 /rpt_family="Alu"
repeat_region 22355..22867 /rpt_family="MERL_type"
repeat_region 22945..23016 /rpt_family="MaLR"
repeat_region 24817..24919 /rpt_family="MIR"
repeat_region 24908..25068 /rpt_family="L2"
repeat_region 25109..25253 /rpt_family="MIR"
repeat_region 26208..26565 /rpt_family="L1"
repeat_region 26896..27135 /rpt_family="L1"
repeat_region 27594..27685
```

```
repeat_region /rpt_family="MIR"
27692..27904 /rpt_family="L2"
28971..29157 /rpt_family="MERL_type"
30167..30420 /rpt_family="MIR"
30886..30945 /rpt_family="(TG)n"
32179..32291 /rpt_family="L2"
32770..32864 /rpt_family="L2"
32907..32970 /rpt_family="MIR"
33065..33123 /rpt_family="MIR"
33266..33289 /rpt_family="AT_rich"
34087..34187 /rpt_family="MERL_type"
34809..34836 /rpt_family="AT_rich"
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Query Match 81.8%; Score 18; DB 86; Length 180568;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ctgtgaaccttagagatg 21
|||||

Db 160426 CTGTGAACCTTAGAGATG 160409

RESULT 12

AC084313

LOCUS AC084313 194026 bp DNA HTG 12-JAN-2001
DEFINITION Homo sapiens chromosome 7 clone RP11-301D21, WORKING DRAFT
SEQUENCE, 12 unordered pieces.

ACCESSION AC084313

VERSION AC084313.3 GI:12084094

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 194026)
AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 194026)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2000)

Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

COMMENT On Jan 12, 2001 this sequence version replaced gi:10954408.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H.NH0301D21

----- Summary Statistics -----

Sequencing vector: M13; 97%

Sequencing vector: plasmid; 0%

Chemistry: Dye-primer ET; 97% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 186566 bases at least Q40

Consensus quality: 188959 bases at least Q30

Consensus quality: 190127 bases at least Q20

Insert size: 193000; agarose-fp

Insert size: 192926; sum-of-contigs
 Quality coverage: 4.67 in Q20 bases; agarose-fp
 Quality coverage: 5.18 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 14547: contig of 14547 bp in length
 * 14548 14647: gap of unknown length
 * 14648 31784: contig of 17137 bp in length
 * 31785 31884: gap of unknown length
 * 31885 50934: contig of 19070 bp in length
 * 50935 51054: gap of unknown length
 * 51055 76962: contig of 25908 bp in length
 * 76963 77062: gap of unknown length
 * 77063 109852: contig of 32790 bp in length
 * 109853 109952: gap of unknown length
 * 109953 148938: contig of 38986 bp in length
 * 148939 149038: gap of unknown length
 * 149039 150656: contig of 1618 bp in length
 * 150657 150756: gap of unknown length
 * 150757 155984: contig of 5198 bp in length
 * 155955 156034: gap of unknown length
 * 156035 162680: contig of 6626 bp in length
 * 162681 162780: gap of unknown length
 * 162781 170137: contig of 7357 bp in length
 * 170138 170237: gap of unknown length
 * 170238 181387: contig of 11150 bp in length
 * 181388 181487: gap of unknown length
 * 181488 194026: contig of 12539 bp in length.

FEATURES

source
 1. .194026
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"
 /clone="RP11-301D21"
 misc_feature
 1. .14547
 /note="assembly_name:Contig10"
 misc_feature
 14648. .31784
 /note="assembly_name:Contig11"
 misc_feature
 31885. .50954
 /note="assembly_name:Contig12"
 misc_feature
 51055. .76962
 /note="assembly_name:Contig13"
 misc_feature
 77063. .109852
 /note="assembly_name:Contig14"
 misc_feature
 109953. .148938
 /note="assembly_name:Contig15"
 misc_feature
 149039. .150656
 /note="assembly_name:Contig14"
 misc_feature
 150757. .155984
 /note="assembly_name:Contig5"
 misc_feature
 156055. .162680
 /note="assembly_name:Contig6"
 misc_feature
 162781. .170137
 /note="assembly_name:Contig7
 clone_end:T7
 vector_side:left
 170238. .181387
 /note="assembly_name:Contig8
 clone_end:SP6
 vector_side:left
 181488. .194026
 /note="assembly_name:Contig9"
 BASE COUNT 60487 a 35185 c 35984 g 61269 t 1101 others
 ORIGIN

Query Match 81.8%; Score 18; DB 77; Length 194026;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ctgtgaaccttagatg 21
 |||||
 Db 146011 CTGTGAACCTTAGAGATG 146028

RESULT 13

AC020873/c AC020873 292420 bp DNA HTG 29-JUN-2000

LOCUS Mus musculus clone RP23-327O23, WORKING DRAFT SEQUENCE, 113
 DEFINITION unorderd pieces.

AC020873 AC020873 2 GI:8810268

VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 292420)

DOE Joint Genome Institute.

Sequencing of Mouse

Unpublished

REFERENCE 2 (bases 1 to 292420)

DOE Joint Genome Institute.

Direct Submission

Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jun 29, 2000 this sequence version replaced gi:6686435.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1862799

Center clone name: RPCI-23_327O23

Summary Statistics

Consensus quality: 193189 bases at least Q40

Consensus quality: 233546 bases at least Q30

Consensus quality: 244455 bases at least Q20

Estimated insert size: 190000; pulse field gel estimation

Estimated insert size: 281220; sum-of-contigs estimation

Quality coverage: 5.6 in Q20 bases; pulse field gel estimation.

Quality coverage: 3.78 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 113 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1059: contig of 1059 bp in length

* 1060 1159: gap of unknown length

* 1160 2247: contig of 1088 bp in length

* 2248 2347: gap of unknown length

* 2348 3573: contig of 1226 bp in length

* 3574 3673: gap of unknown length

* 3674 4728: contig of 1055 bp in length

* 4729 4828: gap of unknown length

* 4829 6441: contig of 1613 bp in length

* 6442 7697: contig of 1156 bp in length

* 7698 7797: gap of unknown length

* 7798 8850: contig of 1053 bp in length

* 8851 8950: gap of unknown length

* 8951 10178: contig of 1228 bp in length

* 10179 10278: gap of unknown length

* 10279 11293: contig of 1015 bp in length

* 11294 11393: gap of unknown length
* 11394 13001: contig of 1608 bp in length
* 13002 13101: gap of unknown length
* 13102 13101: contig of 1429 bp in length
* 14531 14630: gap of unknown length
* 14631 15697: contig of 1067 bp in length
* 15698 15797: gap of unknown length
* 15798 15873: contig of 1076 bp in length
* 16874 16973: gap of unknown length
* 16974 18287: contig of 1314 bp in length
* 18288 18387: gap of unknown length
* 18388 19408: contig of 1021 bp in length
* 19409 19508: gap of unknown length
* 19509 20618: contig of 1110 bp in length
* 20619 20718: gap of unknown length
* 20719 22224: contig of 1506 bp in length
* 22225 22324: gap of unknown length
* 22325 23378: contig of 1054 bp in length
* 23379 23478: gap of unknown length
* 23479 24903: contig of 1425 bp in length
* 24904 25003: gap of unknown length
* 25004 26371: contig of 1368 bp in length
* 26372 26471: gap of unknown length
* 26472 27690: contig of 1219 bp in length
* 27691 27790: gap of unknown length
* 27791 28904: contig of 1114 bp in length
* 28905 30554: contig of 1550 bp in length
* 30555 30654: gap of unknown length
* 30655 32119: contig of 1465 bp in length
* 32120 32219: gap of unknown length
* 32220 33397: contig of 1178 bp in length
* 33398 33497: gap of unknown length
* 33498 34545: contig of 1048 bp in length
* 34546 34645: gap of unknown length
* 34646 35665: contig of 1020 bp in length
* 35666 37665: gap of unknown length
* 37666 37129: contig of 1364 bp in length
* 37130 37229: gap of unknown length
* 37230 38398: contig of 1169 bp in length
* 38399 38498: gap of unknown length
* 38499 39512: contig of 1014 bp in length
* 39513 39612: gap of unknown length
* 39613 40750: contig of 1138 bp in length
* 40751 40850: gap of unknown length
* 40851 41950: contig of 1000 bp in length
* 41951 43306: contig of 1356 bp in length
* 43307 43406: gap of unknown length
* 43407 44461: contig of 1055 bp in length
* 44462 44561: gap of unknown length
* 44562 46308: contig of 1747 bp in length
* 46309 46408: gap of unknown length
* 46409 47905: contig of 1497 bp in length
* 47906 48005: gap of unknown length
* 48006 49428: contig of 1423 bp in length
* 49429 49528: gap of unknown length
* 49529 50895: contig of 1367 bp in length
* 50896 50995: gap of unknown length
* 50996 52180: contig of 1185 bp in length
* 52181 52280: gap of unknown length
* 52281 53377: contig of 1097 bp in length
* 53378 53478: gap of unknown length
* 53479 54808: gap of unknown length
* 54809 56126: contig of 1318 bp in length
* 56127 56226: gap of unknown length
* 56227 57615: contig of 1389 bp in length
* 57616 57715: gap of unknown length
* 57716 59193: contig of 1478 bp in length
* 59194 59293: gap of unknown length
* 59294 60341: contig of 1048 bp in length
* 60342 60441: gap of unknown length

* 60442 62061: contig of 1620 bp in length
* 62062 62161: gap of unknown length
* 62162 64114: contig of 1953 bp in length
* 64115 64214: gap of unknown length
* 64215 65794: contig of 1580 bp in length
* 65795 65894: gap of unknown length
* 65895 67375: contig of 1481 bp in length
* 67376 67475: gap of unknown length
* 67476 68572: contig of 1097 bp in length
* 68573 68672: gap of unknown length
* 68673 69900: contig of 1228 bp in length
* 69901 70000: gap of unknown length
* 70001 71201: contig of 1201 bp in length
* 71202 71301: gap of unknown length
* 71302 73060: contig of 1759 bp in length
* 73061 73160: gap of unknown length
* 73161 74510: contig of 1250 bp in length
* 74511 74510: gap of unknown length
* 74511 76795: contig of 2285 bp in length
* 76796 76895: gap of unknown length
* 76896 78854: contig of 1959 bp in length
* 78855 78954: gap of unknown length
* 78955 80435: contig of 1481 bp in length
* 80436 80535: gap of unknown length
* 80536 81758: contig of 1223 bp in length
* 81759 81858: gap of unknown length
* 81859 82958: gap of unknown length
* 82959 84059: contig of 1100 bp in length
* 84059 84158: gap of unknown length
* 84159 86426: contig of 2268 bp in length
* 86427 86526: gap of unknown length
* 86527 88314: contig of 1788 bp in length
* 88315 88414: gap of unknown length
* 88415 89802: contig of 1388 bp in length
* 89803 89902: gap of unknown length
* 89903 91515: contig of 1613 bp in length
* 91516 92934: contig of 1319 bp in length
* 92935 93034: gap of unknown length
* 93035 94461: gap of unknown length
* 94461 94560: gap of unknown length
* 94561 96081: contig of 1521 bp in length
* 96082 96181: gap of unknown length
* 96182 97318: contig of 1137 bp in length
* 97319 97418: gap of unknown length
* 97419 99350: contig of 1932 bp in length
* 99351 99450: gap of unknown length
* 99451 100979: contig of 1529 bp in length
* 100980 101079: gap of unknown length
* 101080 102260: contig of 1181 bp in length
* 102261 102360: gap of unknown length
* 102361 103407: contig of 1047 bp in length
* 103408 103507: gap of unknown length
* 103508 105016: contig of 1509 bp in length
* 105017 105116: gap of unknown length
* 105117 106848: contig of 1732 bp in length
* 106849 106948: gap of unknown length
* 106949 109545: contig of 2597 bp in length
* 109546 109645: gap of unknown length
* 109646 114995: contig of 1850 bp in length
* 11496 111595: gap of unknown length
* 111596 113429: contig of 1834 bp in length
* 113430 113529: gap of unknown length
* 113530 114998: contig of 1469 bp in length

Query Match 81.8%; Score 18; DB 66; Length 292420;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ctgtgaaccttagagatg 21
|||||
Db 280795 CTGTGAACCTTAGAGATG 280778

JOURNAL

COMMENT

Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jul 29, 2000 this sequence version replaced gl:7630919.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: saplens@wustl.wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0264A13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The position of this clone was established as part of a collaboration between the Human Chromosome Y Mapping Project (Tomoko Kawaguchi, Helen Skaltsky, Laura G. Brown, Steve Rosen, and David C. Page at the Whitehead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenoe, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-292P9, 200 bp overlap; the clone sequenced to the right is RP11-53K10. Actual start of this clone is at base position 99669 of RP11-292P9; actual end is at base position 103108 of RP11-264A13.

A well-conserved inverted repeat extends from RP11-292P9 to 39737 of RP11-264A13 with the intervening unique sequence from base 1084 to 4503. Due to the large size of the inverted repeat PCR and digest data could not confirm the orientation of the loop.

FEATURES

source

1..103108
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="Y"
 /map="Y"

repeat_region

497..807

repeat_region

1760..1824

repeat_region

2054..2604

repeat_region

3189..3298

repeat_region

3563..3873

repeat_region

3975..4063

RESULT 14
 AX083681 22 bp DNA PAT 28-FEB-2001
 LOCUS Sequence 7 from Patent WO0112223.
 DEFINITION
 AX083681
 ACCESSION
 AX083681.1 GI:13185413
 VERSION
 synthetic construct.
 SOURCE
 synthetic construct.
 ORGANISM
 1 (bases 1 to 22)
 van Nest, G.
 METHODS of modulating an immune response using immunostimulatory s
 equences and compositions for use therein
 Patent: WO 0112223-A 7 22-FEB-2001;
 Dynavax Technologies Corporation (US)
 JOURNAL
 FEATURES
 Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 11
 /note="5-bromocytosine"
 /mod_base=OTHER

BASE COUNT 6 a 2 c 7 g 6 t 1 others

ORIGIN

Query Match 80.9%; Score 17.8; DB 10; Length 22;
 Best Local Similarity 86.4%; Pred. No. 40;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22

Db 1 TGACTGTGAAGTTTCGAGATGA 22

RESULT 15

AC018677 103108 bp DNA PRI 30-SEP-2000
 LOCUS Homo sapiens BAC clone RP11-264A13 from Y, complete sequence.
 DEFINITION
 AC018677
 ACCESSION
 AC018677.3 GI:9581959
 VERSION
 HTG.
 KEYWORDS
 human.
 SOURCE
 Homo sapiens

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103108)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

REFERENCE
 2 (bases 1 to 103108)

Ozersky, P., Drone, K. and Wedgeworth, P.

The sequence of Homo sapiens BAC clone RP11-264A13

Unpublished

3 (bases 1 to 103108)

Waterston, R.H.

Direct Submission

Submitted (16-DEC-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 103108)

Waterston, R.H.

Direct Submission

Submitted (29-JUL-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

5 (bases 1 to 103108)

Waterston, R.

Direct Submission

```
repeat_region 4120..4303 /rpt_family="Alu"
repeat_region 4772..5084 /rpt_family="Alu"
repeat_region 11636..11799 /rpt_family="L1"
repeat_region 11824..12039 /rpt_family="L1"
repeat_region 12083..12119 /rpt_family="MaLR"
repeat_region 12366..12445 /rpt_family="MaLR"
repeat_region 13243..13307 /rpt_family="ERV1"
repeat_region 13408..13545 /rpt_family="MER1_type"
repeat_region 13547..13635 /rpt_family="Alu"
repeat_region 13556..14014 /rpt_family="MIR"
misc_feature 14536..14929 /note="similar to EST AI807575 (NID:g5394141) wx43a10.x1"
misc_feature 14536..14900 /note="similar to EST AW448974 (NID:g6989750)"
misc_feature 14538..14980 /note="similar to EST AW339341 (NID:g6835888) x289a01.x1"
repeat_region 14596..14747 /rpt_family="MER1_type"
misc_feature 16533..16805 /note="similar to EST AA827461 (NID:g2899902) of28g01.s1"
repeat_region 16668..16765 /rpt_family="L1"
repeat_region 16766..17053 /rpt_family="Alu"
repeat_region 17054..17655 /rpt_family="L1"
repeat_region 17727..18038 /rpt_family="Alu"
repeat_region 18054..18345 /rpt_family="Alu"
repeat_region 19063..19266 /rpt_family="MER1_type"
repeat_region 20519..20812 /rpt_family="Alu"
repeat_region 22275..22455 /rpt_family="MER1_type"
repeat_region 22552..23757 /rpt_family="SVA"
repeat_region 24382..24671 /rpt_family="L1"
repeat_region 24685..24858 /rpt_family="L1"
repeat_region 25148..25516 /rpt_family="L1"
repeat_region 25518..25903 /rpt_family="MaLR"
repeat_region 25909..25975 /rpt_family="L1"
repeat_region 26444..26521 /rpt_family="L2"
repeat_region 26903..26972 /rpt_family="Mariner"
repeat_region 28311..28496 /rpt_family="Alu"
repeat_region 28497..28590 /rpt_family="Alu"
repeat_region 29127..29379 /rpt_family="Alu"
repeat_region 29831..30017 /rpt_family="ERV1"
repeat_region 30255..30636 /rpt_family="ERV1"
repeat_region 31048..31292 /rpt_family="ERV1"
```

```
repeat_region /rpt_family="ERV1"
repeat_region 31301..31386 /rpt_family="MaLR"
repeat_region 31394..31446 /rpt_family="L1"
repeat_region 31463..31673 /rpt_family="Alu"
repeat_region 32354..32548 /rpt_family="MaLR"
repeat_region 32556..32708 /rpt_family="L1"
repeat_region 32733..32777 /rpt_family="L1"
repeat_region 32786..33061 /rpt_family="MER2_type"
repeat_region 33167..33690 /rpt_family="L1"
repeat_region 33691..34012 /rpt_family="Alu"
repeat_region 34013..34024 /rpt_family="L1"

Query Match 80.9%; Score 17.8; DB 87; Length 103108;
Best Local Similarity 90.5%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatg 21
    ||||| | ||||| |||||
Db 47135 TGACTGTGAGCTTAGAGATG 47155
```

Search completed: October 9, 2001, 16:21:38
Job time: 2668 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 18:20:29 ; Search time 6788.49 Seconds
(without alignments)
30.635 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
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21: gb_est21:*
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23: gb_est23:*
24: gb_est24:*
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26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
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254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL
COMMENT

Unpublished (1999)
Other_GSSs: RPCI-24-97J15.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end plate: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 97 row: J column: 15
Seq primer: SP6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..489
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="RPCI-24-97J15"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."
131 a 96 c 93 g 169 t

BASE COUNT
ORIGIN

Query Match 83.6%; Score 18.4; DB 248; Length 489;
Best Local Similarity 95.0%; Pred. NO. 85;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gactgtgaaccttagatg 21
||||| ||||||| |||||||

Db 157 GACTTTGAACCTTAGAGATG 138

RESULT 2

AZ881693 570 bp DNA GSS 05-MAR-2001
LOCUS
DEFINITION RPCI-23-204F1.TV RPCI-23 Mus musculus genomic clone RPCI-23-204F1,
DNA sequence.
ACCESSION AZ881693
VERSION W88250.1 GI:13200638
KEYWORDS GSS,
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 570)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret,
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.,
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-204F1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	83.6	489	AZ749943	AZ749943 RPCI-24-9
C 2	18.4	83.6	570	AZ881693	AZ881693 RPCI-23-2
C 3	17.8	80.9	431	AZ052737	AZ052737 RPCI-23-3
C 4	17.8	80.9	507	BG552950	BG552950 dab81h04
C 5	17.8	80.9	535	AZ479424	AZ479424 IM0300H03
C 6	17.8	80.9	561	AZ755668	AZ755668 ev02909.x
C 7	17.4	79.1	422	AQ245899	AQ245899 HS_2056.B
C 8	17.2	78.2	142	BB484411	BB484411 BB484411
C 9	17.2	78.2	236	AU053757	AU053757 AU053757
C 10	17.2	78.2	254	AU053032	AU053032 AU053032
C 11	17.2	78.2	265	AU054169	AU054169 AU054169
C 12	17.2	78.2	270	AU053754	AU053754 AU053754
C 13	17.2	78.2	340	AU040059	AU040059 AU040059
C 14	17.2	78.2	371	AU039239	AU039239 AU039239
C 15	17.2	78.2	398	BF010530	BF010530 NXCI_085
C 16	17.2	78.2	424	BF723539	BF723539 193384.NA
C 17	17.2	78.2	429	BF523228	BF523228 UT-R-C3-t
C 18	17.2	78.2	449	AQ114479	AQ114479 CIT-HSP-2
C 19	17.2	78.2	457	AU034234	AU034234 AU034234
C 20	17.2	78.2	463	AU083559	AU083559 AU083559
C 21	17.2	78.2	474	AU052381	AU052381 AU052381
C 22	17.2	78.2	474	BF963693	BF963693 PM4-NN120
C 23	17.2	78.2	479	AU089685	AU089685 AU089685
C 24	17.2	78.2	509	AU039788	AU039788 AU039788
C 25	17.2	78.2	513	AU034515	AU034515 AU034515
C 26	17.2	78.2	515	AA769863	AA769863 z118b04.s
C 27	17.2	78.2	520	AU039823	AU039823 AU039823
C 28	17.2	78.2	521	AQ567409	AQ567409 HS_2111.B
C 29	17.2	78.2	535	AQ804943	AQ804943 HS_3150.A
C 30	17.2	78.2	539	BE755006	BE755006 208706.NA
C 31	17.2	78.2	574	BE496465	BE496465 NXCI_018
C 32	17.2	78.2	669	C22959	C22959 C22959 Dict
C 33	17.2	78.2	681	AU140713	AU140713 AU140713
C 34	17.2	78.2	681	AW349092	AW349092 GW210003B
C 35	17.2	78.2	699	AU034932	AU034932 AU034932
C 36	17.2	78.2	714	AU033417	AU033417 AU033417
C 37	17.2	78.2	936	CNS03417	AL227305 Tetraodon
C 38	17.2	78.2	996	CNS02760	AL184630 Tetraodon
C 39	17.2	78.2	1106	CNS05GCO	AL336129 Tetraodon
C 40	16.8	76.4	105	AA094019	AA094019 cl1619.se
C 41	16.8	76.4	224	BB185712	BB185712 BB185712
C 42	16.8	76.4	256	W04058	W04058 T2023.MVAT4
C 43	16.8	76.4	368	AQ646701	AQ646701 RPCI93-EC
C 44	16.8	76.4	390	W88250	W88250 T1546.MVAT4
C 45	16.8	76.4	435	AA230196	AA230196 nc13b11.s

ALIGNMENTS

RESULT 1
AZ749943/3/C
LOCUS
DEFINITION RPCI-24-97J15.TJ RPCI-24 Mus musculus genomic clone RPCI-24-97J15,
DNA sequence.
ACCESSION AZ749943
VERSION AZ749943.1 GI:12535102
KEYWORDS GSS,
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 489)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24

Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 204 row: F column: 1
 Seq primer: T7
 Class: BAC ends.

Location/Qualifiers
 1. .570

FEATURES source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-204F1"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 159 a 125 c 117 g 169 t

BASE COUNT ORIGIN

Query Match 83.6%; Score 18.4; DB 251; Length 570;
 Best Local Similarity 95.0%; Pred. No. 87;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 gactgtgaaccttagatg 21
 |||||
 DB 124 GACTTTCACCTTAGATG 143

RESULT 3

AZ052737/c
 LOCUS 431 bp DNA GSS 30-MAR-2000
 DEFINITION RPCI-23-136P2.TVB RPCI-23 Mus musculus genomic clone RPCI-23-336P2,
 DNA sequence.
 AZ052737
 VERSION AZ052737.1 GI:7343904
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 431)
 Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
 ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
 and Fraser,C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSs: RPCI-23-336P2.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 336 row: P column: 2
 Seq primer: T7
 Class: BAC ends.

FEATURES source

Location/Qualifiers
 1. .431
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="RPCI-23-336P2"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 107 a 107 c 93 g 124 t

BASE COUNT ORIGIN

Query Match 80.9%; Score 17.8; DB 237; Length 431;
 Best Local Similarity 90.5%; Pred. No. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gactgtgaaccttagatga 22
 |||||
 DB 386 GACTGTGACCATAGAGATTA 366

RESULT 4

BG552950 507 bp mRNA EST 09-APR-2001
 LOCUS dabB1h04.y1 NICHD XGC Emb4 Xenopus laevis cDNA clone IMAGE:4203511
 DEFINITION 5', mRNA sequence.
 ACCESSION BG552950
 VERSION BG552950.1 GI:13564730
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 507)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 380.

FEATURES source

Location/Qualifiers
 1. .507
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4203511"
 /clone_lib="NICHD XGC Emb4"
 /dev_stage="embryo, stage 31-32"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
 dt. Average insert size 2.1 kb. Constructed by Life
 Technologies. Note: This is a Xenopus gene collection (XGC
) library."
 149 a 90 c 112 g 155 t

BASE COUNT ORIGIN

Query Match 80.9%; Score 17.8; DB 155; Length 507;
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatg 21
| | | | | | | | | | |
Db 438 TCACTGTGAACCTTAGCGATG 458

RESULT 5

AAZ479424	535 bp	DNA	GSS	04-OCT-2000
LOCUS	1M0300H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0300H03 F, DNA sequence.			
DEFINITION	clone UUGC1M0300H03 F, DNA sequence.			
ACCESSION	AAZ479424			
VERSION	AAZ479424.1			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 535)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA			

FEATURES
source

```

Location/Qualifiers
1. .535
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300H03"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
144 a 118 c 123 g 150 t

```

	Matches	19: Conservative	0: Mismatches	2: Indels	0: Gaps	0:
Oy	2	gactgtgaaccttagatga	22			
D6	91	GACTGTCAACCATAGAGATTA	111			

RESULT 6

AZ755668/c	AZ755668	561 bp	DNA	GSS	01-MAR-2001
LOCUS	ev02g09.x1	PAX3 CASTING Library 'ev'	Homo sapiens	genomic clone	
DEFINITION	ev02g09	random, DNA sequence.			
ACCESSION	AZ755668				
VERSION	AZ755668.1	GI:13175090			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	1 (bases 1 to 561)				
	Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.F., Ruben,S. and Friedman,T.B.				
TITLE	Cyclic amplification and selection of target genes regulated by PAX3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Friedman TB				
	Laboratory of Molecular Genetics				
	National Institute on Deafness and Other Communication Disorders,				
	National Institutes of Health				
	5 Research Court, Room 2A-15, Rockville, MD 20850, USA				
	Tel: 301 402 7580				
	Fax: 301 496 7882				
	Email: friedman@nidcd.nih.gov				
	Place: 02 row: 9 column: 09				
	Seq primer: -21m13 forward primer (ABI)				
	Class: random plasmid subclone.				

FEATURES
SOURCE

```

source
1. .561
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ev02g09"
/clone_lib="PAX3 CASTing Library 'ev'"
/sex="Male"
/lab_host="DH10b"
/note="Vector: pGEM-T Easy; Human genomic DNA was
partially digested with Sau3AI, ligated to ds linkers,
and enriched for binding to human PAX3dQ+ protein using a
whole Genome PCR-based strategy. DNA fragments containing
putative PAX3dQ+ binding sites were amplified by PCR and
cloned into pGEM-T Easy (Promega). The ligation products
were transformed into DH10b electrocompetent cells (Life
Technologies)."
```

BASE COUNT	126 a	149 c	152 g	134 t
ORIGIN				

Query Match	80.9%	Score 17.8;	DB 249;	Length 561;
Best Local Similarity	90.5%	Pred. No. 1.7e+02;		
Matches 19: Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 tgactgtgaaccttagagatg 21
|||||
Db 461 TGACTGTGAACGTCAGAGATG 441

RESULT

LOCUS	AQ245899	422 bp	DNA	GSS	06-OCT-1998
DEFINITION	HS-2056_B2.F12.T7 Cit Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2056 Col-24 Row-L, DNA sequence.				
ACCESSION	AQ245899				
VERSION	AQ245899.1	GI:3696081			
KEYWORDS	GSS.				

```
Query Match      80.9%; Score 17.8; DB 244; Length 535;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
```



```

REFERENCE 1 (bases 1 to 236)
AUTHORS Yoshino,R., Morio,T. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1..236
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLJ623"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 91 a 42 c 36 g 64 t 3 others
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 236;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
||||| ||| ||| ||| ||| ||| |||
Db 104 TGACCGTAACTTTAGAGATGA 83

RESULT 10
AU053032/c
LOCUS AU053032 254 bp mRNA EST 28-APR-1999
DEFINITION AU053032 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLF551, mRNA sequence.
ACCESSION AU053032
VERSION AU053032.1 GI:4701515
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 254)
AUTHORS Yoshino,R., Morio,T. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1..254
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLF551"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 103 a 45 c 40 g 66 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 254;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
||||| ||| ||| ||| ||| ||| |||
Db 127 TGACCGTAACTTTAGAGATGA 106

```

```

RESULT 11
AU054169/c
LOCUS AU054169 265 bp mRNA EST 28-APR-1999
DEFINITION AU054169 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLK852, mRNA sequence.
ACCESSION AU054169
VERSION AU054169.1 GI:4702650
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 265)
AUTHORS Yoshino,R., Morio,T. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1..265
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SLK852"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 108 a 48 c 42 g 67 t
ORIGIN
Query Match 78.2%; Score 17.2; DB 107; Length 265;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
||||| ||| ||| ||| ||| ||| |||
Db 134 TGACCGTAACTTTAGAGATGA 113

RESULT 12
AU053754/c
LOCUS AU053754 270 bp mRNA EST 28-APR-1999
DEFINITION AU053754 Dictyostellium discoideum SL (H.Urushihara) Dictyostellium
discoideum cDNA clone SLJ617, mRNA sequence.
ACCESSION AU053754
VERSION AU053754.1 GI:4702236
KEYWORDS EST.
SOURCE Dictyostellium discoideum.
ORGANISM Dictyostellium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 270)
AUTHORS Yoshino,R., Morio,T. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostellium discoideum
JOURNAL Unpublished (1997)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.

FEATURES
source
1..270
/organism="Dictyostellium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLJ617"
/clone_lib="Dictyostellium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 111 a 48 c 43 g 68 t
ORIGIN

```


primed cDNA was directionally cloned into the EcoRI-XhoI
Bluescript SK vector arms. NOTE: The sequences contain a
'cDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTCGGCAGAG'.

BASE COUNT 97 a 124 c 101 g 76 t

ORIGIN

Query Match 78.2%; Score 17.2; DB 143; Length 398;
Best Local Similarity 86.4%; Pred. No 3.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
|||||
Db 220 TGACTGTGAACCTTGATGATGA 199

Search completed: October 9, 2001, 18:20:30
Job time: 9800 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 16:26:51 ; Search time 515.84 Seconds
(without alignments)
26.779 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22
Sequence: 1 tgactgtgaaccttagatga 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0601.*

1: /SIDS8/gcgdata/geneseq/geneseq/NA1980.DAT.*
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3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT.*
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21: /SIDS8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAV55790	Immunostimulatory
2	22	100.0	22	AAV55790	Mutant immunostimu
3	22	100.0	22	AAV55790	Immunostimulatory
4	20.4	92.7	22	AAV55791	Immunostimulatory
5	20.4	92.7	22	AAV55791	Oligo used in expe
6	20.4	92.7	22	AAV55791	Non-immunomodulat
7	18.8	85.5	22	AAV55791	Nucleotide sequenc
8	18.8	85.5	22	AAV55791	ISS-ODN DY1018 nuc
9	18.8	85.5	22	AAV55791	Immunostimulatory
10	18.8	85.5	22	AAV55791	Immunostimulatory
11	18.8	85.5	22	AAV55791	Immunostimulatory

12	18.8	85.5	22	20	AAV80106	Oligo used in expe
13	18.8	85.5	22	20	AAV80097	Immunomodulatory o
14	18.8	85.5	22	20	AAV80102	Immunomodulatory o
15	18.8	85.5	22	20	AAV80103	Immunomodulatory o
16	18.8	85.5	22	20	AAV80104	Oligo used in expe
17	18.8	85.5	22	21	AAV80105	Immunostimulatory
18	18.8	85.5	22	21	AAV80106	Non-cpg control ph
19	18.8	85.5	22	21	AAV80107	Sequence of a stab
20	18.8	85.5	22	21	AAV80108	Sequence of a stab
21	18.8	85.5	22	21	AAV80109	Sequence of a stab
22	18.8	85.5	22	21	AAV80110	CpG adjuvant oligo
23	18.8	85.5	22	21	AAV80111	CpG adjuvant oligo
24	18.8	85.5	22	21	AAV80112	Immunostimulatory
25	18.8	85.5	22	21	AAV80113	Immunostimulatory
26	18.8	85.5	22	21	AAV80114	Immunostimulatory
27	18.8	85.5	22	21	AAV80115	Immunostimulatory
28	18.8	85.5	22	21	AAV80116	Immunostimulatory
29	18.8	85.5	22	21	AAV80117	Immunostimulatory
30	18.8	85.5	22	22	AAV80118	Immunostimulatory
31	18.8	85.5	22	22	AAV80119	Cholera toxin immu
32	18.8	85.5	22	22	AAV80120	Oligonucleotide OD
33	18.8	85.5	22	22	AAV80121	CG motif and CFA c
34	18.8	85.5	22	22	AAV80122	CG motif and CFA c
35	18.8	85.5	22	21	AAV80123	Immunostimulatory
36	18.8	85.5	22	22	AAV80124	Immunostimulatory
37	18.8	85.5	22	22	AAV80125	Immunostimulatory
38	18.8	85.5	22	21	AAV80126	Immunostimulatory
39	18.8	85.5	22	19	AAV80127	Nucleotide sequenc
40	18.8	85.5	22	20	AAV80128	ISS-ODN mutant DY1
41	18.8	85.5	22	20	AAV80129	Oligo used in expe
42	18.8	85.5	22	20	AAV80130	Oligo used in expe
43	18.8	85.5	22	20	AAV80131	Immunomodulatory o
44	18.8	85.5	22	20	AAV80132	Immunomodulatory o
45	18.8	85.5	22	22	AAV80133	CG motif and CFA c

ALIGNMENTS

RESULT	1
AAV55790	
ID	AAV55790 standard; DNA; 22 BP.
XX	
AC	AAV55790;
XX	
DT	29-MAR-1999 (first entry)
XX	
DE	Immunostimulatory sequence oligodeoxynucleotide Inhibitor DY1040.
XX	
KW	Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW	Immunostimulatory activity; gene therapy; genetic immunisation;
KW	autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
XX	
OS	Synthetic.
XX	
PN	WO9855609-A1.
XX	
PD	10-DEC-1998.
XX	
PF	05-JUN-1998; 98WO-US11391.
XX	
PR	06-JUN-1997; 97US-0048793.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Ray E, Roman M;
XX	
DR	WPI; 1999-080827/07.
XX	
PT	New oligonucleotide that inhibits action of immunostimulatory
PT	sequence oligonucleotides - particularly those present in gene
PT	therapy vectors or microbial pathogens, used to prolong gene therapy
PT	expression and to treat e.g. infections or autoimmune disease

XX PS Example 1; Fig 1; 50pp; English.

XX CC This sequence represents an example of an immunostimulatory sequence

CC CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN

CC CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or

CC CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by

CC CC ISS-ODNs that contain a hexamer region consisting of at least one CpG

CC CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;

CC CC Y = any natural or synthetic nucleotide other than C; Z = any natural or

CC CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.

CC CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs

CC CC when this is present in (i) a recombinant expression vector (being used

CC CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly

CC CC one in a host and associated with an autoimmune disease). Particularly

CC CC the inhibitors prolong gene expression from the vector and reduce

CC CC inflammation caused by microbial infection. They also modulate activity

CC CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune

CC CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes

CC CC or monocytes by reducing the Th1-type response and stimulating the

CC CC Th2-type response to an antigen (including antigen-stimulated

CC CC immunoglobulin G1 production). Prolonged expression from the gene therapy

CC CC vector avoids the need for repeated treatments and re-engineering of the

CC CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over

CC CC the effect of ISS-ODN-based adjuvants and can be used even where the

CC CC existence, identity and location of the ISS-ODNs are unknown. The

CC CC inhibitors are effective at very low doses.

XX CC

XX CC Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

XX CC

Query Match 100.0%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaaccttagagatga 22

RESULT 2

AAAI4469

ID AAAI4469 standard; DNA; 22 BP.

XX AC AAAI4469;

XX DT 21-AUG-2000 (first entry)

XX DE Mutant immunostimulatory oligonucleotide, M-ODN.

XX KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;

XX KW secretory immunoglobulin A production; sigA; Th1 phenotype; mutant; ds.

XX OS Synthetic.

XX PN WO200020039-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US21203.

XX PR 05-OCT-1998; 98US-0167039.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Raz E, Horner AA, Carson DA;

XX DR WPI; 2000-303647/26.

XX DR

XX CC Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to

PT an antigen in a mammalian host through production of secretory

PT immunoglobulin A -

XX PT

PS Example 1; Page 21; 64pp; English.

XX CC The invention relates to a method of inducing mucosal immunity to an

CC CC antigen in a mammalian host, including the production of secretory

CC CC immunoglobulin A (sigA). Immune protection in the mucosa (the principal

CC CC site of entry of most foreign antigens) is mediated by mucosa-associated

CC CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory

CC CC cell sub-populations. The primary immune response which characterises

CC CC the induction of mucosal immunity to an antigen is sigA production by

CC CC activated B-cells. The method comprises introducing an immunostimulatory

CC CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the

CC CC ISS-ODN includes a core nucleotide sequence. The core nucleotide

CC CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific

CC CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID Nos 1-3). A

CC CC specific example of an ISS-ODN is DY1018 (AAAI4467). The ISS-ODN is used

CC CC as an adjuvant with an antigen for stimulating mucosal immunity. The

CC CC level of sigA production induced in the host is at least 3 times the

CC CC magnitude of sigA production achievable in response to introduction of

CC CC antigen alone into the mucosal tissue and is equivalent or greater than

CC CC the magnitude of sigA production achievable in response to introduction

CC CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The

CC CC host immune response is stimulated to antigen-specific IgA production,

CC CC biased towards the Th1 phenotype while antigen-induced IgE production is

CC CC avoided. The adjuvant has little or no known toxicity in mammals and its

CC CC efficacy is comparable to that of cholera toxin which is used as a

CC CC mucosal adjuvant. The present sequence represents a mutant ISS-ODN,

XX CC M-ODN, used in an exemplification of the invention.

XX CC

XX CC Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

XX CC

Query Match 100.0%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaaccttagagatga 22

RESULT 3

AAFI31345

ID AAFI31345 standard; DNA; 22 BP.

XX AC AAFI31345;

XX DT 12-APR-2001 (first entry)

XX DE Immune response enhancement method related sequence.

XX KW Immunostimulatory nucleotide sequence; immune response; cancer;

XX KW antibody production; IFNgamma release; CTL activity; Th1 response;

XX KW infection; allergy; ds.

XX OS Synthetic.

XX PN WO200102007-A1.

XX PD 11-JAN-2001.

XX PF 30-JUN-2000; 2000WO-US18229.

XX PR 02-JUL-1999; 99US-0347343.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Raz E, Kobayashi H;

XX DR WPI; 2001-138056/14.

XX DR

XX CC Enhancing immune response against pathogen or antigen associated with

PT infectious diseases, an allergen or cancer, involves administering

PT immunostimulatory nucleotide sequence prior to antigen exposure -

XX PT

XX
PS
XX
CC

Example 1: Page 14; 47pp; English.

The present invention describes a method for enhancing an immune response to a substance, comprising administering an immunostimulatory nucleotide sequence to a subject prior to exposure to the substance. This can be used to enhance antibody production, IFN γ release, CTL activity and Th1 related effects. The method can be used in the prevention and treatment of allergies, cancer and infections.

XX
SQ Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 22; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.044; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagatga 22

Db 1 tgactgtgaaccttagatga 22

RESULT 4

AAV55791
ID AAV55791 standard; DNA; 22 BP.

XX
AC AAV55791;

XX
DT 29-MAR-1999 (first entry)

XX
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1041.

XX
KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW Immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
XX
OS Synthetic.

XX
PN WO9855609-A1.

XX
PD 10-DEC-1998.

XX
PF 05-JUN-1998; 98WO-US11391.

XX
PR 06-JUN-1997; 97US-0048793.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Ray E, Roman M;

XX
DR WPI; 1999-080827/07.

XX
PT New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease

XX
PS Example 1: Fig 1: 50pp; English.

XX
CC This sequence represents an example of a immunostimulatory sequence
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or
CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
CC motif flanked by two 5'-Pu and two 3'-Py. Pu - purine; Py - pyrimidine;
CC Y - any natural or synthetic nucleotide other than C; Z - any natural or
CC synthetic nucleotide, but if Y is not G or inosine (I), then Z is G or I.
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
CC when this is present in (i) a recombinant expression vector (being used
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
CC one in a host and associated with an autoimmune disease). Particularly
CC the inhibitors prolong gene expression from the vector and reduce
CC inflammation caused by microbial infection. They also modulate activity

CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
CC or monocytes by reducing the Th1-type response and stimulating the
CC Th2-type response to an antigen (including antigen-stimulated
CC immunoglobulin G1 production). Prolonged expression from the gene therapy
CC vector avoids the need for repeated treatments and re-engineering of the
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
CC the effect of ISS-ODN-based adjuvants and can be used even where the
CC existence, identity and location of the ISS-ODNs are unknown. The
CC inhibitors are effective at very low doses.

XX
SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;

Best Local Similarity 95.5%; Pred. No. 0.28; Mismatches 21; Conservative 0; Indels 1; Gaps 0;

Qy 1 tgactgtgaaccttagatga 22

Db 1 tgactgtgaaccttagatga 22

RESULT 5

AAV80110
ID AAV80110 standard; DNA; 22 BP.

XX
AC AAV80110;

XX
DT 12-MAR-1999 (first entry)

XX
DE Oligo used in experiments for stimulation of cytokine production.

XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX
OS Synthetic.

XX
PN WO9855495-A2.

XX
PD 10-DEC-1998.

XX
PF 05-JUN-1998; 98WO-US11578.

XX
PR 06-JUN-1997; 97US-0048793.

XX
PA (DYNA-) DYNVAX TECHNOLOGIES CORP.

XX
PI Dina D, Roman M, Schwartz D;

XX
DR WPI; 1999-059898/05.

XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases

XX
PS Example 2: Page 30; 63pp; English.

XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
CC GAGTTC, and GAGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent

CC oligonucleotides that were tested for immunostimulatory activity. These
 CC were used in experiments for the stimulation of cytokine production and
 CC were found to lack immunostimulatory activity. The invention provides
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.
 XX
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.28;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccccttagagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaagccttagagatga 22

RESULT 6
 AA255878
 ID AA255878 standard; DNA; 22 BP.
 AC AA255878;
 DT 10-APR-2000 (first entry)
 DE Non-immunomodulatory oligonucleotide SEQ ID NO: 3.
 DE Non-immunomodulatory; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KW asthma; immunocontraception; ss.
 XX Mus musculus.
 OS Synthetic.

Key Location/Qualifiers
 modified_base 1..22
 /*tag= a
 /note= "Phosphorothioate linkages"

WO9962923-A2.
 09-DEC-1999.
 04-JUN-1999; 99WO-US12538.
 05-JUN-1998; 98US-0088310.
 01-JUN-1999; 99US-0324191.
 (DYNA-) DYNAX TECHNOLOGIES CORP.
 Schwartz D;
 WPI; 2000-105687/09.
 Novel immunomodulatory oligonucleotide used to induce a Th1-type immune response, e.g. to tumor antigens -
 Example 1; Page 35; 54pp; English.

Sequences AA255878-255879 represent oligonucleotides which do not contain an immunostimulatory sequence (ISS, e.g., AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GCGGTT, AACGTTC and GACGTTC), and which did not exhibit immunomodulatory activity in an exemplification of the present invention. The invention relates to oligonucleotides comprising one or more ISSs, where the ISS comprises at least one modified cytosine with an electron-withdrawing moiety at position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886 contain ISSs comprising at least one bromocytosine, whereas sequence AA255876 contains an unmodified ISS. The immunomodulatory oligonucleotides have an adjuvant-like effect: when formulated with an antigen, the oligonucleotides stimulate production of Th1-type cytokines, and induce a Th1-type immune response (activation of cytotoxic T cells), while simultaneously downregulating the Th2-type response. The Th1

CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.
 XX
 SQ Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 other;

Query Match 92.7%; Score 20.4; DB 21; Length 22;
 Best Local Similarity 95.5%; Pred. No. 0.28;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccccttagagatga 22
 ||||| ||||| ||||| ||||| |||||
 Db 1 tgactgtgaagccttagagatga 22

RESULT 7
 AAV32079
 ID AAV32079 standard; DNA; 22 BP.
 AC AAV32079;
 DT 09-SEP-1998 (first entry)
 DE Nucleotide sequence of DY1018.
 DE
 KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
 KW immunisation; anaphylaxis; IgE; retinopathies; ss.
 XX Synthetic.

Key Location/Qualifiers
 modified_base 1..22
 /*tag= a
 /note= "phosphothioate backbone"

WO9816247-A1.
 23-APR-1998.
 09-OCT-1997; 97WO-US19004.
 11-OCT-1996; 96US-0028118.
 (REGC) UNIV CALIFORNIA.
 Carson DA, Raz E, Roman M;
 WPI; 1998-261028/23.
 New immunomodulatory compositions - comprising an antigen conjugated to a polynucleotide that contains an immunostimulatory sequence
 Example 1; Page 36; 69pp; English.

This is the nucleotide sequence of DY1018, which is conjugated to beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM), which comprises an antigen conjugated to a polynucleotide (PN) that contains at least one immunostimulatory nucleotide sequence (ISS). The conjugate synergistically boost the magnitude of the host immune response against an antigen to a level greater than the host immune response to either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM conjugates are particularly acute during the important early phase of the host immune response to an antigen. The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular (Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE

CC production in response to the antigen challenge. The conjugates can
 CC also be used to combat pathogenic infection and to stimulate
 CC therapeutic angiogenesis to treat conditions in which localised blood
 CC flow plays a significant etiological role, e.g. retinopathies.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 Other;

Query Match 85.5%; Score 18.8; DB 19; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22
 |||||

RESULT 8
 AAX36624
 ID AAX36624 standard; DNA; 22 BP.

XX
 AC AAX36624;
 XX
 DT 09-JUL-1999 (first entry)
 XX

DE ISS-ODN DY1018 nucleotide sequence.

XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypereosinophilic syndrome;
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.

XX Synthetic.

XX WO9911275-A2.

XX 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18382.

XX 05-SEP-1997; 97US-0927120.

XX (REGC) UNIV CALIFORNIA.

PI Ray E;

XX WPI; 1999-312404/26.

XX Reducing antigen-stimulated granulocyte-mediated inflammation

PS Example 2; Page 30; 69pp; English.

XX This is the ISS-ODN DY1018 nucleotide sequence.

CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypereosinophilic syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte
 CC adhesion to endothelia.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 85.5%; Score 18.8; DB 20; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22
 |||||

RESULT 9

AAV55792
 ID AAV55792 standard; DNA; 22 BP.

XX
 AC AAV55792;

XX 29-MAR-1999 (first entry)

XX Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1042.

XX Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
 KW immunostimulatory activity; gene therapy; genetic immunisation;
 KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
 XX Synthetic.

XX WO9855609-A1.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11391.

XX 06-JUN-1997; 97US-0048793.

XX (REGC) UNIV CALIFORNIA.

XX Ray E, Roman M;

XX WPI; 1999-080827/07.

XX New oligonucleotide that inhibits action of immunostimulatory
 PT sequence oligonucleotides - particularly those present in gene
 PT therapy vectors or microbial pathogens, used to prolong gene therapy
 PT expression and to treat e.g. infections or autoimmune disease

XX Example 1; Fig 1; 50pp; English.

XX This sequence represents an example of a immunostimulatory sequence
 CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
 CC sequences have a hexamer region of sequence 5'-pu-pu-y-2-py-py or
 CC 5'-pu-pu-y-2-py-poly for inhibiting immunostimulation caused by
 CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
 CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;
 CC y = any natural or synthetic nucleotide other than C; z = any natural or
 CC synthetic nucleotide, but if y is not G or Inosine (I), then z is G or I.
 CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
 CC when this is present in (i) a recombinant expression vector (being used
 CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
 CC one in a host and associated with an autoimmune disease). Particularly
 CC the inhibitors prolong gene expression from the vector and reduce
 CC inflammation caused by microbial infection. They also modulate activity
 CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
 CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
 CC or monocytes by reducing the Th1-type response and stimulating the
 CC Th2-type response to an antigen (including antigen-stimulated
 CC immunoglobulin G1 production). Prolonged expression from the gene therapy
 CC vector avoids the need for repeated treatments and re-engineering of the
 CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
 CC the effect of ISS-ODN-based adjuvants and can be used even where the
 CC existence, identity and location of the ISS-ODNs are unknown. The
 CC inhibitors are effective at very low doses.

```
SQ Sequence 22 BP; 5 A; 3 C; 6 G; 8 T; 0 other;
Query Match      85.5%; Score 18.8; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tgactgtgaaccttagagatga 22
    ||||| ||||| |||||
DB 1 tgactgtgttccttagagatga 22
    ||||| ||||| |||||

RESULT 10
AAV55797
ID AAV55797 standard; DNA; 22 BP.
XX
AC AAV55797;
XX
DT 29-MAR-1999 (first entry)
XX
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1061.
XX
KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
OS Synthetic.
XX
PN WO9855609-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11391.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Ray E, Roman M;
XX
DR WPI; 1999-080827/07.
XX
PT New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease
XX
PS Example 1; Fig 3; 50pp; English.
XX
CC This sequence represents an example of a immunostimulatory sequence
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or
CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;
CC Y = any natural or synthetic nucleotide other than C; Z = any natural or
CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
CC when this is present in (i) a recombinant expression vector (being used
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
CC one in a host and associated with an autoimmune disease). Particularly
CC the inhibitors prolong gene expression from the vector and reduce
CC inflammation caused by microbial infection. They also modulate activity
CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
CC or monocytes by reducing the Th1-type response and stimulating the
CC Th2-type response to an antigen (including antigen-stimulated
CC immunoglobulin G1 production). Prolonged expression from the gene therapy
CC vector avoids the need for repeated treatments and re-engineering of the
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
CC the effect of ISS-ODN-based adjuvants and can be used even where the
CC existence, identity and location of the ISS-ODNs are unknown. The
CC inhibitors are effective at very low doses.
XX
SQ Sequence 22 BP; 7 A; 1 C; 7 G; 7 T; 0 other;
Query Match      85.5%; Score 18.8; DB 20; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tgactgtgaaccttagagatga 22
    ||||| ||||| |||||
DB 1 tgactgtgaatgttagagatga 22
    ||||| ||||| |||||

RESULT 11
AAV55788
ID AAV55788 standard; DNA; 22 BP.
XX
AC AAV55788;
XX
DT 29-MAR-1999 (first entry)
XX
DE Immunostimulatory sequence oligodeoxynucleotide inhibitor DY1019.
XX
KW Immunostimulatory sequence oligonucleotide; ISS-ODN; inhibitor;
KW immunostimulatory activity; gene therapy; genetic immunisation;
KW autoimmune disease; inflammation; microbial infection; immunotherapy; ss.
OS Synthetic.
XX
PN WO9855609-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11391.
XX
PR 06-JUN-1997; 97US-0048793.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Ray E, Roman M;
XX
DR WPI; 1999-080827/07.
XX
PT New oligonucleotide that inhibits action of immunostimulatory
PT sequence oligonucleotides - particularly those present in gene
PT therapy vectors or microbial pathogens, used to prolong gene therapy
PT expression and to treat e.g. infections or autoimmune disease
XX
PS Example 1; Fig 1; 50pp; English.
XX
CC This sequence represents an example of a immunostimulatory sequence
CC oligodeoxynucleotide (ISS-ODN) inhibitor of the invention. The ISS-ODN
CC sequences have a hexamer region of sequence 5'-Pu-Pu-Y-Z-Py-Py or
CC 5'-Pu-Pu-Y-Z-Py-polyPy for inhibiting immunostimulation caused by
CC ISS-ODNs that contain a hexamer region consisting of at least one CpG
CC motif flanked by two 5'-Pu and two 3'-Py. Pu = purine; Py = pyrimidine;
CC Y = any natural or synthetic nucleotide other than C; Z = any natural or
CC synthetic nucleotide, but if Y is not G or Inosine (I), then Z is G or I.
CC The inhibitors are used to inhibit immunostimulatory activity of ISS-ODNs
CC when this is present in (i) a recombinant expression vector (being used
CC for gene therapy or genetic immunisation) or (ii) a microbe (particularly
CC one in a host and associated with an autoimmune disease). Particularly
CC the inhibitors prolong gene expression from the vector and reduce
CC inflammation caused by microbial infection. They also modulate activity
CC of ISS-ODNs, e.g. where these are used as adjuvants to boost an immune
CC response, e.g. in immunotherapy, in contact with vertebrate lymphocytes
CC or monocytes by reducing the Th1-type response and stimulating the
CC Th2-type response to an antigen (including antigen-stimulated
CC immunoglobulin G1 production). Prolonged expression from the gene therapy
CC vector avoids the need for repeated treatments and re-engineering of the
CC vector to eliminate ISS-ODNs. The inhibitors provide precise control over
CC the effect of ISS-ODN-based adjuvants and can be used even where the
CC existence, identity and location of the ISS-ODNs are unknown. The
CC inhibitors are effective at very low doses.
```

CC Inhibitors are effective at very low doses.
 XX Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 other;
 SQ

Query Match 85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaaggttagagatga 22

RESULT 12

AAV80106
 ID AAV80106 standard; DNA; 22 BP.

XX AAV80106;

XX 12-MAR-1999 (first entry)

XX Oligo used in experiments for stimulation of cytokine production.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

PN 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

PS Example 1; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
 CC GACGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
 CC oligonucleotides that were tested for immunostimulatory activity. These
 CC were used in experiments for the stimulation of cytokine production and
 CC were found to lack immunostimulatory activity. The invention provides
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match

85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttagcgatga 22

RESULT 13

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX AAV80097;

XX 12-MAR-1999 (first entry)

XX Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.

XX Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTC, AACGTTCG,
 CC GACGTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match

85.5%; Score 18.8; DB 20; Length 22;

Best Local Similarity 90.9%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 tgactgtgaaccttagagatga 22
 ||||| ||||| ||||| |||||
 Db 1 tgactgtgaacgttagcgatga 22

RESULT 14

AAV80102
 ID AAV80102 standard; DNA: 22 BP.
 XX AC AAV80102;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 11
 FT /*tag= a
 FT /note= "5-bromocytosine"
 XX
 PN W09855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Dina D, Roman M, Schwartz D;
 XX
 DR WPI: 1999-059898/05.
 XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 23; Page 30; 63pp; English.
 XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AAGTTCC, AACGTTCC,
 CC GAGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus. Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 XX
 Query Match 85.5%; Score 18.8; DB 20; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22
 |||||
 RESULT 15
 AAV80102
 ID AAV80103 standard; DNA: 22 BP.
 XX AC AAV80103;
 XX

XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 11
 FT /*tag= a
 FT /note= "5-bromocytosine"
 XX
 PN W09855495-A2.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Dina D, Roman M, Schwartz D;
 XX
 DR WPI: 1999-059898/05.
 XX
 PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 XX
 PS Claim 24; Page 30; 63pp; English.
 XX
 CC The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AAGTTCC, AACGTTCC,
 CC GAGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus. Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 XX
 Query Match 85.5%; Score 18.8; DB 20; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.8;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 tgactgtgaaccttagagatga 22
 |||||
 Db 1 tgactgtgaacgttcgagatga 22
 |||||

Search completed: October 9, 2001, 16:26:52
 Job time: 2982 sec

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:12:48 ; Search time 10334.3 Seconds
(without alignments)
31.457 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22

Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099G_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US099H_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US099I_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US099J_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US099K_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US6015_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US6016_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US6017_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US6023_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	100.0	22	1	PCT-US00-18229-33
2	22	100.0	22	1	PCT-US01-06034-3
3	22	100.0	22	1	PCT-US01-10118-7
4	22	100.0	22	1	PCT-US01-14508-9
5	22	100.0	22	17	US-09-347-343-33
6	22	100.0	22	22	US-09-570-325-21
7	22	100.0	22	28	US-09-713-136-10
8	22	100.0	22	30	US-09-791-500-3
9	22	100.0	22	31	US-09-820-484-7
10	20.4	92.7	22	1	PCT-US01-06034-5
11	20.4	92.7	22	1	PCT-US01-06034-6
12	20.4	92.7	22	1	PCT-US01-10118-2
13	20.4	92.7	22	1	PCT-US01-10118-6
14	20.4	92.7	22	1	PCT-US01-14508-10
15	20.4	92.7	22	1	PCT-US01-14508-11
16	20.4	92.7	22	16	US-09-296-477-13
17	20.4	92.7	22	17	US-09-324-191A-3
18	20.4	92.7	22	30	US-09-791-500-5
19	20.4	92.7	22	31	US-09-820-484-2
20	20.4	92.7	22	31	US-09-820-484-6
21	20.4	92.7	22	1	PCT-US01-14508-2
22	19	86.4	20	1	PCT-US00-18229-32
23	18.8	85.5	22	1	PCT-US00-35064-1
24	18.8	85.5	22	1	PCT-US01-03029-1
25	18.8	85.5	22	1	PCT-US01-03029-3
26	18.8	85.5	22	1	PCT-US01-06034-1
27	18.8	85.5	22	1	PCT-US01-06034-2
28	18.8	85.5	22	1	PCT-US01-06034-8
29	18.8	85.5	22	1	PCT-US01-10118-1
30	18.8	85.5	22	1	PCT-US01-10118-3
31	18.8	85.5	22	1	PCT-US01-11290-1
32	18.8	85.5	22	1	PCT-US01-11290-4
33	18.8	85.5	22	1	PCT-US01-14508-1
34	18.8	85.5	22	1	PCT-US01-14508-12
35	18.8	85.5	22	1	PCT-US01-14508-13
36	18.8	85.5	22	1	PCT-US01-14508-14
37	18.8	85.5	22	1	PCT-US99-21203-19
38	18.8	85.5	22	13	US-08-927-120-19
39	18.8	85.5	22	15	US-09-167-039-19
40	18.8	85.5	22	16	US-09-235-742-19
41	18.8	85.5	22	16	US-09-296-477-2
42	18.8	85.5	22	16	US-09-296-477-3
43	18.8	85.5	22	16	US-09-296-477-8
44	18.8	85.5	22	31	US-09-828-503-4
45	18.8	85.5	22	31	US-09-828-503-4

ALIGNMENTS

```

RESULT 1
PCT-US00-18229-33
; Sequence 33, Application PC/TUS0018229
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Kobayashi, Hiroko
; TITLE OF INVENTION: Method for Enhancing an Immune Response
; FILE REFERENCE: 6510-189W01
; CURRENT APPLICATION NUMBER: PCT/US00/18229
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
PCT-US00-18229-33

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 2
PCT-US01-06034-3
; Sequence 3, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202W0
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-3

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 3
PCT-US01-10118-7
; Sequence 7, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay

```

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; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188W01
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modN
PCT-US01-10118-7

```

```

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

```

```

RESULT 4
PCT-US01-14508-9
; Sequence 9, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168W01
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: M-ODN
PCT-US01-14508-9

```

```

Query Match      100.0%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 tgactgtgaaccttagagatga 22
   |||||
DB 1 tgactgtgaaccttagagatga 22

```

```

RESULT 5
US-09-347-343-33
; Sequence 33, Application US/09347343A
; GENERAL INFORMATION:

```

; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 22
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-33

Query Match 100.0%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
|||||
DB 1 tgactgtgaaccttagatga 22

RESULT 6
US-09-570-325-21
; Sequence 21, Application US/09570325
; GENERAL INFORMATION:
; APPLICANT: Eyal Raz
; APPLICANT: Anthony A. Horner
; APPLICANT: Dennis A. Carson
; TITLE OF INVENTION: METHODS AND ADJUVANTS FOR STIMULATING
; TITLE OF INVENTION: MUCOSAL IMMUNITY TO HIV
; FILE REFERENCE: 30448.92US11
; CURRENT APPLICATION NUMBER: US/09/570,325
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 09/167,039
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: 08/927,120
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 08/593,554
; PRIOR FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-570-325-21

Query Match 100.0%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
|||||
DB 1 tgactgtgaaccttagatga 22

RESULT 7
US-09-713-136-10
; Sequence 10, Application US/09713136
; GENERAL INFORMATION:
; APPLICANT: Tuck, Stephen
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: Immunomodulatory Compositions Containing
; TITLE OF INVENTION: An Immunostimulatory Sequence Linked To Antigen And Methods
; FILE REFERENCE: 377882001500
; CURRENT APPLICATION NUMBER: US/09/713,136

; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,467
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-713-136-10

Query Match 100.0%; Score 22; DB 28; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
|||||
DB 1 tgactgtgaaccttagatga 22

RESULT 8
US-09-791-500-3
; Sequence 3, Application US/09791500
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-3

Query Match 100.0%; Score 22; DB 30; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagatga 22
|||||
DB 1 tgactgtgaaccttagatga 22

RESULT 9
US-09-820-484-7
; Sequence 7, Application US/09820484
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mODN
US-09-820-484-7

Query Match 100.0%; Score 22; DB 31; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 10
PCT-US01-06034-5
; Sequence 5, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-5

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 11
PCT-US01-06034-6
; Sequence 6, Application PC/TUS0106034
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202WO
; CURRENT APPLICATION NUMBER: PCT/US01/06034
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
PCT-US01-06034-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 12
PCT-US01-10118-2
; Sequence 2, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188WO
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated ODN
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
PCT-US01-10118-2

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22

RESULT 13
PCT-US01-10118-6
; Sequence 6, Application PC/TUS0110118
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Methods for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188WO
; CURRENT APPLICATION NUMBER: PCT/US01/10118
; CURRENT FILING DATE: 2001-03-17
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated control ODN
PCT-US01-10118-6

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
|||||

RESULT 14
PCT-US01-14508-10
; Sequence 10, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168W01
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
PCT-US01-14508-10

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
|||||

RESULT 15
PCT-US01-14508-11
; Sequence 11, Application PC/TUS0114508
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510/168W01
; CURRENT APPLICATION NUMBER: PCT/US01/14508
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/262,321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 22

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: methylated ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: m5C
PCT-US01-14508-11

Query Match 92.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
|||||
DB 1 tgactgtgaaccttagagatga 22
|||||

Search completed: October 9, 2001, 21:12:48
Job time: 20073 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 21:36:23 ; Search time 1391.6 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22
Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 204985 seqs, 1141153189 residues

Total number of hits satisfying chosen parameters: 4093770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2.6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2.6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2.6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 7: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 8: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	6	US-09-770-943-3
2	22	100.0	22	7	US-09-802-359-4
3	22	100.0	22	7	US-09-802-359-10
4	22	100.0	22	7	US-09-802-376-10
5	20.4	92.7	22	6	US-09-770-943-2
6	20.4	92.7	22	6	US-09-770-943-4
7	18.8	85.5	22	6	US-09-770-943-1
8	18.8	85.5	22	6	US-09-770-943-5
9	18.8	85.5	22	6	US-09-770-943-10
10	18.8	85.5	22	7	US-09-802-518-1
11	18.8	85.5	22	7	US-09-802-518-10
12	18.8	85.5	22	7	US-09-802-359-1
13	18.8	85.5	22	7	US-09-802-359-9
14	18.8	85.5	22	7	US-09-802-376-1
15	18.8	85.5	22	7	US-09-802-376-9
16	18.8	85.5	533	8	US-60-253-652-3007
17	18.4	83.6	22	7	US-09-802-518-8
18	18.4	83.6	22	7	US-09-802-359-8
19	18.4	83.6	22	7	US-09-802-376-8
20	17.8	80.9	22	7	US-09-802-518-7
21	17.8	80.9	22	7	US-09-802-359-7
22	17.8	80.9	22	7	US-09-802-376-7
23	17.8	80.9	352	8	US-60-253-378-36285
24	17.2	78.2	22	7	US-09-802-518-2
25	17.2	78.2	22	7	US-09-802-518-4

Sequence 2, Appl1
Sequence 4, Appl1
Sequence 2, Appl1
Sequence 4, Appl1
Sequence 31699, A
Sequence 2488, Ap
Sequence 2489, Ap
Sequence 2446, Ap
Sequence 1, Appl1
Sequence 9, Appl1
Sequence 2275, Ap
Sequence 168, App
Sequence 427, App
Sequence 586, App
Sequence 426, App
Sequence 500, App
Sequence 28028, A
Sequence 47271, A
Sequence 172, App
Sequence 702, App

26 17.2 78.2 22 7 US-09-802-359-2
27 17.2 78.2 22 7 US-09-802-359-4
28 17.2 78.2 22 7 US-09-802-376-2
29 17.2 78.2 22 7 US-09-802-376-4
30 17.2 78.2 445 6 US-09-909-629-31699
31 17.2 78.2 601 5 US-09-948-933-2488
32 17.2 78.2 601 5 US-09-948-933-2489
33 17.2 78.2 2318 1 PCT-US01-08656-2446
34 17.2 78.2 6909 5 US-09-165-019-1
35 17.2 78.2 6909 7 US-09-880-107-2275
36 17.2 78.2 6914 5 US-09-948-933-9
37 17.2 78.2 6987 5 US-09-948-933-168
38 17.2 78.2 76321 5 US-09-948-933-427
39 17.2 78.2 76638 5 US-09-948-933-586
40 17.2 78.2 179904 5 US-09-948-933-426
41 17.2 78.2 179905 5 US-09-948-933-500
42 16.8 76.4 252 7 US-09-540-213-28028
43 16.8 76.4 285 7 US-09-540-213-47271
44 16.8 76.4 43982 6 US-09-803-736-172
45 16.8 76.4 78172 6 US-09-803-736-702

ALIGNMENTS

RESULT 1
US-09-770-943-3
; Sequence 3, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE OF INVENTION: Sequence Activity
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-3

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
|||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 2
US-09-802-518-11
; Sequence 11, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; FILE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10

```
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-11

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 3
US-09-802-359-10
; Sequence 10, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-10

Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 4
US-09-802-376-10
; Sequence 10, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-10
```

```
Query Match      100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 5
US-09-770-943-2
; Sequence 2, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

Query Match      92.7%; Score 20.4; DB 6; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   |||||
Db 1 tgactgtgaaccttagagatga 22

RESULT 6
US-09-770-943-4
; Sequence 4, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-4

Query Match      92.7%; Score 20.4; DB 6; Length 22;
```

Best Local Similarity 95.5%; Pred. No. 0.87;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22
||||||| |||||||
Db 1 tgactgtgaagccttagagatga 22

RESULT 7

US-09-770-943-1
; Sequence 1, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-1

Query Match 85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22
||||||| |||||||
Db 1 tgactgtgaagccttagagatga 22

RESULT 8

US-09-770-943-5
; Sequence 5, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-5

Query Match 85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22
||||||| |||||||
Db 1 tgactgtgtcccttagagatga 22

RESULT 9

US-09-770-943-10
; Sequence 10, Application US/09770943
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/770,943
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/092,314
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-770-943-10

Query Match 85.5%; Score 18.8; DB 6; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22
||||||| |||||||
Db 1 tgactgtgaatgttagagatga 22

RESULT 10

US-09-802-518-1
; Sequence 1, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-518-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccccttagagatga 22
||||||| |||||||
Db 1 tgactgtgaagccttagagatga 22

RESULT 11
US-09-802-518-10
; Sequence 10, Application US/09802518
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF AMELIORATING SYMPTOMS OF
; TITLE OF INVENTION: HERPES INFECTION USING IMMUNOMODULATORY POLYNUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 377882001100
; CURRENT APPLICATION NUMBER: US/09/802,518
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,556
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-518-10

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 12
US-09-802-359-1
; Sequence 1, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 13
US-09-802-359-9
; Sequence 9, Application US/09802359
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201400

; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-359-9

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggttagagatga 22

RESULT 14
US-09-802-376-1
; Sequence 1, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match 85.5%; Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
||||| ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgttcgagatga 22

RESULT 15
US-09-802-376-9
; Sequence 9, Application US/09802376
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-376-9

Query Match      85.5%   Score 18.8; DB 7; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaaccttagagatga 22
   |||||  |||||  |||||  |||||
Db 1 tgactgtgaaggtagagatga 22

Search completed: October 9, 2001, 21:36:24
Job time: 21244 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 15:42:11 ; Search time 217.64 Seconds
(without alignments)
19.136 Million cell updates/sec

Title: US-09-713-136-10

Perfect score: 22

Sequence: 1 tgactgtgaaccttagagatga 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/prodata/1/lna/5A-COMB.seq.*
- 2: /cgn2_6/prodata/1/lna/5B-COMB.seq.*
- 3: /cgn2_6/prodata/1/lna/5A-COMB.seq.*
- 4: /cgn2_6/prodata/1/lna/6B-COMB.seq.*
- 5: /cgn2_6/prodata/1/lna/PCTUS-COMB.seq.*
- 6: /cgn2_6/prodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	4 US-09-092-314-3	Sequence 3, Appli
2	20.4	92.7	22	4 US-09-092-314-2	Sequence 2, Appli
3	20.4	92.7	22	4 US-09-092-314-4	Sequence 4, Appli
4	18.8	85.5	22	4 US-09-092-314-1	Sequence 1, Appli
5	18.8	85.5	22	4 US-09-092-314-5	Sequence 5, Appli
6	18.8	85.5	22	4 US-09-092-314-10	Sequence 10, Appli
7	17.2	78.2	6909	2 US-08-804-196-1	Sequence 1, Appli
8	17.2	78.2	6909	2 US-08-558-340-1	Sequence 1, Appli
9	17.2	78.2	6909	3 US-08-746-111-26	Sequence 26, Appli
10	16.2	73.6	913	2 US-08-975-316-61	Sequence 61, Appli
11	15.8	71.8	2088	1 US-08-331-394-1	Sequence 1, Appli
12	15.8	71.8	2088	1 US-08-250-858-1	Sequence 1, Appli
13	15.8	71.8	2088	1 US-08-446-915-1	Sequence 1, Appli
14	15.8	71.8	2088	2 US-08-744-139-1	Sequence 1, Appli
15	15.8	71.8	2088	5 PCR-US95-06639-1	Sequence 1, Appli
16	15.6	70.9	22	4 US-09-092-314-7	Sequence 7, Appli
17	15.6	70.9	22	4 US-09-092-314-8	Sequence 8, Appli
18	15.6	70.9	1653	1 US-08-218-026-3	Sequence 3, Appli
19	15.6	70.9	1653	2 US-08-653-632-3	Sequence 3, Appli
20	15.6	70.9	1813	1 US-08-030-644-1	Sequence 1, Appli
21	15.6	70.9	1813	1 US-08-013-801-1	Sequence 1, Appli
22	15.6	70.9	1813	1 US-08-072-063-1	Sequence 1, Appli
23	15.6	70.9	1813	1 US-08-212-132-1	Sequence 1, Appli
24	15.6	70.9	1813	1 US-08-414-924-1	Sequence 1, Appli
25	15.6	70.9	1813	1 US-08-311-611A-145	Sequence 145, App
26	15.6	70.9	1813	1 US-08-232-527-1	Sequence 1, Appli
27	15.6	70.9	1813	1 US-08-372-783-145	Sequence 145, App

ALIGNMENTS

RESULT 1

US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

Query Match 100.0%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22

Db 1 tgactgtgaaccttagagatga 22

RESULT 2

US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06

Sequence 145, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 145, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 264, App


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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match      92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.084;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
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Db 1 tgactgtgaacgcttagagatga 22

RESULT 3
US-09-092-314-4
; Sequence 4, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-4

Query Match      92.7%; Score 20.4; DB 4; Length 22;
Best Local Similarity 95.5%; Pred. No. 0.084;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaacgcttagagatga 22

RESULT 4
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1.

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.52;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgaaggcttagagatga 22

RESULT 5
US-09-092-314-5
; Sequence 5, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-5

Query Match      85.5%; Score 18.8; DB 4; Length 22;
Best Local Similarity 90.9%; Pred. No. 0.52;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tgactgtgaaccttagagatga 22
   ||||| ||||| ||||| |||||
Db 1 tgactgtgttccttagagatga 22

RESULT 6
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-1730S1
; CURRENT APPLICATION NUMBER: US/09/092.314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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RESULT 8
US-08-658-340-1/c
; Sequence 1, Application US/08658340
; Patent No. 5910576
; Patent No. 5910576 5861489

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RESULT          9
US-08-746-111-26/c
; Sequence 26, Application US/08746111
; Patent No. 6066778
; GENERAL INFORMATION:
;   APPLICANT: Ginsburg, David
;   TITLE OF INVENTION: Compositions And Methods For Screening
;   TITLE OF INVENTION: Compounds For Anticoagulant Activity
;   NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Meelen & Carroll, LLP
;   STREET: 220 Montgomery Street, Suite 2200
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:

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US-08-973-316;61

US-08-5-319-19

APPLICANT: ROCHE, MIKE

APPLICANT: KOTHE, MIKE

```

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-250-858-1

Query Match 71.8%; Score 15.8; DB 1; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
   ||| ||||| |||||
DB 336 CTGAGAACTGAGAGATGA 354

RESULT 13
US-08-446-915-1
; Sequence 1, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-250-858-1

Query Match 71.8%; Score 15.8; DB 1; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
   ||| ||||| |||||
DB 336 CTGAGAACTGAGAGATGA 354

RESULT 14
US-08-744-139-1
; Sequence 1, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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US-08-744-139-1

Query Match 71.8%; Score 15.8; DB 2; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
||| ||||| |||||

Db 336 CTGAGAACCTGAGAGATGA 354

RESULT 15

PCT-US95-06639-1
; Sequence 1, Application PC/TUS9506639
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-06639-1

Query Match 71.8%; Score 15.8; DB 5; Length 2088;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ctgtgaaccttagagatga 22
||| ||||| |||||

Db 336 CTGAGAACCTGAGAGATGA 354

Search completed: October 9, 2001, 15:42:12
Job time: 302 sec